

CREATION RESEARCH SOCIETY



QUARTERLY

Volume 57 Fall 2020 Number 2

- *SUPERNOVA DRIVEN ACCELERATED DECAY*
- *A CORRECT UNDERSTANDING OF SYMMETRY IN ORGANIC SYNTHESIS*
- *THE DISTRIBUTION OF GENETIC VARIANTS IN THE HUMAN GENOME*
- *COMPUTER MODEL OF Y-CHROMOSOME*
- *MAGNETIC ORBITAL DECAY OF SOLAR TYPE BINARIES: THEIR GEOCHRONOLOGY*
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# Creation Research Society Quarterly

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**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*

# Creation Research Society Quarterly

**Volume 57**

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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*.

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ISSN 0092-9166

Printed in the United States of America

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# Magnetic Orbital Decay of Solar Type Binaries: Their Gyrochronology

R.G. Samec

## Abstract

This study is the final installment of the previously CRS-funded projects, involving an observational study of the apparent age of the universe as indicated by gyrochronology. It involves estimating ages due to magnetic orbital decay of solar type binaries. The scenario used is in a time dilation scenario applying the RATE results (accelerated radiometric aging). Three CRSQ papers have resulted from this study. It was also presented twice at summer Creation Research Society meetings. Additionally, it has been presented at secular meetings of the Interna-

tional Astronomical Union general assembly (IAUGA) and was well received by individual astronomers. In the 2018 IAUGA in Vienna Austria, we reported in a poster paper a compendium of 200 binaries. We conclude this study here by presenting recently analyzed binaries to the previous study, publishing the full group of binaries directing these results through the *Creation Research Society Quarterly*. These give strong evidence that the age of universe even in a time dilated scenario is grossly exaggerated and amounts to only 0.3% of the accepted age of the universe to the secular astronomer. Here, an age is computed for each binary,  $\Delta t$ , based on the difference in the current orbital period and the proposed initial period,  $\Delta P$  and the rate of orbital decay,  $dP/dt$ ,  $\Delta t = -\Delta P / (dP/dt)$ . The result is that the evolution of solar type binaries, from formation to the present configuration, average more than two magnitudes faster than theory suggests. Further implications are explored.

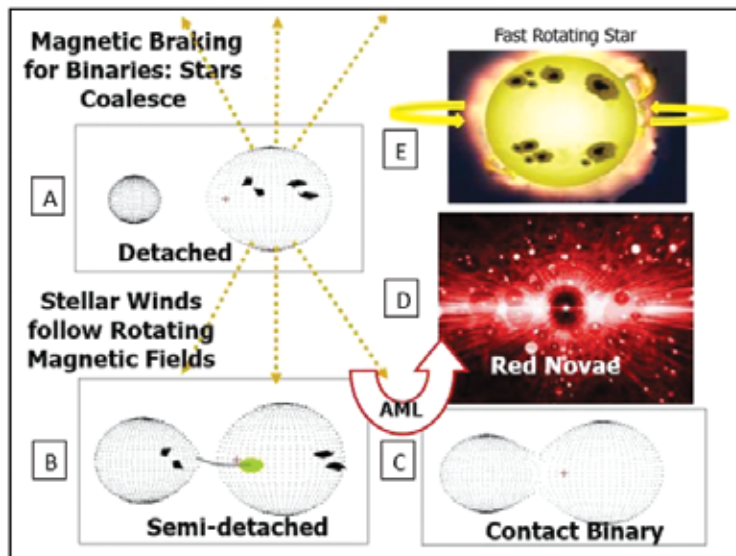


Figure 1. Depiction of a binary star made up of two solar-type stars undergoing magnetic braking which results in angular momentum loss (AML). (A) Plasmas leave along north and south magnetic field (dipole) lines cause the magnetically active binary (detached spotted binary in the upper left-hand corner) to lose angular momentum and steadily fill their Roche lobe and move to a (B) semidetached and then a (C) contact binary configuration. (D) The binary becomes unstable and a Luminous Red Novae (LRNe) event erupts finally resulting in a (E) fast-rotating single star.

## Introduction

This study is the final installment of the previously CRS-funded projects, which included the papers, “The Apparent Age of the Time-Dilated Universe I: Gyrochronology, Angular Momentum Loss In Close Solar Type Binaries” (Samec-1 = Samec and Figg, 2012), “The Apparent Age of the Time Dilated Universe II: Gyrochronology, Magnetic Orbital Decay of Close Solar Type Binaries and Errata” (Samec-2 = Samec, 2016a), and *Magnetic Orbital Decay of Solar Type Binaries and Creation Implications, 2018* (Samec-3 = Samec, 2018a) which involved the CRS undergraduate research initiative, allowing undergraduate mentors and their research students to request research grants from the Society Research Committee (see section VI.). The first paper made a calculation correction to the original paper and increased the number of binaries included in the study to 124 binaries. This time a simpler kinematic approach [instead of a complicated angular momentum approach (See Samec-1, 2012)] is taken to extend the number of systems surveyed. An estimate of the age of the time-dilated universe was made. The second study included system analyses in which students performed the analysis of eleven eclipsing binaries. The average of the ages of these came out to be  $3.6 \times 10^7$  years. Otherwise, we first reported an initial statistical study was begun with a poster session at the 2015 International Astronomical Union General Assembly (IAUGA)—a compendium of more than 75 solar type binaries was presented—each with a clearly decreasing orbital period as indicated by magnetic braking. Later in the 2018 IAUGA in Vienna, Austria, we reported in a poster paper a compendium of 200 binaries, *Magnetic Orbital Decay Of Solar Type Binaries, Their Gyrochronology And Red Novae*. We conclude this study here by presenting new recently analyzed binaries to the previous study, publishing the full group of binaries. In an article in *Publications of the Astronomical Society of Japan*, Tian et al. (2009) noted that the rate of decay of orbits is “1–2 orders of magnitude faster” than expected in binary star evolution (e.g., Guinan and Bradstreet, 1987). We find here that this is nearer to 2–3 orders, but their general observation is correct, i.e., binaries are decaying. at a rapid and easily observable rate. Thus, binary evolution occurs in real time—easily perceptible by human observers during their lifetimes and on the order of decades. This all has strong young-Earth creation implications.

## Magnetic Braking

W U Ma (solar type) binaries are believed to be undergoing steady but slow angular momentum ( $\Sigma m\vec{r} \times \vec{v}$ )<sup>1</sup> losses. This is

due to *magnetic braking* as stellar winds blow radially away on stiff bipolar magnetic field lines. This torques the binary similar to that occurring to a spinning speed skater slowly spreading his/her arms. The skater’s angular rotation slows as the radial distance of the hands/arms increase. But we also know that as the skater brings her arms in, the rotation speeds back up due to conservation of angular momentum. But in the case of stars, plasma (charged mass particles) never return but completely leave the star at about 15 times the radius of the star, called the Alfvén radius. So as stellar winds leave the star, the star also loses mass and angular momentum—it spins down. This is called angular momentum loss (AML). Solar type binaries are magnetic in nature. They have sunspots and a host of magnetic phenomena including facula, plages (bright spots), sun (dark) spots, prominences, flares, coronal mass ejections and solar winds (here, we say stellar winds). The Sun is undergoing AML. In the case of a single star, much like the speed skater extending his/her arms, is slowing its rotation. This is magnetic braking. In the case of solar type binaries which obey Kepler’s laws ( $r^3 \propto P^2$ , where P is the orbital period). They slowly coalesce (decreasing r) and speed up their rotation (decreasing P) as they undergo AML.

Solar-type binaries are believed to begin their existence as well-detached fast-spinning stars in groups that undergo gravitational interactions which leave them as binaries with several day periods. Since they are highly magnetic in nature, due to their convective envelopes and fast rotation, they undergo magnetic braking as plasma winds stream away from the stars on stiff rotating dipole fields. This action torques the binary, eventually bringing the components into contact (contact or W UMa binaries, see Figure 1). During the contact stage, the atmospheres of both stars are shared, not only nearly equalizing the surface temperatures of the two stars but causing mass transfer between the stars. The secondary component may decrease in mass as it is absorbed by the primary, more massive, component. Heavy, dark-spot activity on the primary star can act to mask the initial surface temperature actually making it appear as the cooler component. In this case, the binary is called a W-Type W UMa binary. Later, when the primary component returns to appear as the hotter component, it is called an A-type W UMa binary (primary component, is hotter) and are believed to be among the most ancient of stars. They continue to coalesce and finally merge and undergo a cataclysmic event called a *red nova* (see Samec-2, 2016a), the aftermath of which is a single, earlier spectral type star (usually F or A); see Samec-3, 2018a.

## Approach

A simple but effective method was taken in this project. In this methodology, we use the following equation to make our age calculations:

<sup>1</sup> For a single particle orbiting in a circular motion about a center, L (angular momentum) = mvr, where m is the mass of the particle, v is its orbital speed and r is the radius of orbit.

$$\Delta t = \frac{-\Delta P}{\dot{P}} \quad (1)$$

Here the  $\Delta P$  is the change of period of the binary.  $\Delta P$  is equal to the present orbital period less the initial period.  $\dot{P} = \frac{dP}{dt}$  is the rate of change of period in the binary. The elapsed time interval or age of the binary is the change in period divided by the negative rate of change since the rate is negative. Only the actual period and the assumed initial period and rate of period change were needed. The method only assumes that the chosen systems have a continuous, quadratically decreasing period.  $\Delta P$  is the difference in the present orbital period of the binary minus its initial period. The quantity,  $\dot{P}$  is the rate of change in the period,  $\frac{dP}{dt}$ , in Equation (1). I undertook a survey of the literature and internet sites including the American Association of Variable Stars (AAVSO) O-C files which was created and maintained by Dr. Bob Nelson.<sup>2</sup> I also included additional binaries from 34 years of my personal observations. The binary star community is indebted to Dr. Nelson's continued work in handling thousands of period studies of eclipsing binary stars. Of importance was Pietrukowicz et al. (2017). I was able to cover some 202 binaries with orbital periods present ranging in  $P = 0.21$  days to 9.3 days. We have added more systems recently analyzed to this group. The additional analyzed binaries are summarized in this paper.

## 2018–2020 Analyses

In our 2018 submitted and accepted paper, *Magnetic Orbital Decay of Solar Type Binaries and Creation Implications*, 2018, (Samec-3 of this study = 2018a) we summarized 11 more solar type binaries that we analyzed and published with the aid of undergraduate college students as a part of a funded CRS project during 2015–2018. That brought our total up to 93 eclipsing binaries. During the intermediate time interval, we were adding several more analyzed systems and gathered many more from the recent literature. The systems analyzed by this author included NSVS 103152 (V616 Cam), NSVS 10541123, V385 Cam, AE Cas, NS Cam and SZ Scl. We summarize the results of their analyses here.

## NSVS 103152 (V616 Cam)

NSVS 103152 (V616 Cam) is a  $F5V \pm 2$  type ( $T \sim 6500K$ ) eclipsing binary. It was observed on March 5, 6, 9, and 30, 2017, at Dark Sky Observatory in North Carolina with the 0.81-m reflector of Appalachian State University. It is a totally eclipsing binary with a period of 0.52835d. A total eclipse of

## NSVS 103152 Quadratic Fit

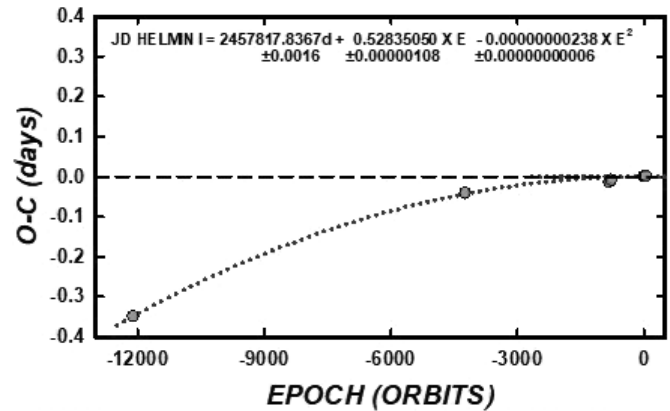


Figure 2. The period study of 17.5 years indicates continuous period decrease.

38 minutes occurs at phase 0.5. Five times of minimum light were determined from our present observations, which include three primary eclipses and two secondary eclipses. It is likely a detached near-contact binary and has spots. The spectral type is  $\sim F5 \pm 2V$ . This yields a temperature of  $6500 \pm 250K$ .

The period study covers a time interval of some 17.5 years and shows a period that is decreasing. A plot of the quadratic residuals (Observed-Calculated, or O-C's) is given in Figure 6. The quadratic fit carried a precision of 27 sigma although the study consists of only 11 times of minimum light. This system was given as a poster paper at the American Astronomical Society, AAS Meeting #233 (Samec, 2019b) and was published in the *Journal of the American Association of Variable Star Observers* (Samec, 2019c).

## NSVS 10541123

NSVS 10541123 (TYC 1488-0693-1) is an  $\sim F2$  type ( $T \sim 6750K$ ) eclipsing binary. It was observed in April and May 2015 at Dark Sky Observatory in North Carolina with the 0.81-m reflector of Appalachian State University. Six times of minimum light were determined from our present observations, which include two primary eclipses and four secondary eclipses. A  $BVR_{cI_c}$  simultaneous Wilson-Devinney (W-D) Program solution indicates that the system has a mass ratio ( $q = M_2/M_1$ ) of  $\sim 0.58$ , and a component temperature difference of 2350 K. The large  $\Delta T$  in the components verify that the binary is not in contact. A Binary Maker fitted hot spot was maintained in the WD Synthetic Light Curve Computations. It remained on

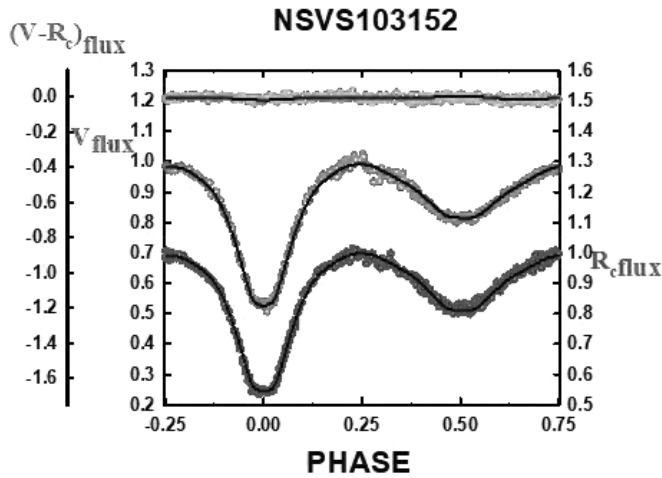


Figure 3. V,  $R_c$  Normalized Fluxes and the V-R color curves overlaid by our solution of NSVS 103152 (V1616 Cam).

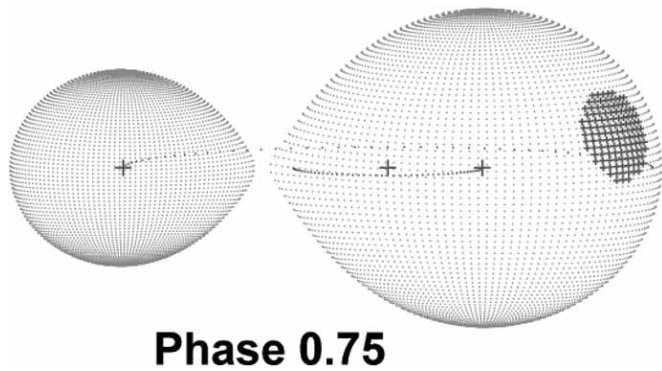


Figure 4. Geometrical Representation at phase 0.75 of NSVS 103152 or TYC 1488-0693-1.

the larger component at the equator on the correct (following) side for a stream spot directed from the secondary component (as dictated by the Coriolis effect). This could indicate that the components are near filling their respective Roche Lobes. The fill-outs are nearly identical, 96% for the primary component and 95% for the secondary component. The inclination is  $\sim 79^\circ$  which is not enough for the system to undergo a total eclipse.

Improved linear and quadratic ephemerides were calculated from these times of minimum light which gave a rapid period change of  $dP/dt = -5.2(1.5) \times 10^{-6}$  d/yr. The rapid period decrease may indicate that the binary is undergoing magnetic

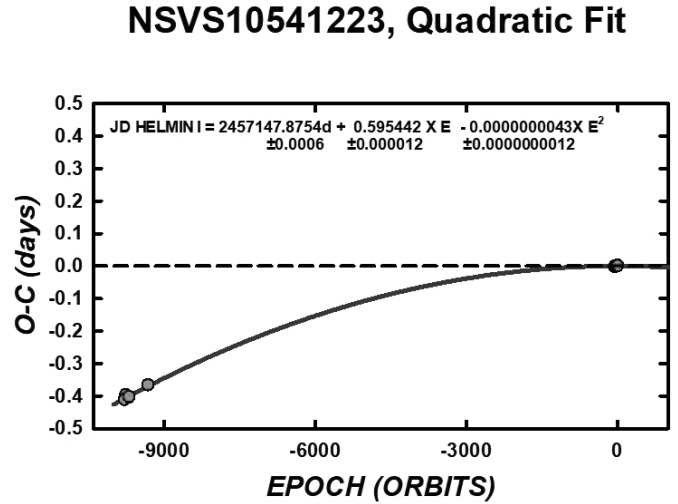


Figure 5. Residuals from quadratic term, NSVS 10541223 (TYC 1488-0693-1).

braking and is approaching a contact configuration due to the angular momentum loss.

The spot on the primary component is at the physical position that a stream spot would be expected, so it is possible that a weak plasma stream is being emitted from the secondary component with the secondary component as the gainer. The inclination is  $79^\circ$  which allows only 2% of the light of the system to be contributed by the secondary component at phase 0.5. The iterated hot spot region has a  $9^\circ$  radius and a mean T-factor of 1.05 ( $T \sim 7100$ K). The mass ratio and the component temperatures indicate that the secondary is somewhat oversized so that interactions may have occurred in the past.

This system was published in the *Journal of the American Association of Variable Star Observers* (Samec et al., 2018d).

### V385 Camelopardalis

V385 Cam is a  $G7 \pm 2$  type ( $T \sim 5500$ K) eclipsing binary. It was observed on December 15, 16, 17, and 18, 2017, at Dark Sky Observatory in North Carolina with the 0.81-m reflector of Appalachian State University. Three times of minimum light were determined from our present observations, which include two primary eclipses and one secondary eclipse. Eight times of low light were calculated using least squares fits to archived data from the Sky Patrol All-Sky Automated Survey for Supernovae (ASAS-SN, hereafter, ASAS, <https://asas-sn.osu.edu/>).

The following quadratic ephemeris was determined from the available times of minimum light:

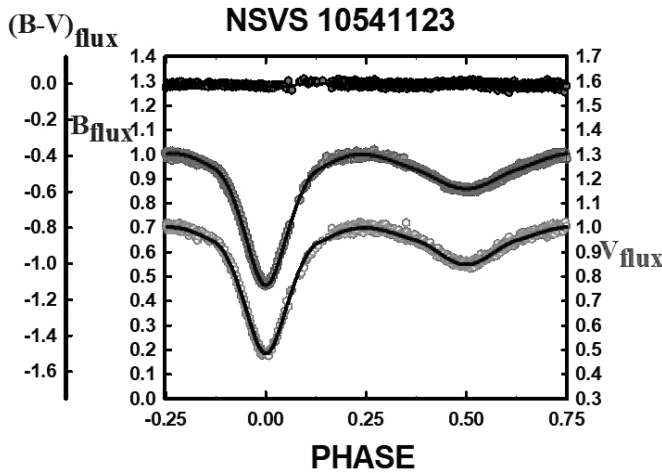


Figure 6. Solution overlaying B, V normalized flux light curves or TYC 1488-0693-1.

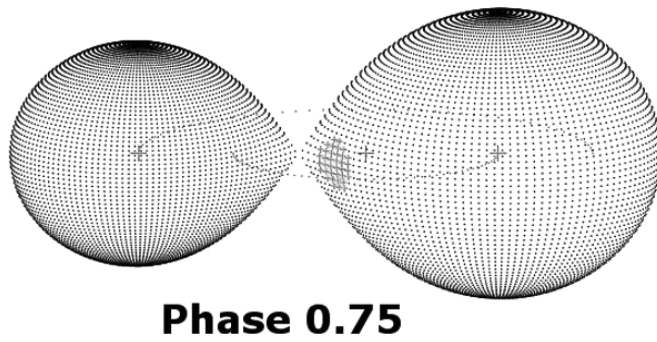


Figure 7. Geometrical representation at phase 0.75 of NSVS 10541123.

$$\begin{aligned} \text{JD Hel Min I} &= 2451\,57372.61838 \pm 0.00063\text{d} \\ &+ 0.61527012 \pm 0.00000077 \times E \\ &- 0.00000000014 \pm 0.00000000008 \times E^2 \end{aligned}$$

The weak period decrease may indicate AML and/or that the mass is flowing from the secondary Lagrangian point to the primary component.  $\text{BVR}_{\text{c}}\text{I}_{\text{c}}$  simultaneous 2015 Wilson-Devinney Program (W-D) solutions gives a mode 5 classical Algol solution (secondary component filling its Roche Lobe, primary underfilling). The semidetached solution gives a primary component with a 95% fill-out. The solution gives a mass

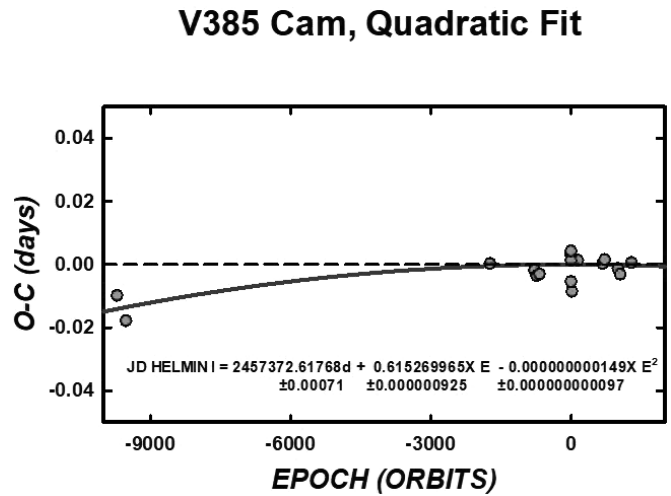


Figure 8. Residuals from quadratic term, V385 Cam.

ratio of  $0.288 \pm 0.001$ , and a component temperature difference of  $\sim 1300$  K. The large  $\Delta T$  in the components verify that the binary is not yet in contact. A Binary Maker fitted dark spot did not persist in the WD Synthetic Light Curve Computations even though there is a definite asymmetry at phase  $\sim 0.75$ . The inclination is  $\sim 81.7 \pm 0.2^\circ$ , resulting in a total eclipse (secondary component) of 16.3 minutes in duration. The systems distance is  $854 (\pm 13)$  pc as determined from GAIA DR2.

This was published in the *The American Association of Variable Stars Observers Journal* (Samec et al., 2019a).

## AE Cassiopeiae

AE Cas was observed some 40 years ago by Srivastava and Kandpal (1984) and was analyzed by a Fourier technique. This study represented the first modern synthetic analysis of light curves using the 2016 version of the Wilson-Devinney Program. It was observed on October 3, 4, and 23, 2016, at Dark Sky Observatory in North Carolina with the 0.81-m reflector of Appalachian State University and the 0.9-m reflector at KPNO remotely through the SARA consortia. V,  $R_{\text{c}}$ ,  $I_{\text{c}}$  observations were taken. Five times of minimum light were determined from our present observations, which include three primary eclipses and two secondary eclipses.

In addition, eight observations at minima were introduced as low-weighted times of low light taken from archived ASAS data and 74 times of minimum light from the literature, some of which were from visual observations. The quadratic residual plot is given in Figure 20. This study covers an interval of

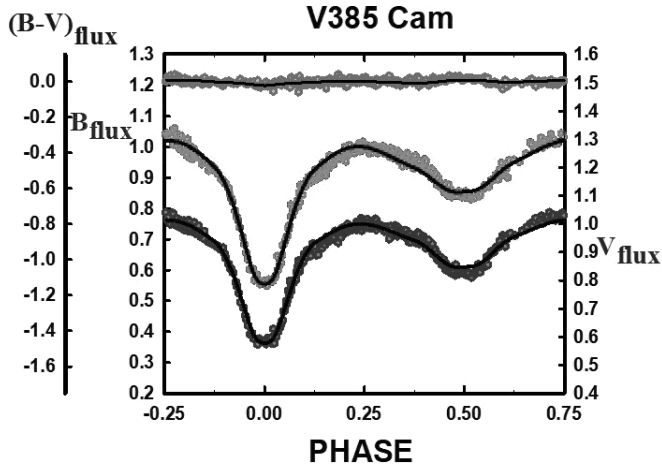


Figure 9. Solution overlaying B, V normalized flux light curves

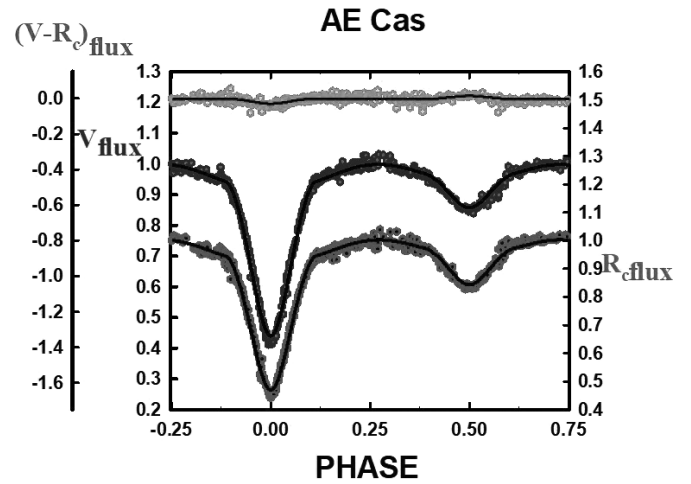


Figure 11. Solution overlaying B, V normalized flux light curves.

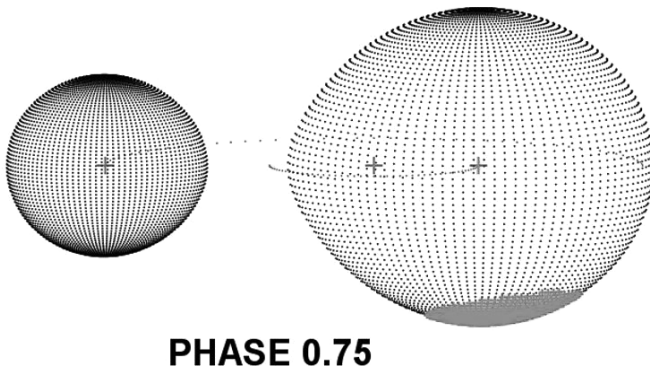


Figure 10. Geometrical representation at phase 0.75 of V385 Cam.

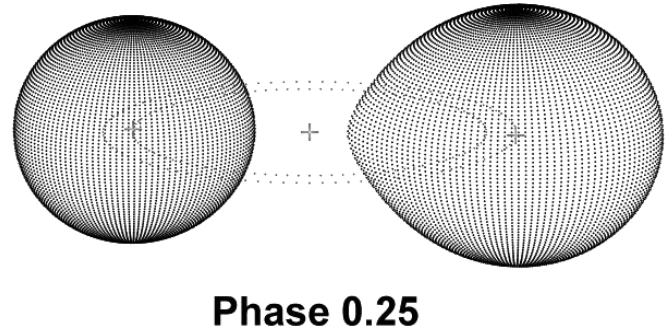


Figure 12. Geometrical representation at phase 0.25 of AE Cas.

some 89 years. The following quadratic ephemerides were determined from all available times of minimum light:

$$\begin{aligned} \text{JD Hel Min I} &= 2457684.75610 \pm 0.00085\text{d} \\ &+ 0.75911881 \pm 0.00000014 \text{ X E} \\ &- 0.00000000047 \pm 0.00000000003 \text{ X E}^2 \end{aligned}$$

The period decrease (see Figure 20) may indicate that the binary is undergoing magnetic braking and is approaching its contact configuration. Alternately, the near contact secondary

component may be streaming matter onto the primary, more massive component.

A  $\text{VR}_{\text{Ic}}$  simultaneous Wilson-Devinney Program (W-D) solution indicates that the system has a mass ratio somewhat less than unity ( $q=0.856 \pm 0.001$ ), and a component temperature difference of  $\sim 2060$  K. A q-search was performed and the mass ratio minimized at the above q-value. The large  $\Delta T$  in the components verifies that the binary is not yet in contact. No spots were needed for the solution, so if the stream exists it is weak as verified by the decreasing period. The fill-out of our model is 83.2% for the primary component (smaller radius) and 99.1% for the secondary component. The inclination is

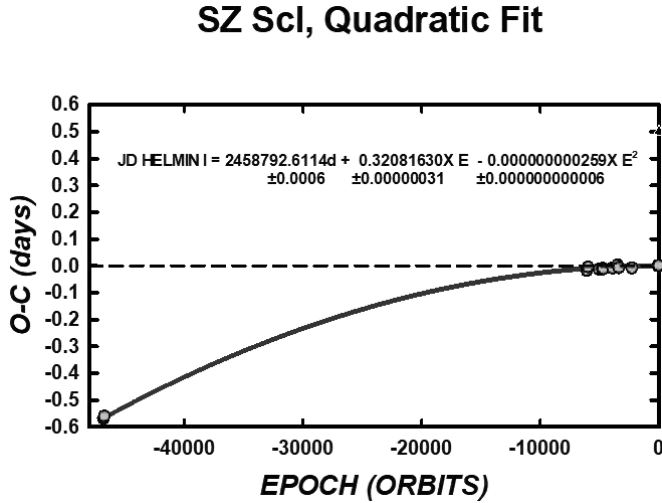


Figure 13. A plot of the quadratic term overlying the linear residuals of Equation 3. Note there is a gap in the observations from -46000 to -7000 orbits.

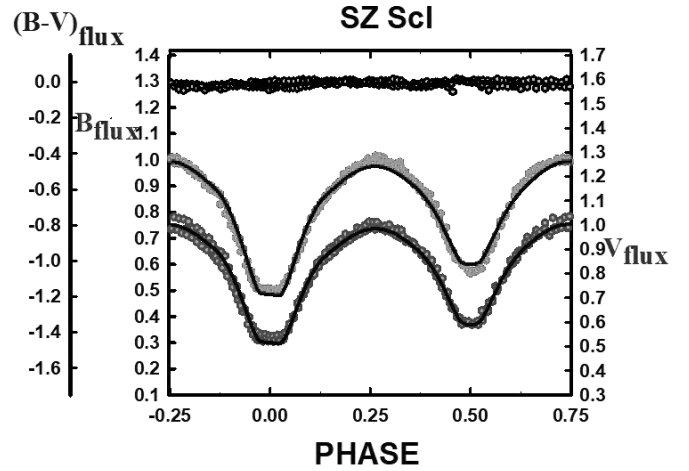


Figure 14. B,V and B-V normalized flux overlaid by the WD solution.

$\sim 76^\circ$ , not enough for the system to undergo a total eclipse. The light curve in V is more than one magnitude in amplitude. The B,V and B-V plot of the the solution is given in Figure 11. The geometrical representation is given in Figure 12.

### SZ Sculptoris

SZ Sculptoris (GSC 6990–0597), a solar type ( $T \sim 5040\text{K}$ ), shallow-contact, eclipsing binary. It was observed on October 5 and 6 and November 7, 2019, in remote mode with the Cerro Tololo InterAmerican Observatory, 0.6-m SARA South reflector by R. Samec. The amplitude of the light curves were 0.74, 0.67, 0.65 and 0.61 mags in BVRI, respectively. Six times of minimum light were calculated from three primary eclipses and secondary eclipses with our present observations. Eight times of low light were also taken from ASAS observations. Two additional timings were taken from the BBSAG bulletin #39 and from APASS (the AAVSO Photometric All-Sky Survey) observations. From this 41-year-interval orbital period study, it was found that the period is decreasing.

$$\text{JD Hel Min I} = 2458792.6114(6)\text{d} + 0.32081630(31) \\ \times \text{E} - 0.000000000259(6) \times \text{E}^2$$

This may be due to angular momentum loss (AML) resulting from rotating ion streams leaving along stiff magnetic

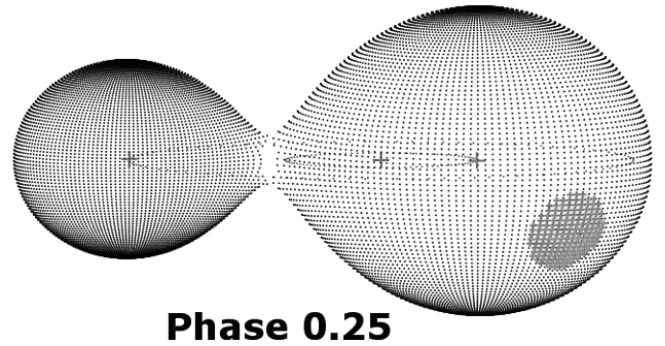


Figure 15. Geometrical representation of the solution for SZ Scl at phase 0.25.

bipolar field lines from the system. The quadratic residuals are given in Figure 13. A linear ephemeris was also calculated. A BVRI Bessel filtered Wilson-Devinney Program (W-D) solution gives a mass ratio,  $m_1/m_2 = 0.3800 \pm 0.0007$ , a large component temperature difference of 350 K and a contact fill-out of only 11%. Thus, the system is in poor thermal contact. A near equatorial spot (colatitude of  $112.5 \pm 0.5^\circ$ ), radius of  $15.04 \pm 0.45^\circ$  and T-factor of  $0.84 \pm 0.01$  was calculated. The B,V and B-V color curves are given as Figure 14. The system is an unusual shallow-contact A-type W UMa binary, albeit, the amplitudes

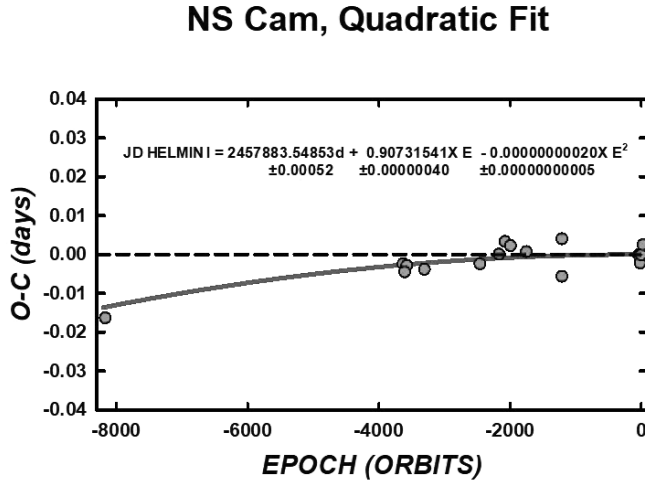


Figure 16. The linear residuals from quadratic equation (Equation 2) overlaying a plot of the quadratic term versus the orbital epoch in the period study of NS Cam.

of the primary and secondary eclipse are equal within the errors. An eclipse duration of ~21 minutes was determined for the secondary eclipse and the light curve solution. The geometrical representation at phase 0.25 is given in Figure 15.

### NS Camelopardalis

CCD, BVR<sub>I</sub> light curves of NS Cam were taken on January 1, 20, 21, 22, 23, February 4, 22, and 23, March 1, and April 7, 2020, at the Dark Sky Observatory, North Carolina, with the 0.81-m reflector of Appalachian State University by D. Caton. The initial study (light curves, classification, ephemeris etc.) of NS Cam (NSV 3771, GSC 4373 0708) was given by Khruslov and Tula of the SKYdot team (IBVS 5699). They classified it as an EB system with a maximum magnitude of 12.9 and minima of 13.5 and 13.2 for the primary and secondary eclipses. The period was 0.90733d.

Five times of minimum light were determined from our present observations, which include three primary eclipse and two secondary eclipses. We selected 4 times of low light from parabola fits of ASAS observations. From these we determined a quadratic ephemeris. The residuals are given in Figure 16.

$$\begin{aligned} \text{JD Hel MinI} = & 2458883.54853 \pm 0.00052d + \\ & 0.90731541 \pm 0.00000040 \times E \\ & - 0.0000000020 \pm 0.0000000005 \times E^2 \quad (1) \end{aligned}$$

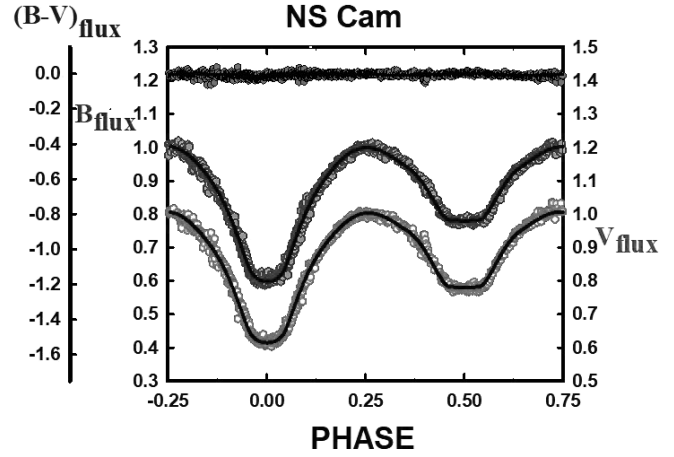


Figure 17. B, V normalized fluxes and B-V and R-I color curves overlaid by our solution curves of NS Cam.

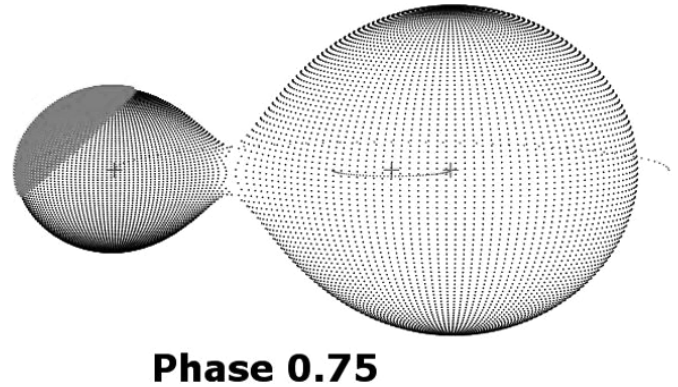


Figure 18. Geometrical representation of the surface of the binary at phase 0.75 for NS Cam with spot.

Thus, from our 20.3-year study, the period is found to be decreasing. Since the spectral types are ~F7V and ~G4V, this is probably due to magnetic braking. A Wilson-Devinney analyses reveals that the system is a W UMa shallow contact binary. The component temperature difference is 566K. The mass ratio is also somewhat extreme,  $M_2/M_1 = 0.2130 \pm 0.0001$ . The total eclipses make this a firm determination. The geometric representation of the solution is given in Figure 18. Its Roche Lobe fill-out is 15%. The dark spot was at midlatitude (co-latitude = 48°), but overlaps the pole with a large radius

of  $\sim 60^\circ$  and a T-factor of only  $\sim 0.67$ . The binary inclination is high,  $83.5 \pm 0.2^\circ$ , resulting in total eclipses. As a result, the primary minimum has a time of constant light with an eclipse duration of 104 minutes. The B, V and B-V color curves with the solution overlaid are given in Figure 17.

## Results

Figure 19 shows the typical theoretical thinking for magnetic braking of close binary (Guinan and Bradstreet, 1988). The observed rate of angular momentum loss has a much greater effect on the ages of short period binaries than proposed by the binary star community. We have recently been studying pre-contact W UMa binaries—that is, solar type stars—which exist in detached (separated) binary orbits with periods up to  $\sim 10$  days. Thus, our study extends to longer periods than usual accorded to close binaries. Due to the inclusion of these longer period binaries, we have extended our range of initial periods to 20 days. In our final results (See Samec-2 = 2016a), we assumed 5 days as the birth period for binaries of period 0.2–0.5 days. Further, we assumed an initial period of 8 days for periods of 0.5–0.8 days, 10 days for 0.8–1.5 day periods 15 and 20 days for periods from 2.0–9.3 days. Our final results begin in Table 1. The over-all average age of our extended sample is about 40 million years. This is only 0.3 % (0.003) of the evolutionary age of the universe (13.8 Gyr). Figure 20 shows example results: O-C figure showing evolution of the orbit of AE Cas that is decaying over the 89-year-period study (Samec et. al, 2019d).

In the example given by Guinan and Bradstreet (1988), shown in Figure 19, using their magnetic braking equations, the scenario of a present contact binary with a 0.315-day period is calculated. The sample calculation shows the decrease in the orbits over time of 5 different initial periods  $P_0$  from 1 day to 5 days. It is of interest here that they state that systems having periods  $P_0 > 6$  d may not experience this braking effect as main sequence stars since the tidal effects are small due to their relatively large separations. They cut off their initial period at 5d. We note that all of the stars except for two studied here have periods less than 5d. Here, selected systems were limited to those appearing to be undergoing magnetic braking. Thus, my unwitting selection may lend credibility to their prediction. As shown in the figure, the time to reach contact depends strongly on the initial period. Their calculations yield an age of 17 Gyr for an initial period of 5 days and 30 Myr for  $P_0 = 1$  d. In our sample, using binaries with periods from 0.30 to 0.32 days, we find, from observational rates of decay, that the time to attain contact ranges from 5 to 260 Myr, averaging 42 Myr, nearer to the prediction for initial 1 d periods. Our result for this transition (braking from a 5-day period to 0.32 days) is far short of 17 (now 13.8) Gyr. In fact, it is only

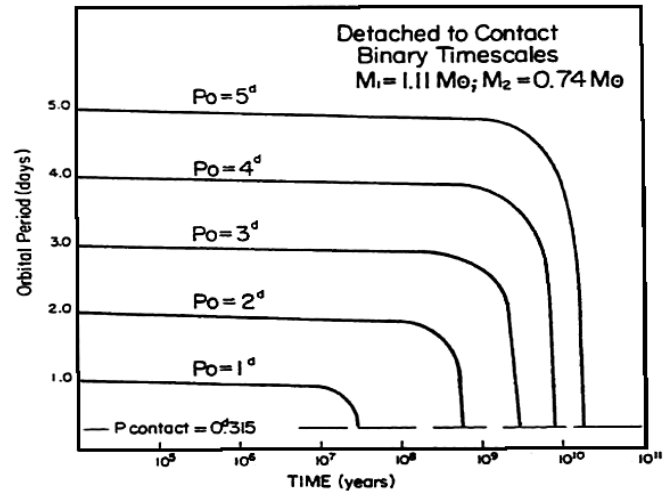


Figure 19. Typical theoretical thinking for magnetic braking of close binary: The time need to brake from a, 1–5 d period binary to a 0.315 period binary with 1.11 and 0.74 solar masses for the primary component and the secondary component, respectively (Guinan and Bradstreet, 1988).

## AE Cas

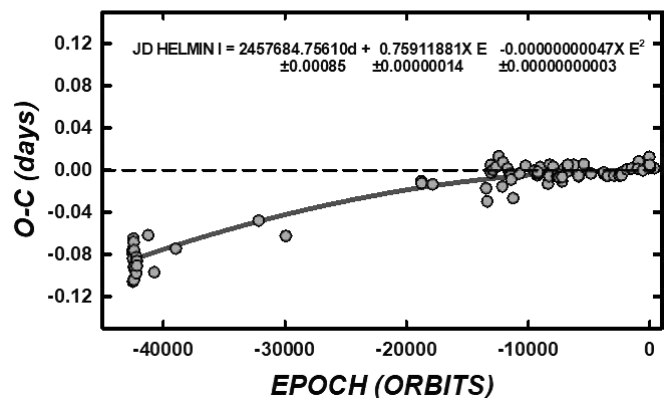


Figure 20. Example Results: O-C figure showing evolution of the orbit of AE Cas that is decaying over the 89-year-period study. Since this system is of solar type, we concluded in our paper that the period is decreasing and angular momentum loss is occurring. We include AE Cas in our calculation of the age of such binaries. This was published in *The Astronomical Journal* (Samec et. al, 2019d).

**Table I. Additional Eclipsing Binary Systems.** (Not all #s are in numerical order; some numbers are also missing.)

| Number | System              | Ref | dp/dE<br>(d/E) | dP/dt<br>(d/yr) | period<br>(d) | Est. Spec.<br>Type |
|--------|---------------------|-----|----------------|-----------------|---------------|--------------------|
| 1      | 279326              | 55  | -1.03E-10      | -3.29E-07       | 0.227733      | K9V                |
| 2      | V1107 Cas           | 64  | -5.69E-11      | -1.52E-07       | 0.273411      | K1V                |
| 3      | 187430              | 55  | -1.20E-10      | -3.18E-07       | 0.275312      | K9V                |
| 4      | RW Dor              | 48  | 0.00E+00       | -9.27E-09       | 0.285463      | K2V                |
| 5      | 238356              | 55  | -5.89E-10      | -1.47E-06       | 0.292658      | K6V                |
| 6      | 294795              | 55  | -1.95E-10      | -4.84E-07       | 0.293658      | K0V                |
| 7      | 238356              | 55  | -5.89E-10      | -1.47E-06       | 0.292658      | K6V                |
| 8      | 294795              | 55  | -1.95E-10      | -4.84E-07       | 0.293658      | K0V                |
| 29     | IK Boo              | 53  | -1.36E-10      | -3.28E-07       | 0.303118      | G2V                |
| 10     | 190636              | 55  | -8.19E-10      | -1.96E-06       | 0.305221      | K9V                |
| 11     | 215121              | 55  | -2.32E-10      | -5.51E-07       | 0.3078.42     | K7V                |
| 36     | ASAS J083241+2332.4 | 62  | -3.77E-10      | -8.85E-07       | 0.311321      | F5V                |
| 13     | V1187 Her           | 63  | -1.4E-10       | -3.34E-07       | 0.310763      | F7V                |
| 14     | 149279              | 55  | -8.75E-10      | -2.03E-06       | 0.314728      | K9V                |
| 83     | SZ Scl              | -   | -2.59E-10      | -5.90E-07       | 0.3208163     | K2V                |
| 15     | V474 Cam            | 42  | -4.2E-10       | -9.4E-07        | 0.328207      | K0V                |
| 16     | V658 Lyr            | 41  | -1.3E-10       | -3E-07          | 0.330258      | G2V                |
| 17     | V1007 Cas           | 40  | -8.1E-11       | -1.8E-07        | 0.332008      |                    |
| 18     | 181083              | 55  | -4.9E-10       | -1E-06          | 0.349391      | K6V                |
| 19     | 218785              | 55  | -1.2E-09       | -2.5E-06        | 0.353455      | K9V                |
| 20     | 2172596             | 55  | -1.5E-10       | -3.1E-07        | 0.354705      | K6V                |
| 21     | 162594              | 55  | -3E-10         | -6.2E-07        | 0.356191      | K3V                |
| 22     | QW Gem              | 50  | -1.3E-10       | -2.6E-07        | 0.358123      | F8V                |
| 23     | 233821              | 55  | -7.8E-10       | -1.6E-06        | 0.35992       | K2V                |
| 24     | 246693              | 55  | -3.5E-10       | -7E-07          | 0.363524      | G0V                |
| 25     | 347999              | 55  | -2.2E-09       | -4.3E-06        | 0.365383      | K3V                |
| 26     | MT Cam              | 64  | -4.6E-11       | -9.2E-08        | 0.366139      | G8V                |
| 27     | 130708              | 55  | -1E-09         | -2.1E-06        | 0.366826      | K9V                |
| 28     | GSC 3108-0057       | 28  | -1.9E-10       | -3.8E-07        | 0.368751      | G6V                |
| 29     | Omega Cen V150      | 46  | -9.5E-11       | -1.9E-07        | 0.369         | F7V                |
| 30     | 168012              | 55  | -1.9E-10       | -3.8E-07        | 0.371039      | K9V                |
| 31     | 241306              | 55  | -3.6E-10       | -7.1E-07        | 0.371268      | K3V                |
| 32     | NSVS 5066754        | 65  | -2.4E-08       | -4.7E-05        | 0.37478       | G5V                |
| 33     | 339765              | 55  | -6.1E-09       | -1.2E-05        | 0.37784       | K6V                |
| 34     | 351804              | 55  | -1.1E-09       | -2.1E-06        | 0.38542       | K6                 |
| 35     | 320382              | 55  | -1.4E-09       | -2.6E-06        | 0.388373      | K7V                |
| 36     | 207879              | 55  | -3E-10         | -5.5E-07        | 0.393082      | K6V                |
| 37     | 119460              | 55  | -1.3E-09       | -2.5E-06        | 0.394387      | K6V                |

Table I (cont.)

| Number | System         | Ref | dp/dE<br>(d/E) | dP/dt<br>(d/yr) | period<br>(d) | Est. Spec.<br>Type |
|--------|----------------|-----|----------------|-----------------|---------------|--------------------|
| 38     | 229500         | 55  | -9.3E-10       | -1.7E-06        | 0.398365      | K5V                |
| 39     | 192437         | 55  | -8.8E-10       | -1.6E-06        | 0.402313      | K9V                |
| 40     | 243151         | 55  | -2.4E-09       | -4.4E-06        | 0.403628      | K5V                |
| 41     | 217990         | 55  | -6.4E-10       | -1.1E-06        | 0.412545      | K9V                |
| 42     | MR Com         | 57  | -3E-10         | -5.3E-07        | 0.412744      | F7V                |
| 43     | V1695 Aql      | 66  | -9.8E-10       | -1.7E-06        | 0.412816      | G8V                |
| 44     | 212252         | 55  | -2.2E-09       | -3.9E-06        | 0.41325       | K9V                |
| 45     | V573 Peg       | 67  | -2.7E-10       | -4.8E-07        | 0.417449      | G7V                |
| 46     | 225278         | 55  | -4.1E-10       | -7.2E-07        | 0.417923      | K6V                |
| 47     | GQ Cnc         | 68  | -2.9E-11       | -5E-08          | 0.422208      | K0V                |
| 48     | 181311         | 55  | -8.3E-10       | -1.4E-06        | 0.422617      | K6V                |
| 49     | 195664         | 55  | -2.7E-09       | -4.6E-06        | 0.4369        | K5V                |
| 50     | 198303         | 55  | -2.3E-10       | -3.8E-07        | 0.438734      | K2V                |
| 51     | FF Vul         | 69  | -6E-11         | -9.8E-08        | 0.444976      | F4V                |
| 52     | NSVS 10083189  | 70  | -4.9E-10       | -7.9E-07        | 0.452189      | F8V                |
| 53     | 114280         | 55  | -6.2E-10       | -1E-06          | 0.453031      | K5V                |
| 55     | 183004         | 55  | -1.3E-09       | -2E-06          | 0.467429      | K3V                |
| 56     | V532 Mon       | 52  | -1.1E-10       | -1.7E-07        | 0.466976      | F5V                |
| 57     | 183004         | 55  | -1.3E-09       | -2E-06          | 0.467429      | K3V                |
| 58     | 184767         | 55  | -5.6E-10       | -8.6E-07        | 0.473305      | M1V                |
| 59     | 106230         | 55  | -5.9E-10       | -8.9E-07        | 0.489019      | K3V                |
| 60     | 163655         | 55  | -1.1E-09       | -1.6E-06        | 0.492482      | K9V                |
| 61     | 201682         | 55  | -1.3E-09       | -1.9E-06        | 0.497314      | K9V                |
| 62     | 168049         | 55  | -1.9E-09       | -2.7E-06        | 0.506522      | K7V                |
| 64     | NSVS 103152    | 64  | -2.4E-09       | -3.3E-06        | 0.528378      | F5V                |
| 65     | 192939         | 55  | -3.2E-09       | -4.4E-06        | 0.531934      | K9V                |
| 66     | 287671         | 55  | -1.4E-09       | -1.9E-06        | 0.532926      | K2V                |
| 67     | 182438         | 55  | -8.3E-10       | -1.1E-06        | 0.549392      | K9V                |
| 68     | 159116         | 55  | -1.4E-09       | -1.7E-06        | 0.587393      | K2V                |
| 69     | 176119         | 55  | -1.2E-09       | -1.4E-06        | 0.594569      | K7V                |
| 70     | TYC 1488-693-1 | 63  | -4.3E-09       | -5.2E-06        | 0.595442      | F2V                |
| 72     | V385 Cam       | 65  | -1.5E-10       | -1.8E-07        | 0.615271      | G7.5V              |
| 73     | 172659         | 55  | -5E-09         | -5.9E-06        | 0.626226      | K5V                |
| 74     | AE Cas         | 66  | -4.8E-11       | -4.6E-08        | 0.759121      | F7V                |
| 75     | V1073 Cyg      | 45  | -1.04E-10      | -9.7E-08        | 0.78585       | F2V                |

Table I (cont.)

| Number | System | Ref | $dp/dE$<br>(d/E) | $dP/dt$<br>(d/yr) | period<br>(d) | Est. Spec.<br>Type |
|--------|--------|-----|------------------|-------------------|---------------|--------------------|
| 76     | 175354 | 55  | -1.2E-08         | -1.1E-05          | 0.840163      | K7V                |
| 84     | N Cam  | -   | -2.00E-10        | -1.61E-07         | 0.90781541    | F7V                |
| 77     | 220028 | 55  | -7.6E-09         | -6E-06            | 0.920792      | K4V                |
| 78     | 154749 | 55  | -1.3E-08         | -1E-05            | 0.932247      | M1V                |
| 79     | 344477 | 55  | -2.1E-08         | -1.5E-05          | 1.032195      | K5V                |
| 80     | 176377 | 55  | -2.4E-08         | -1.4E-05          | 1.245946      | K9V                |
| 81     | 299145 | 55  | -2.9E-08         | -1.7E-05          | 1.252603      | K5V                |
| 82     | 170070 | 55  | -2.2E-08         | -1.2E-05          | 1.401907      | K9V                |

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 57. Qian et al., 2003  
 62. Sriram et al., 2016b  
 63. Samec et al., 2018a  
 64. Samec et al., 2019b  
 65. Samec et al., 2019a  
 66. Samec et al., 2019d  
 67. Samec et al., 2018c  
 69. Samec et al., 2016b  
 70. Samec et al., 2018d

Table 2. Average values from Samec-1 and 2 (2012, 2016a), including this paper.

|                   | $P_0$ 5d<br>(initial) | $P_0$ 8d<br>(initial) | $P_0$ 10d<br>(initial) | $P_0$ 15d<br>(initial) | $P_0$ 20d<br>(initial) | Average  |
|-------------------|-----------------------|-----------------------|------------------------|------------------------|------------------------|----------|
| AGE (Years)       | 4.12E+07              | 6.05E+07              | 4.74E+07               | 1.97E+07               | 2.22E+07               | 3.82E+07 |
| Maximum           | 7.15E+08              | 2.86E+08              | 2.18E+08               | 1.02E+08               | 1.45E+08               | 7.15E+08 |
| Minimum           | 1.33E+01              | 2.20E+05              | 5.09E+05               | 6.28E+04               | 8.86E+04               | 5.09E+05 |
| % age of Universe | 0.3                   | 0.4                   | 0.3                    | 0.1                    | 0.2                    | 0.3      |

0.4% of the current estimated age of the universe, (some 2–3 orders of magnitude)!

Binary evolution is taking place at a rate of ~300 times that predicted by theory! Using the 5-day limiting period of Guinan and Bradstreet, our sample decreases to 133 binaries and the age of this group is about 40 million years. This is only 0.3% (0.003) of the present estimate of the evolutionary age of the universe (13.8 Gyr). So, our results remain at same order of magnitude.

## Creation Implications

This paper gives physical confirmation of the youthful age, in a creationary sense, of the universe in a time-dilation scenario. We have determined the age of solar type binaries from a large sample which comprise the most abundant of the binaries in the universe (probably 90%) and about 50% of all stars. A scheme was developed which estimated the age of such binaries and thus apparent age of the time-dilated universe. The average age result is on the order of ~38.2 million years as the apparent age of the time-dilated universe. Although this seems large for a creation-based paper, it is much, much smaller than the proposed age of W UMa binaries of some 5–10 billion years. The age is about 1/200th of their theoretical age! The 5-day initial period binaries (including 135 eclipsing solar type binaries) have an average age of  $4.12 \times 10^7$  years or 0.3% of the age of the universe proposed by secular astronomers, 13.8 Gyr. I reiterate the statement given in Samec-2 (2016a) as a footnote here with the present results.<sup>3</sup> This shows that even in a time-dilated view of the cosmos that the universe “evolves” at a much higher rate than the evolutionist imagines. As I have noted before, someone called to our attention at a recent meeting much of this prehistory took place during Creation Week following the creation of the first stars on Day 4. So, the time-dilation events postulated by Humphreys (1994, 2005, 2008) fall into the category of a Creation Week event. Regardless, the aging phenomena did actually take place in a scientific-historical sense and it is not due to an apparent, ex nihilo, created history. The events we see truly took place and are objects of legitimate scientific inquiry that the Lord has al-

lowed His children to study. I firmly believe as stated in Exodus 20:11, “For in six days the LORD made heaven and earth, the sea, and all that in them is, and rested the seventh day:” and Isaiah 45:12, “I have made the earth, and created man upon it: I, even my hands, have stretched out the heavens, and all their host have I commanded.”

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<sup>3</sup> Although this does not equal the oft-cited age of 6000–10,000 years in creation literature, I remind the reader that this value is the *apparent age* of a time-dilated universe. The Earth and, I believe, the entire Solar System remains in the range of ages last mentioned. And only some ~100 million years (not 13.8 billion!) years of *apparent* history is exhibited at least in the nearby (<2 kiloparsec’s, or about 6000 LY) cosmos—and probably for the “deep” universe as well. I also believe that some celestial bodies were created so that they defy being dated by evolutionary time schemes, such as our Sun.

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# Supernova Driven Accelerated Decay Confronts the Evidence

Eugene Chaffin\*

## Abstract

Supernova explosions emit debris including neutrinos and anti-neutrinos. In a previous paper these were linked to a hypothetical accelaron field and the variations in this accelaron field as the blast reached Earth were investigated as a cause for accelerated nuclear decays. In this paper some of the collateral reactions which would result are investigated to see if they are consistent with known things. This includes the known detections which are associated with Supernova 1987A and other supernovae. Also, the rate of supernova detections on Earth is considered. One cannot induce stars to explode, so we must be content with what has been observed. We find that there are no observations available at present which would rule out the existence of the accelaron field and the associated particle, as long as it has a mass within a specified range. Also, the recent discovery of uranium's presence in the spectra of some galactic halo stars is discussed in the context of the accelaron mechanism. A separate paper will discuss the dependence of supernova light curves on the nuclear decay of relevant nuclei.

## Introduction

In order to match the evident amount of decay that has occurred in Earth rocks, and fit the Biblical timescale, the RATE project emphasized an accelerated decay episode, perhaps beginning early in the year of the Genesis Flood, and tapering off somewhere between a minimum of about ten years and a maximum somewhat less than a thousand years after the Flood (Vardiman, Snelling, and Chaffin, 2005). The exact mechanism of

the accelerated decay was left an open question. It would be desirable to pinpoint more precisely the mechanism of accelerated decay. In Chaffin (2017), a possible origin of the accelerated decay was sought by considering the effects of a nearby supernova when fields and materials from the explosion arrived at Earth. This necessarily involved study of the *weak interaction*, since neutrinos escaping from a supernova remove

prodigious amounts of energy and are considered the prime suspect in allowing the collapse and “bounce” of the interior of the star that “goes supernova” (Heger et al., 2001). As Heger et al. discussed, a number of different nuclei can undergo electron capture, a type of nuclear decay where a proton absorbs an electron, becoming a neutron and emitting a neutrino. The energy of the neutrino has a large probability of leaving the star, decreasing “pressure support and, all else being equal, decreases the effective Chandrasekhar mass that can be supported without collapsing” (Heger et al., 2001, p. 307).

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Accepted for publication November 24, 2020

It may be that a time dilation cosmology, a rapid expansion of space, or a larger speed of light prior to the Flood would be necessary to build a consistent history of the chronology of events in our galaxy. However, that is outside the scope of this paper.

The work discussed in this paper, a follow-up to the Chaffin (2017) paper, majors on showing that it is reasonable to postulate that the scalar field, the acceleron field introduced in that paper, decays over a time scale of ten to a thousand years. The relaxation time for the scalar field is related to how it couples to other fields. In modern physics, the established theory for this involves *Feynman diagrams*: drawings with lines, wavy lines, vertices, etc. representing, via the *Feynman rules*, calculational expressions for a physical process (Feynman, 1949a, 1949b; 1985). In this investigation it thus becomes necessary to consider some simple Feynman diagrams, see Figures 1 and 2. Our progress is aided by the small mass of our hypothetical acceleron particle. We shall see that the small value restricts the possible decays of the acceleron, and hence the possible diagrams.

It is prudent to point out that the acceleron field and its associated particle may not exist. That is a question for future experimental and observational work. However, as in any science we try to examine our hypothesis to see if it agrees with known things. It is no disgrace to discover disagreement of observation with a suggested model; the possibility of agreement and increasing our explanatory abilities makes the endeavor exciting.

There is a spectrum of three known neutrino masses, and there may also exist one or more sterile neutrinos. The sterile neutrinos, if they exist, do not couple to the  $W^\pm$  or  $Z$  bosons and hence are referred to as “sterile.” They might be compared to “ghosts” in that they interact only feebly (or weakly). Their importance may be that they would

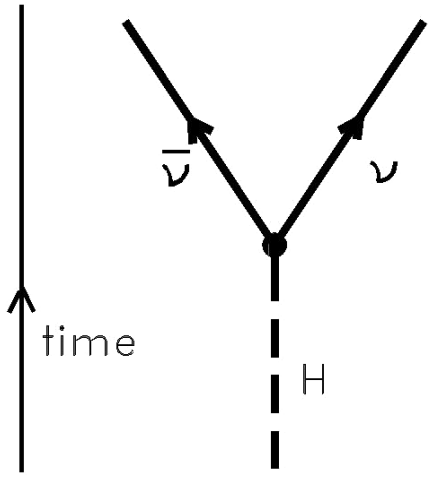


Figure 1. Feynman diagram of a Higgs particle decaying into a neutrino and an antineutrino. Here we replace the Higgs by an acceleron particle, which is much lighter.

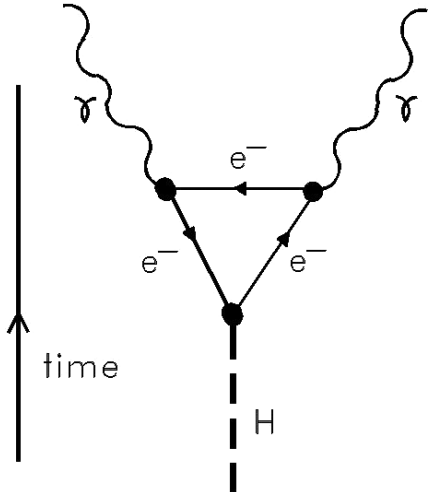


Figure 2. The Higgs-boson decay into two zero-mass photons must involve a loop of charged particles, here an electron and a positron. The backwards-in-time arrow on one of the electrons means that it represents a positron. Here we replace the Higgs by a much lighter acceleron particle.

interact via gravity and they could carry off energy when emitted in decays.

The three known neutrino types, called “flavors,” are the electron neutrino, muon neutrino, and tau neutrino, partnering with the electron (mass 0.510 electron volts (eV) in energy units), muon (105.66 eV), and tau (1777 eV). The muon and tau are not stable particles. The tau can decay into a muon with the emission of muon antineutrino and a tau neutrino, or follow other decay modes including decaying directly to an electron plus electron antineutrino and tau neutrino. The most probable decay mode for the muon is to an electron plus electron antineutrino and muon neutrino.

These neutrino types correspond to the three known “generations” of particles that make up the known roster of elementary particles. Everyday matter that we encounter on Earth is made from first generation particles: protons, neutrons and electrons. The higher generation particles can be created in

| Lepton            | Lifetime (seconds)     |
|-------------------|------------------------|
| Electron          | stable                 |
| Muon              | $2.197 \times 10^{-6}$ |
| Tau               | $3.3 \times 10^{-13}$  |
| Electron neutrino | stable                 |
| Muon neutrino     | stable                 |
| Tau neutrino      | stable                 |
| Sterile neutrino  | ?                      |

Figure 3. The known leptons plus the hypothetical *sterile* neutrino. Antiparticles of these leptons may also exist, but this is still an experimental question for the neutrinos.

particle accelerators (that is how they were discovered), but they rapidly decay back to the first generation due to their larger mass. However, neutrinos may

have an “inverted hierarchy” where the tau neutrino is lighter than the muon neutrino which is lighter than the electron neutrino. This needs to be decided experimentally.

Neutrinos can also morph amongst, or oscillate between, the three (or more if sterile neutrinos exist) flavors. This is the accepted solution to the solar neutrino problem described by the late John Bahcall (1989). The Sun only produces electron neutrinos. However, the neutrinos undergo a “flavor” oscillation during their travel out of the Sun and through space to Earth. Experiments show that this reduces the probability of detection of electron neutrinos at Earth.

The neutrinos could possibly also oscillate to sterile neutrinos, and experiments have placed limits on this possibility but have not ruled it out (Chang, 2016; Carlson, 2020). Experiments such as Liquid Scintillator Neutrino Detector (LSND) at Los Alamos, New Mexico, and Mini Booster Neutrino Experiment (MiniBooNE) at the Fermi National Accelerator Laboratory in Batavia, Illinois, which had a relatively short beam length, have produced results favorable to the sterile neutrino hypothesis which other experiments cannot corroborate (Aguilar-Arevalo et al., 2018; Cho, 2018a). Originally (Schwarzschild, 1995) the Liquid Scintillator Neutrino Detector experimental collaboration reported evidence for antineutrino oscillation over a very short distance, which was not confirmed for a long time by any other group, including the MiniBoone collaboration. However, the MiniBoone group eventually switched from using a muon neutrino beam to a muon antineutrino beam in order to match more exactly what LSND had done (Schwarzschild, 2010), and then after several years of data collection was able to confirm the LSND results (but see Chang, 2016). Several years were required because of the low event rates. No one initially expected that the oscillations would give different results for antineutrinos than

neutrinos, but that is what was found, experimentally.

The LSND and MiniBoone experiments find antineutrino oscillation over a distance of a hundred meters or so, while other experiments are concerned with distances much larger, including the distance to the Sun. The sterile neutrino, or neutrinos (if there is more than one), are a way to model these various results which mathematically cannot be done with just the three conventional types of neutrinos.

An effort currently in progress is the Karlsruhe Tritium Neutrino (KATRIN) experiment (Arenz et al., 2018). Tritium is the isotope of hydrogen,  $^3\text{H}$ , with two neutrons and one proton; it has a very low energy release of 18.6 kiloelectron volts (keV) and some other useful properties for the experimental objectives. The primary objective is to find the absolute neutrino mass scale, with a sensitivity of 0.2 eV. Indications were that the neutrino masses should be, in

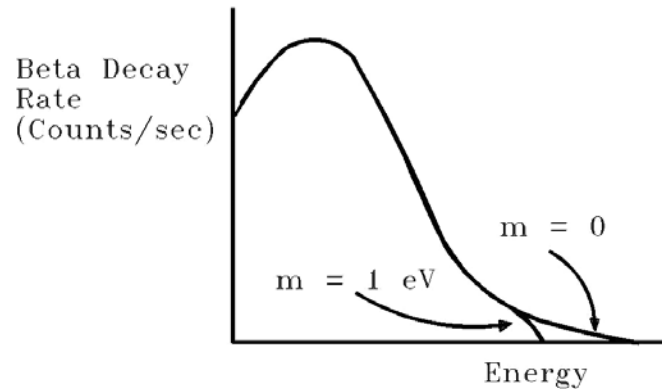


**Figure 4.** The projected electron energy spectrum of tritium decay, showing the count rate for beta decay versus the electron kinetic energy. Tritium has a comparatively low endpoint energy of 18.6 kiloelectron volts (keV) and a half life of 12.3 years. Near the endpoint, the form of the graph depends on the neutrino mass. The graph shows two curves for the cases of neutrino masses of 0 and 1 eV. When the neutrino mass is nonzero, the graph drops abruptly down at the endpoint, as shown for the 1 eV case, since a portion of the energy is tied up in the rest mass energy. This is what would enable the measurement of the rest mass. After Osipowicz et al. (2001).

energy units, between 10 milli-electron volts and 2 electron volts (eV). In late 2019, there was already enough data for the Karlsruhe Tritium Neutrino (KATRIN) collaboration to put an upper limit of 1.1 eV on the neutrino mass, improving by a factor of 2 the mass limits derived by previous measurements that directly characterized the particle mass (Aker et al., the KATRIN collaboration, 2019). This announcement was based on initial data, and in four or five years the collaboration should have enough data to reduce the sensitivity down to 0.2 eV, either finding the value for the mass or giving a new upper limit.

According to results from several experiments, at least two of the three neutrino masses are larger than about  $8 \times 10^{-3}$  eV (Aker et al., the KATRIN collaboration, 2019; Brugnera, 2019). In interpreting experiments, sometimes an average or “effective” neutrino mass is referenced, since morphing between neutrino flavors may occur. If the effec-

tive mass is greater than 0.2 eV, KATRIN should eventually be able to measure it; otherwise, it will just establish a new upper limit. It depends on a precise measurement of the endpoint spectrum of tritium beta-decay (Figure 4).

In the following discussion we will use the word “neutrino” for both neutrinos and antineutrinos, unless otherwise specified.

The circumstance that neutrinos are now known to have nonzero rest masses changes our views about how they affect our universe. According to the Standard Model, the unification of weak and electromagnetic forces for which Weinberg, Salam, and Glashow received the 1979 Nobel Prize for physics, the neutrino mass should be exactly zero. The modern circumstances are thus pointing to a need to extend the Standard Model. More than that, neutrinos cannot be the “Dark Matter,” as was thought in the 1990’s (Roulet, 1993, p. 5247), because their rest mass is restricted to be less than 1.1 electron volts. Nevertheless, their non-zero rest mass means that they can slow down over time and clump together in clouds (Fardon et al., 2004). Quantum mechanically, neutrinos are a superposition of at least three mass eigenstates. The components of different mass move through space at slightly different speeds, which means that passing through high density regions can destroy neutrino oscillations (Beacom, 2010, p. 9), as can travel over large distances (Anada and Nishimura, 1989, pp. 60–61; 1990).

In the next section, we will discuss the decay modes available to the acceleron and the timescale involved. This controls the duration of the disturbance. Then we will consider the reported detections of uranium in galactic halo stars, and the implications regarding the acceleron. After that we will discuss some criticisms of various neutrino theories by Zhou (2011), which are relevant to our acceleron theory, and some relevant criticism of Firestone (2014) by Melott

et al. (2015), as it relates to what was said in Chaffin (2017). We shall see that the acceleron-based model of an accelerated decay episode seems to survive these unanticipated criticisms. In a separate paper Chaffin (2020, submitted), we will relate the decline of supernova light curves to the radioactive decay of the important isotopes Ni-56 and Co-56.

### The Duration of the Supernova Effect

In Chaffin (2017) a neutrino burst from a supernova was hypothesized to cause a change in the scalar acceleron field. Although the neutrino burst is quickly over, we shall see that the relaxation time for the associated acceleron field can be ten to a thousand years. This is negligible on an evolutionary timescale, but very significant on a recent creation timescale. The humans who lived through a supernova burst would not find an interval of ten to a thousand years negligible. We find that the accelerated decay may be initiated by the neutrino burst, but lasts long past the passing of the neutrino burst.

According to the Fardon et al. (2004) theory, discussed in Chaffin (2017), the neutrino mass is simply inversely proportional to the neutrino density. In their theory, there is background of neutrinos left over from the big bang. Since the density cannot be lower than that of the background, neutrinos in a region restricted only by this background have the heaviest mass possible.

The hypothetical acceleron field will have an increased value as a result of the supernova emission of neutrinos, and a pulse in the field will travel towards Earth along with the neutrino burst. As pointed out by Abbott, Farhi, and Wise (1982), such a pulse in the scalar field, the acceleron field in our case, may be thought of as a *coherent* state which decays by particle emissions. Dicke (1954) explained that in such a *coherent* state all the emitters are interacting with

common fields and hence cannot be treated as independent. The decay rate of the acceleron field is the decay rate of an acceleron, considered as a particle. These rates may be found by evaluating the relevant Feynman diagrams. In quantum theory, each scalar particle has an associated wave packet. For the scalar acceleron field to be nonzero requires the wave packets of different acceleron particles to interfere constructively. If the wave packets were emitted chaotically rather than coherently, the waves would interfere destructively and an overall zero acceleron field would result (Figure 5). *Indistinguishability* of different sources is also involved.

When we are considering a field which is nonzero in empty space, a description in terms of only a few field quanta is inadequate. To approach such a problem, it is appropriate to consider the coherent states approach of Glauber (1963), suitably adapted to the type of field one is considering, the acceleron field in our case. As Glauber (1963, p. 2784) pointed out, electromagnetic radiation from a prescribed electric current distribution will lead invariably to a coherent state for that radiation. The same should apply to our acceleron field for a suitable source distribution or neutrino distribution.

As Fardon et al. (2004) discussed, a typical supernova produces a density of  $10^{35}$  to  $10^{37}$  neutrinos per cubic centimeter. Annihilation of neutrinos with antineutrinos producing pairs of accelerons, interaction of neutrinos with other neutrinos producing acceleron pairs, and inelastic scattering of neutrinos with nuclei producing accelerons are occurring during the supernova explosion. These processes rapidly increase the acceleron field in a burst traveling outward away from the explosion.

The decay lifetime for the scalar field is what controls future decrease in the scalar field, hence the change in the neutrino mass. For the acceleron, we will find a mass, in energy units, of the

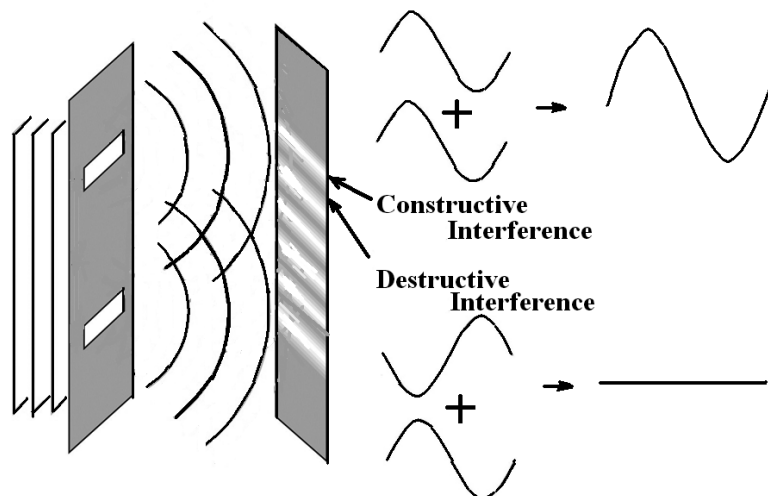


**Figure 5.** Addition of waves from different slits can involve constructive or destructive interference. This corresponds to coherent radiation versus chaotic addition of the source radiation.

order of tens to hundreds of eV, electron volts. For such a small mass, the only allowed decays of a scalar particle are decays into two photons (Resnick, Sundaresan, and Watson, 1973; Freund and Nandi, 1974; Sato and Sato, 1975; Ellis, Gaillard, and Nanopoulos, 1976; Gunion and Haber, 1993) or decays into a neutrino and antineutrino (Ellis, Gaillard, and Nanopoulos, 1976; Davidson and Logan, 2009; Ng and Beacom, 2014; Dawson, Englert, and Plehn, 2018). The Higgs boson, discovered experimentally in 2012, is also a scalar particle, similar to the acceleron but with a much larger mass, and hence totally different decay modes (Cho, 2018b). However, in the 1970's a Higgs particle mass of the order of 125 gigaelectron volts (125 GeV) had not yet been ruled out and was still thought possible, which makes study of these very old papers useful for application to our model.

The lifetime for decay to neutrino and antineutrino becomes infinite as the neutrino mass approaches zero, but it is known that the effective neutrino mass is not zero (Hecht, 2003). As Hecht ex-

plained, zero-mass particles would travel at the speed of light, and time stops for them. Hence, mixing between different neutrino types, electron, muon, and tau neutrinos, which has been experimentally observed, could not occur because the particles would travel without any passage of time. For this reason we know that the neutrino masses are not zero, even though the exact value remains to be determined. According to Osipowicz et al. (2001), the effective mass-energy of the three neutrino types must lie between 0.05 and 0.34 electron volts. For non-zero rest mass of the neutrino, the acceleron can decay into neutrino and antineutrino, as in the Feynman diagram shown in Figure 1.

A scalar particle cannot decay directly into two photons. However, Butterworth (2015, p. 186), while discussing the decay of the Higgs particle (a scalar particle), explained that this decay occurs nonetheless: "But since the photon's mass is zero, the Higgs really ought not to decay into photons at all. And it does not, directly. It has to go through a loop of some other particle,..." The

intervening loop that Butterworth mentions must involve charged particles as shown in Figure 2. One of the arrows in Figure 2 is backwards, which Feynman interpreted as a positron, an electron moving backwards in time (Feynman, 1949a; 1985).

The lifetime for decay into two photons can be calculated by following the Feynman rules which go with the Feynman diagram (Figure 2). This was done, for example, by Resnick, Sundaresan, and Watson (1973), and the resulting lifetime is Planck's constant over  $2\pi$ , called  $\hbar$  [h-bar], divided by the decay width given in their paper. Sato and Sato (1975), in the case of a small scalar mass particle such as our acceleron, specified that according to the Resnick et al. equation the lifetime in seconds is inversely proportional to the cube of the mass  $m_\phi$  of the scalar, and is  $6.6 \times 10^{16} / m_\phi^3$ . Here  $m_\phi$  is in the energy units of electron volts in order to get the lifetime in seconds.

Appendix A contains some equations leading to a formula for the lifetime for decay into two photons.

If we change the Appendix A results to years, the lifetime formula is  $1.06 \times 10^8 / m_\phi^3$ . In order to fit the Biblical timescale, the RATE project would specify an accelerated decay episode, beginning early in the Flood year, and ending somewhere between ten and a thousand years after the Flood at the outset. However, let us expand this interval to from ten to ten thousand years for the decay to two photons, since we will see that the other decay mode is more restrictive. We can calculate straightforwardly that this requires our acceleron mass, in energy units, to be between 59 eV and 590 eV, where eV stands for electron volts, a unit of mass-energy. For unknown reasons, Sato and Sato (1975) reported values off by a factor of 19.7 from ours, and accepting their results alters these limits to 21.96 eV to 219.7 eV. The cube root of 19.7 is 2.7.

Resnick et al. stated that if the mass of the scalar meson  $m_\phi$  is less than  $2m_\pi$ ,

then it cannot decay into an  $e^+e^-$  pair, and the only decay mode available is into two photons. In 1973, the date for the Resnick et al. work, the Weinberg model, today called the Standard Model, prevailed in which the neutrino mass is exactly zero, and consequently the lifetime for decay into neutrino plus antineutrino was infinite or that decay mode could not occur. This is now known to be false. The neutrino mass is between 0.01 eV and 1.1 eV, and the scalar meson has a lifetime for decay into neutrino plus antineutrino comparable to the lifetime for decay into two photons.

We therefore see that a second decay mode, the decay of the acceleron into neutrino and antineutrino (Figure 1), is possible. It turns out that this mode is even more restrictive. Butterworth (2015, p. 240) cited Ellis, Gaillard, and Nanopoulos (1976) for the calculation of the Feynman diagram (Figure 1) for the decay of the Higgs boson by this mode. Since the acceleron is a scalar, it follows the same Feynman diagram as the Higgs. Of course, the Higgs discovered at the Large Hadron Collider (LHC), is much more massive than our hypothetical acceleron, which opens up more possible decay modes for the Higgs particle which are not available to the acceleron. Using Ellis et al.'s equations, the decay width that they gave is the Fermi constant  $G_F$  times the fermion (the neutrino in our case) mass squared, times the acceleron mass, all divided by four  $\pi$  times the square root of two. The lifetime is then Planck's  $\hbar$  [ $\hbar = h/2\pi$ ] divided by this decay width. For simplicity, assume that the Fermi constant was the same as the modern value. This may not be the case (Chaffin, 2001). Then we find that an acceleron mass between 59 and 590 electron volts yields an acceleron lifetime between 217 and 21.7 years. There is a discrepancy between this result and that of Sato and Sato (1975), and the reason is obscure. If my calculations were off by a factor of 19.7, then

59 and 590 become 21.96 and 219.7 eV. The cube root keeps this from being a huge change. The acceleron lifetimes become 80.3 years and 8.03 years. The acceleron lifetime for this decay mode is comparable to, but slightly less than the two photon decay mode, where these lifetimes corresponded to ten thousand years and ten years, respectively.

$\Gamma$  [GAMMA] is the rate for the coherent state  $\phi$  to transfer energy into radiation. Abbott, Farhi, and Wise (1982) considered that an extended scalar field could be thought of as a "coherent" combination of scalar particles. As we already said, "coherent" means in this case that the particles have associated wavefunctions which oscillate in synchrony with each other. As discussed by Abbott, Farhi, and Wise, the  $\Gamma$  [GAMMA] is then simply the decay rate for the scalar particle  $\phi$ , with mass  $m_\phi \sim \mu^2/m_p$ , to decay into radiation. In other words,  $\Gamma$  gives the number of particles decaying per unit time.

A decrease in energy of the scalar field could occur through the expansion of the universe or through decay radiation. The universe expansion will be a very slow process compared to the time development of a supernova explosion and dispersal of the debris from the star. Hence, we are mainly concerned with the decay modes of the scalar particles for our model of an accelerated decay episode.

A region of high neutrino density, means a region of large acceleron field. A large  $\phi$  value [corresponding to a large neutrino density] makes  $G_F$  smaller, in the Fardon et al. (2004) model. The decay constant is proportional to  $G_F^2$ , where  $G_F$  is a constant of proportionality which we use for beta decay probability. The decay constant is  $\ln 2/(\text{half-life})$ . The half-life is thus smaller for larger  $G_F$  or larger for smaller  $G_F$ . However, the half-life depends on other considerations besides  $G_F$ , and these other considerations can mean a much more drastic change in half-life. For example,

a change in decay mode may occur, as for U-238 in the scenario discussed in Chaffin (2017, 2019). In that scenario, a change in the neutrino mass, and the associated change in the weak force, might alter the masses of neutrons and protons, and thus of U-238, and thus make beta-minus decay of U-238 energetically possible. One might point out that the alteration in mass could also occur if the change were a change in the strong force rather than the weak force. For other possibilities see Chaffin (2005a, 2005b; 2008; Oliver and Chaffin, 2012).

We should notice that a recent experimental analysis (Aprile et al., 2019), the XENON1T experiment, put an upper limit of 186 electron volts on scalar particles similar to the acceleron. The experiment searched for flashes of light emitted when dark matter particles interact with the two tons of liquid xenon in the detector. No dark matter particles were detected. In the process, the analysis performed ruled out a range of unknown particle candidates of specific masses. Future upgrades of the detector are planned which would increase the sensitivity, possibly either detecting or ruling out acceleron particles in the mass range considered here.

## Uranium Detection in Stars

Miller (2007) pointed out that the only elements that "the Big Bang could have produced are hydrogen, helium, and possibly a trace of lithium, but no other metals." Nevertheless, heavy elements, including uranium, have been detected in some stars, which the standard paradigm explains as due to nucleosynthesis in stars. It has been thought that perhaps Uranium-238 could switch from predominately alpha decay to predominately beta-minus decay (Chaffin, 2017, p. 182) as the result of the change in the acceleron field as it reached our location from a supernova. If this could occur at Earth, other supernovae occurring elsewhere should affect the uranium in

the surrounding stars. The Milky Way Galaxy has been described as having a spherical halo centered on the same central bulge as the disk in which the Sun is found. The stars in the halo are on average farther apart than those in the disk. We may not be able to pinpoint every supernova in the history of our galaxy, but one would expect on average less accelerated decay of the uranium in halo stars than on Earth, due to their probable location farther from historic supernovae. Halo stars are spread over a huge volume. Uranium has not been directly detected in solar spectra, but its presence in small concentrations in the Sun has been inferred from its concentration in meteorites (Asplund, 2009, Table 1).

However, uranium has been detected in a handful of halo stars, including Cayrel's star CS31082-001 (Cayrel et al., 2001; Chaffin, 2001), J09544277+5246414 (Holmbeck et al., 2018), and CS29497-004 (Hill et al., 2016). The measured value of  $\log(U/Th)$  in CS31082-001 is  $-0.74 \pm 0.15$ , and it is about 4 kiloparsecs away. CS29497-004 is located at about  $26^\circ$  below the celestial equator and Hill et al. (2016) reported  $\log \epsilon(U) = -2.20 \pm 0.30$ . Uranium detection in J09544277+5246414 was reported as  $[U/Fe] = +1.40$  (Holmbeck et al., 2018). Here Holmbeck et al. were using the usual spectroscopic notations that  $[A/B] = \log_{10}(N_A/N_B)_* - \log_{10}(N_A/N_B)_{\text{sun}}$ , and that  $\log \epsilon(A) = \log_{10}(N_A/N_H) + 12.0$ , for elements A and B, where N represents abundance. In other words, the abundance of hydrogen is arbitrarily set to 12.0, or the logarithm to base 10 of the hydrogen abundance is made to be 12.0, and all other elements are given relative to this standard. Cowan et al. (2002) reported uranium in the star BD+17°324. The detection of such large amounts of uranium in these instances leads one to suspect that not as much accelerated decay occurred at those locations as on Earth, and perhaps is a step toward validation of our logic.

## Overcoming Some Criticism Regarding Neutrinos and Their Interactions

In modern times, particle-physics models have been proposed in which there are more than one neutral scalar particle, with the Higgs boson being the one discovered in 2012 at the Large Hadron Collider (LHC). A hypothetical extra "light Higgs particle" has been proposed by Wang et al. (2006), Gabriel and Nandi (2007), Davidson and Logan (2009), and Sher and Triola (2011). This light scalar particle is very similar to our acceleron, while not necessarily having all of its characteristics. The motivation of these authors for introducing their extra scalar particle was to explain the small masses of the neutrinos, without the necessity of the usual very small *Yukawa coupling*. A Yukawa coupling is a constant occurring in the dynamical equations, named after the late Japanese physicist Hideki Yukawa, which also is a proportionality constant between the Higgs expectation value and the particle mass, the neutrino mass in this case, and the Yukawa coupling in the usual theory is about  $10^{-12}$  to  $10^{-13}$ , depending on what the exact neutrino mass is. The new theories said that the neutrinos coupled to the light Higgs rather than the usual one, with the result that the Yukawa coupling could be of order unity instead of  $10^{-12}$  to  $10^{-13}$ . Zhou (2011) submitted a formal comment or criticism of these papers on the basis of several arguments. While Zhou was not directly addressing our acceleron model, his criticisms still seem to need to be addressed. Nandi, in Maitra et al. (2014, p. 3), seemed to acquiesce in Zhou's conclusion, stating that astrophysical bounds on the neutrino Yukawa couplings in such extensions of the Standard Model were contradictory to motivations of the Gabriel and Nandi (2007) paper. The astrophysical bounds which Zhou (2011) mentioned included the fact that neutrinos from the supernova in the Large Magellanic Cloud, SN1987A, were observed by the

Japanese Kamiokande detector as well as others (Woosley and Phillips, 1988; Woosley and Weaver, 1989). That being the case, restrictions are found on the reactions that the neutrinos might undergo in their 168 thousand light-year [51.4 kiloparsecs, where 1 parsec is 3.26 light years] journey to Earth. Sher, in Branco et al. (2012, p. 34) also seems to acquiesce, stating: "In particular, the neutrinos emitted by SN1987A would, if there is a light scalar, interact strongly with the relic neutrino background and would not reach Earth."

Zhou's paper mentioned, in particular, reactions of the neutrinos with relic neutrinos from the big bang, the so-called cosmic neutrino background. Zhou (2011, p. 1) stated:

The observation of neutrinos from Supernova 1987A requires that the mean free path of electron antineutrinos in the presence of cosmic background particles should be larger than the supernova distance, i.e.,  $\lambda_{\nu_e}^{-1}D < 1$  with  $D = 51.4$  kpc, in order to avoid significant reduction of neutrino flux.

If this background of relic neutrinos exists, and if the hypothetical light scalar particles also exist, then certain reactions become possible. In particular, antineutrinos from the distant supernova could react with the relic neutrinos, producing pairs of the scalar particles. Zhou showed that the fact of the detection of the antineutrinos on Earth led to the restriction of the Yukawa couplings of the antineutrinos with the scalar particles. The Yukawa couplings had to be very small, contrary to the reasons given by Gabriel and Nandi (2007) for introducing these light scalar particles. The particles were introduced to explain why the Yukawa couplings might not be small. In essence, if the antineutrino and neutrino masses resulted from a different Higgs boson than that of other particles, a light Higgs particle rather than the one found in 2012, then that would allow the Yukawa coupling to be of the order

of one [1] rather than very small. However, Zhou said that the SN1987A data contradicted this hypothesis. The reason is that, for neutrinos with the standard weak interaction, and for most neutrino energies, there is little hindrance to their propagation over cosmic distances. However, the light scalar particles that were considered should, according to Zhou, cause extra reactions with the cosmic neutrino background which could hinder the neutrinos, preventing their detection on Earth.

One way to discern whether the cosmic neutrino background exists might be the Z-burst phenomenon. In this scenario, high-energy neutrinos or antineutrinos from deep space interact with the cosmic background, or relic neutrinos to produce a  $Z^0$  boson. So far detectors of sufficient sensitivity to detect these cosmic  $Z^0$  particles have not been constructed (Stal et al., 2007). Hence, observational data cannot yet tell us whether these “relic” neutrinos exist.

Recent creationists do not accept the big bang and the scenario that goes with it. Does this mean that we reject the existence of the cosmic neutrino background? Not necessarily. For instance Humphreys (1994, p. 133; 2014) proposed a creationist cosmology in which a cosmic microwave background exists. Also, the origin of the elements, starting from water, in Humphrey’s cosmology involves beta decay, which introduces antineutrino and neutrino backgrounds (Humphreys, 1994, pp. 72–73; 2019, private communication).

Even in the secular literature not everyone agrees that the relic neutrino background exists. It is possible that the reasons given may also apply to creationist models. I will discuss two alternative scenarios, one due to Beacom et al. (2004) and the other due to Davoudiasl et al. (2018).

Basically, in the Beacom et al. scenario reactions between cosmic background or relic neutrinos result in their conversion into the scalar particles.

However, some “secret interactions” have to be assumed. For example, one “secret” interaction is:

$$\bar{\nu}_e + \nu_e \rightarrow \phi + \phi$$

Here the reaction of an electron antineutrino with a relic neutrino destroys both, while producing two light scalar particles. These “secret interactions” either may not exist or may not have the strength that has to be assumed. The reactions will not exist if the light scalar particles  $\phi$  do not exist, or the actual masses of the light scalars may make the above reaction improbable. Future experiments will decide. Beacom has already abandoned this idea (Hannestad, 2005, p. 1; Ng and Beacom, 2005, p. 2), but the reasons involve beliefs about cosmology which creationists may find doubtful.

Davoudiasl et al. (2018) proposed that the cosmic neutrino background left over from the big bang is mostly absent in our galactic neighborhood. Their hypothesis is that neutrino masses can be zero in vacuo and may be generated by the local distribution of dark matter through a feeble long range scalar force. This force is repulsive and expels low energy neutrinos from any region where dark matter has a significant presence, such as our neighborhood. They assume that the local dark matter population generates a neutrino mass of about 0.1 eV. The dark matter population acts like a repulsive potential barrier near the Solar System. The cosmic background neutrinos exist in other parts of the universe and are characterized today by kinetic energies of the order of  $10^{-4}$  electron volts. Such low energy neutrinos and antineutrinos would not have enough energy to enter our region of space and would be repelled from it.

If the Beacom et al. (2004) or the Davoudiasl et al. (2018) scenarios or something like them should prove correct, then that would largely free us from the criticisms of the type that Zhou

(2011) gave for the papers of Wang et al. (2006), Gabriel and Nandi (2007), and Sher and Triola (2011). These theories are vulnerable to falsification by future experimental or observational findings, as all significant theories should be. If they are correct in that there is no relic neutrino background in our neighborhood, or repulsive dark matter is prevalent out to the Large Magellanic Cloud, then the neutrinos from SN1987A should be able to reach us. This would save some basic ideas, including the one of Fardon et al. (2004) and ours from the Zhou (2011) type criticism. However, one notes that in the Fardon et al. model one expects overdensities of neutrinos inside galaxies rather than the Beacom or Davoudiasl et al. regions inside galactic halos where background neutrinos have been either expelled or destroyed in secret reactions. Clustering of neutrinos caused by gravity had been discussed by Wigmans (2002) or Adler (2008, 2009). Wigmans thought that dark matter clumps to form a halo around galaxies, including our own. Adler explored the possibility that it could also clump around the Sun or around planets. At one time, when neutrino masses in the range from 30 to 100 electron volts were thought possible, some considered the possibility that neutrinos were the dark matter (Roulet, 1993). Clumping of neutrinos was modeled, or distributions of neutrinos were found that would explain galaxy rotation curves. Experiments have since ruled out neutrino masses that large. However, clumping of non-zero mass neutrinos is still considered possible although neutrinos are too light to allow them to be dark matter. In the Fardon et al. model there is the circumstance that the neutrino mass is *inversely* proportional to the neutrino density. Fardon et al. expect a larger neutrino density, not a smaller one, contrary to Davoudiasl et al. (2018).

Hence, a good answer to the Zhou criticism is probably not to deny the existence of the cosmic relic neutrinos

in the solar neighborhood, but rather to assume that the masses of the scalar particles, the acceleron particles, are different enough from the neutrino masses that Zhou's assumed reactions are very improbable. The neutrino masses are thought to be less than 1.1 electron volts, and we have seen that the acceleron mass favored by our scenario is considerably larger, at least 59 electron volts. Since the neutrinos from SN1987A have kinetic energies in the MeV range it is possible to convert, during collision with the lower energy background neutrinos, some of this kinetic energy into rest mass of the scalar particles, the ones produced in the reaction considered above [ $\bar{\nu}_e + \nu_e \rightarrow \phi + \phi$ ], and still conserve momentum. However, the reaction becomes less probable when the rest masses of the neutrinos and the scalar particles are found to be more and more different (Weiler, 1982, p. 234; Kolb and Turner, 1987, p. 2895; Yoshida et al., 1997, p. 551).

An analogy of collisions with basketballs or bowling balls may help here. If a basketball collides with another basketball, then in a direct collision, one ball stops losing its kinetic energy and the other ball goes off with a gain in kinetic energy. Kinetic energy is a scalar quantity with no direction. Also, when a golf ball collides with a much heavier bowling ball it glances off with very little change in kinetic energy. When the colliding particles are considerably different in mass, neither particles change their kinetic energy very much.

Zhou also considered reactions where the electron antineutrino is scattered by an acceleron:

$$\nu_i + \phi \rightarrow \nu_i + \phi$$

For this reaction, if the acceleron is much heavier than the antineutrino, then basic physics shows that in most cases there will be very little kinetic energy lost by the antineutrinos as they move past. If there is a direct collision, a

backward scattering can take place, but there will still be antineutrinos detected at Earth from the other cases.

Zhou himself concluded that some other possible reactions were of no consequence or not appropriate for our case. This included consideration of cooling of supernova cores by emission of the scalar particles, but Zhou made some assumptions which are not applicable to our case.

Hence, for the acceleron masses that support our scenario where the acceleron field remains abnormally large for ten to a thousand years, reaction of the SN1987A neutrinos with cosmic relic neutrinos is not very likely. Also we are not concerned with the size of the Yukawa coupling which Zhou tried to rule out. This nullifies any criticism of the type given by Zhou that would claim that the SN1987A data forbid the existence of light scalars such as our acceleron particle.

### Criticism Regarding Supernova Rates in Our Galaxy

Wallner et al. (2016) estimated the rate of supernovae in our local galactic neighborhood within a distance of about 100 parsecs from Earth at 1 supernova every 2–4 million years (Myr), based on the total SN-rate in the Milky Way ( $2.0 \pm 0.7$  per century).

Biblical creation constrains the timeframe of Earth history and standard theories of stellar evolution do not fit the timeframe. In the astronomy literature, these standard theories have been used to estimate the rate of nearby supernovae. Gehrels et al. (2003) gave a value of 1.5 per Gigayear for core-collapse supernovae occurring within 8 parsecs [26 light years] of Earth. Van den Bergh (1993) gave a value of  $1.2^{(+1.7, -0.7)}$  supernovae per century in our galaxy based on theories of stellar evolution, but  $2.6 \pm 1.2$  per century based on historic supernova rates for supernovae that exploded within

4,000 parsecs [about 13,000 light years] of Earth. Several authors have noted that, if mass extinctions occur when supernovae are within a distance  $R$ , which is of the order of 3 to 10 parsecs, then the supernova rate is too small to explain mass extinctions observed in the conventional geologic column (van den Bergh, 1994; Gehrels et al., 2003). Melott (2016) seemed to question these conclusions, pointing to the detection of Fe-60 in ocean-floor crust.

In Chaffin (2017), a paper by Firestone (2014) was cited which gave radiocarbon evidence for numerous (23) nearby ( $d < 300$  parsecs) supernovae. Subsequently, a criticism by Melott et al. (2015) appeared. Interestingly, although the Firestone paper appeared in *The Astrophysical Journal*, the subsequent Melott et al. criticism appeared in the *International Journal of Astrobiology*. Melott et al. point out that, if the rate of supernovae implied by the Firestone (2014) paper were true, this would have strong implications for the irradiation of the Earth. They wrote: "... at this rate, the mass extinction level events due to SNe [supernovae] would be more frequent than 100 Myr." Since this was an unacceptable rate, the data sets used by Firestone were questioned, and it was claimed that Firestone's results were not valid. They did not dispute indications of relatively nearby supernovae, pointing to Fe-60, a likely supernova byproduct, detections on Earth. They only disputed the large number of recent supernovae claimed by Firestone. In Chaffin (2017), only one nearby supernova was needed, hence the Melott et al. criticism of Firestone (2014) would not change the main conclusions, only possibly whether Firestone's results should be accepted.

On a related thread, a paper by Retejum (2019) recently analyzed bristlecone pine tree-ring data from the mountains of the western United States and analyzed growth rates near the known dates for historic supernova, AD 185, 393, 1004, 1054, 1181, 1572,

and 1604. Significant but temporary decreases in tree-growth rates following these supernovae were reported.

## The Local Bubble

Figure 6 shows the Sun in relation to a map of the Milky Way Galaxy. In trying to identify recent supernovae, astronomers recognize features of the Milky Way Galaxy known as the Local Bubble and the nearby Loop I Bubble (Figure 7). This should not be confused with the “heliosphere.” The heliosphere is a bubble-like region of space which surrounds and is formed by the Sun. It is the cavity formed by the Sun in the surrounding interstellar medium. The Local Bubble is a larger region, of average radius 100 parsecs, of low density gas, about 0.005 atoms per  $\text{cm}^3$ , although the density is larger at about 0.1 to 0.3 atoms per cubic centimeter within a local cloud where the Sun resides (Sfeir et al., 1999). Astronomers have attempted to identify candidates for the supernovae which would have blasted out this region of low-density gas within the galactic disk.

We have seen that Firestone was criticized for the high rate of supernova explosions (SNe) that his findings implied. However, to blast out the Local Bubble seems also to be incongruous with expectations for the supernova rate near the Sun. Benítez et al. (2002, p. 1) wrote: “The paucity of SNe in the Galaxy makes it very unlikely that several isolated SN explosions would happen in short succession within such a small region, but about 20% of all SNe originate in OB star associations, and are therefore strongly clustered in time and space.” We will discuss these “OB associations” later.

One clue to the affect of supernovae on the Local Bubble involves the radioactive nucleus  $^{60}\text{Fe}$ . This isotope  $^{60}\text{Fe}$ , with half-life  $t_{1/2} = 2.62 \times 10^6$  years, is produced inside supernova precursors and ejected into space during the explosions (Rugel et al., 2009; Wallner

et al., 2015b). The 2.6 million year half-life caused astronomers to expect that some amount of  $^{60}\text{Fe}$  should survive the light-years of long-distance travel and be deposited on Earth when supernovae debris arrived.

What clues are there for which supernovae carved-out the Local Bubble? There is an emitter of pulsed radio signals, a pulsar, named “Geminga” which is about 250 parsecs from Earth (Faherty et al., 2007). The precursor of Geminga pulsar was initially favored as a candidate star, but it does not seem to fit the evidence. Breitschwerdt et al. (2016) sought to identify these supernova candidates by modeling the motion of radioactive  $^{60}\text{Fe}$  expelled from hypothetical supernovae. This would help explain where the  $^{60}\text{Fe}$  detected in seafloor sediments originated (Knie et al., 2004; Koll et al., 2019). Uncertainties in the history of local gas densities make these simulations difficult. Nevertheless, based on computer simulations, Breitschwerdt et al. proposed an aggregate of candidates including two with location shown in Figure 7 which hypothetically

exploded 2.3 and 1.5 million years ago. The supernovae remnants of such great age would have long since dispersed, so Breitschwerdt et al. were not discouraged

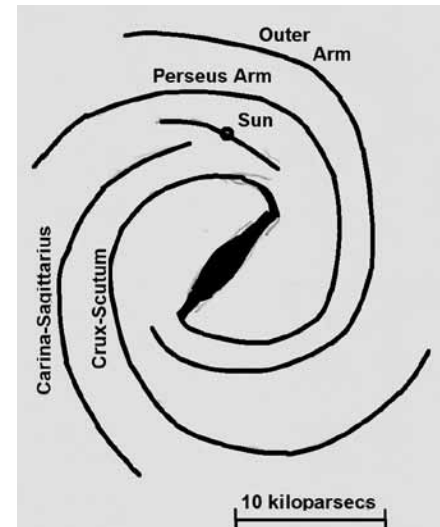


Figure 6. A sketch of the Milky Way Galaxy showing the Sun in relation to the known arms (Perseus Arm, Carina-Sagittarius Arm, Crux-Scutum Arm, and Outer Arm) of the spiral structure. The Sun is in the Orion-Cygnus Arm.

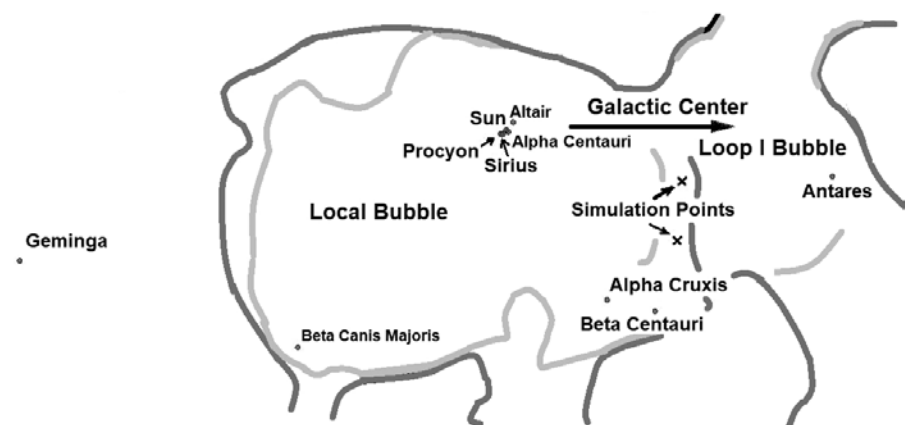


Figure 7. The Local Bubble and Loop I Bubble viewed in the galactic plane. These are regions of the Milky Way Galaxy, including the Sun, where the density of gas is low compared to surrounding space within the galactic disk. Precise data for gas density contours, upon which this sketch is based, may be found in Sfeir et al (1999). Two hypothetical points identified by Breitschwerdt et al. (2016) are labelled “simulation points” in the figure, denoting where some exploding stars were located.

by the lack of anything to be detected at those locations.

The average radial extent of our bubble is about 100 parsecs (Sanders et al. 1977; Snowden et al. 1990; Sfeir et al. 1999), although it is not spherical. The Sun is relatively near to the edge of this bubble and to a neighboring bubble called the “Loop I Bubble.”

Some stars are found in OB associations, such as the nearby Scorpius-Centaurus Association. The letters OB refer to spectral classes O and B. Antares, a name meaning “the enemy of Mars,” is the brightest star in Scorpius, and resides inside the Loop I bubble (Figure 7). Associations such as this are thought to be responsible for a significant fraction of all Galactic supernova progenitors. An increase in supernova frequency would be expected near these associations.

Melott (2017) revised the presumed distance to the primary source of the  $^{60}\text{Fe}$  to about 50 parsecs based on the simulations of Fry et al. (2016). This is about a factor of two smaller than Breitschwerdt et al.’s values of 91 and 96 parsecs. Melott said that the sources were “probably originating within the Tuc-Hor stellar group, which may have been at the appropriate distance at the appropriate time.” This Tuc-Hor group was explored by Krauss et al. (2014). The fact that a factor of two difference in distance estimates is possible shows that there is not very much accuracy in these simulations.

Davies (2007) gave the following description of a typical supernova remnant (SNR):

The diameter of a mid-sized SNR can be as much as twenty parsecs. To put this size into perspective, the distance from the Earth to the star Alpha Centauri is about three-fourths of a parsec. An average SNR is therefore sufficiently large to potentially contain a star cluster containing thousands of stars within its extended volume.

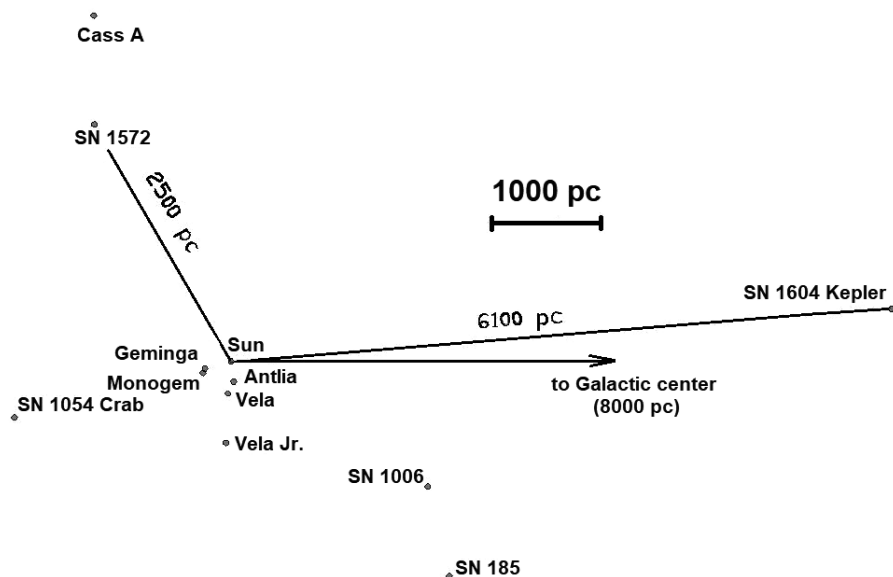


Figure 8. The positions of historic nearby supernovae and remnants projected onto the galactic plane.

Davies went on to discuss models of supernova remnant expansion (Davies, 1994, p. 243): “Using a sample ISM density of  $n=0.001$  gives an expected largest diameter of around 140 parsecs.” This largest diameter would be for a remnant of near 6,000-year age, which the Crab Nebula has not reached, currently being only 20 parsecs in diameter.

Davies (1994, p. 175) described two types of supernova remnants, plerions or “filled center” types and shell types. Furthermore, he wrote:

The shell type comprise those objects distinguished by the conspicuous boundaries that are formed by the expanding cloud of stellar debris as they cause a “snow-plow” effect through the interstellar medium (I.S.M.).

In the case of a supernova occurring within the Local Bubble prior to the Genesis Flood, one would expect the current size of the remnant to be close to Davies’ maximum size of 140 parsecs. Thus, the shell would have merged with the edges of the Local Bubble and

would be difficult to distinguish from it. The Sun would now be encompassed by this large, very diffuse remnant, and one wonders whether observational data could test this conclusion.

One could consider whether our part of the Galaxy is special. If this pulse of neutrinos reached Earth at the time of the Genesis Flood, then we have said that the larger acceleration field in our neighborhood would remain for ten to a thousand years or so, with a resulting change in nuclear decay rates. In other parts of the Galaxy there may have been no such change because no supernova was nearby. Is there evidence for this? Figure 8 shows the distribution of nearby historic supernova and supernova remnants near the Sun.

While this variation in nuclear decay with galactic position is a matter for future study via observational astronomy, one might point to statements regarding galactic structure by Ward and Brownlee (2000, p. 29; 2002, p. 96), Gonzalez, Brownlee, and Ward (2001a, 2001b), and Gonzalez and Richards (2004).

The center of our galaxy, the “bulge,” is a much more violent region laced with ionizing radiation, higher supernova frequency, and the danger from the 4-million solar mass black hole (Ghez [now a Nobel prize winner] et al., 2003, 2005), whereas points farther from the galactic center than the Sun have fewer heavy elements than our location. Thus isotope abundances do vary from place to place in the Galaxy. One could also point to data which show variations in  $^{26}\text{Al}$  (half-life 710,000 years according to Parrington et al., 1996) concentration from place to place in the Galaxy (Prantzos and Diehl, 1996; Diehl et al., 2006). Prantzos and Diehl (2006, pp. 52–55) point to “hotspots” in the 1.8 MeV gamma ray intensity from  $^{26}\text{Al}$ . The same variation is known for  $^{44}\text{Ti}$  (The et al., 2006) and  $^{244}\text{Pu}$  (Wallner et al., 2015a). The half-life of  $^{44}\text{Ti}$  is 128 years, and in most models is one of the isotopes produced abundantly by core-collapse supernovae. It emits a characteristic 1.157 MeV gamma-ray line. The et al. (2006) wrote:

In this paper we estimate what the gamma-ray sky of  $^{44}\text{Ti}$  sources would be expected to look like by adopting an average  $^{44}\text{Ti}$  source model having a characteristic source event recurrence rate,  $^{44}\text{Ti}$  yield per event, and spatial distribution. We compare this to the present-day gamma-ray survey and find apparent and serious conflicts.

There were not enough Galactic supernova remnants detected. In fact the one called Cas A was the only one with appreciable gamma ray intensity that could be identified with  $^{44}\text{Ti}$ . Cas A is at a distance of 3,400 parsecs and the remnant observed on Earth is thought to be 340 years old. Here SN1987A is discounted since it did not occur in the Galaxy but in the Large Magellanic Cloud satellite.  $^{44}\text{Ti}$  was subsequently also detected in the Vela Jr. supernova remnant (Delahaye et al., 2010, p. 29), shown in Figure 8.

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## Appendix A

When I repeat the calculations of Resnick, Sundaresan, and Watson (1973), I find the following.

$$\Gamma(\phi \rightarrow 2\gamma) = \frac{g_{\phi e \bar{e}}^2}{4\pi} \left( \frac{e^2}{4\pi} \right)^2 \frac{m_\phi}{4\pi^2} \left( \frac{m_\phi}{m_e} \right)^2 \left[ \frac{1}{3} \right]^2$$

$$\frac{g_{\phi e \bar{e}}^2}{4\pi} = \frac{1}{2\pi} m_e^2 \frac{G_F}{\sqrt{2}}$$

Apparently,  $(e^2/4\pi)^2$  stands for the square of the fine structure constant  $\alpha$  (alpha in Heaviside Lorentz units),  $(1/137.036)^2$ .

$$G_F \left( \frac{e}{4\pi} \right)^2 = 1.166 \times 10^{-23} \text{eV}^{-2} \left( \frac{1}{137.036} \right)^2$$

$$= 6.209 \times 10^{-28} \text{eV}^{-2}$$

$$G_F (e/4\pi)^2 / (3157.06) = 1.9667 \times 10^{-31}$$

$$\Gamma(\phi \rightarrow 2\gamma) = (1.9667 \times 10^{-31} \text{eV}^{-2}) m_\phi^3$$

$$\tau = \frac{h}{\Gamma} = \frac{6.582173 \times 10^{-16} \text{eV} \cdot \text{s}}{1.9667 \times 10^{-31} \text{eV}^{-2} m_\phi^3}$$

$$= 3.35 \times 10^{15} m_\phi^{-3}$$

This is smaller than Sato and Sato's  $6.6 \times 10^{16} m_\phi^{-3}$ .

# A Correct Understanding of Symmetry-Breaking in Chiral Organic Synthesis

Charles A. McCombs

## Abstract

In recent years, many scientists have referenced the work of mathematicians D.K. Kondepudi and G.W. Nelson who claim that symmetry breaking states are extremely sensitive to small symmetry breaking interactions, and small external influences can play a role in the selection of one outcome from other possible outcomes. Kondepudi and Nelson have previously concluded that the energy barrier for selecting one outcome over the other should be on the order of  $10^{-15}$ – $10^{-17}$   $kT$  based on their earlier calculations. Kondepudi and Nelson then studied mathematically the rate equations from a hypothetical chemical reaction to see if symmetry breaking leading to bifurcation could create new homochirality in that chemical reaction. Although symmetry occurs in some chemical reactions that produce chirality, the breaking of that symmetry as it relates to forming new homochirality, the alleged formation of only one outcome and the bifurcation they propose occurs contrary to the chemical literature. For this reason, it was necessary to evaluate their claims because of the potential impact of their discovery if verifiable. Unfortunately, it had to be concluded that the Kondepudi and Nelson math equations for symmetry breaking are not relevant to chemical systems, and their claims for creating new homochirality were only assumed, never substantiated.

The synthesis of organic molecules has always been an important part of organic chemistry, and in recent years, the synthesis of “chiral” organic molecules has received much attention. The word “chiral” is derived from the word “chirality” meaning handedness, and a chiral carbon exists when that carbon atom has four different bonds attached to it. When four different

bonds exist around a carbon, that carbon atom will exist as two distinctly different structures. Those two structures differ only as each being the non-superimposable mirror image of the other and because they are mirror images of each other, hence the term handedness, those images are designated as either the left-handed isomer or the right-handed isomer. In

this paper, the labels “D” or “L” will be used as subscripts to distinguish between the right-handed and left-handed isomers since that was the method used by Kondepudi and Nelson in their published articles.

[**Author’s Note:** In organic chemistry, mirror image isomers are frequently labeled as either “D” or “L” to distinguish between their handedness, but to be correct, “D” or “L” only refer to the direction that isomer rotates polarized light; rotation to the right is given as “Dextrorotatory” and rotation to the left is “Levorotatory.” Unfortunately, there is no correlation between handedness and polarized light rotation.]

Of special interest in chiral organic synthesis is the topic of homochirality; a homochiral molecule is a molecule existing as one of the two possible mirror-image isomers. The synthesis of such homochiral molecules has become increasingly important for understanding the chemistry of life’s chiral systems, and the need for synthesizing a single chiral isomer is more important than ever because all of the chiral molecules found in the human body are essentially 99.9%+ of a single chiral isomer without exception. For this reason, the evolutionary origin of homochiral molecules is the most difficult topic to explain when it comes to understanding the origin of life on Earth. For many scientists, that is the “mystery” keeping them from knowing the origin of life, and this mystery still exists today (Cohen, 1995, pp. 1265–1266). For a discussion of homochirality, see Coppedge (1971), Helmick (1976), and Murphy (2013). Ever since the presence of unique homochirality was discovered in living organisms, scientists have tried, but failed to explain how unique homochirality came to exist in living organisms. There have been many attempts to explain the origin of homochirality, and all these attempts have failed for one reason. There is no natural process that can explain how new homochirality can be formed without some form of pre-existing homochirality already present, a known fact of chemistry.

In chemistry, there are many examples of how the homochirality of a starting material can be transferred to the final product. Either the homochirality of the starting material is directly incorporated into the final structure, or indirectly as other factors influence how the new chiral carbon bonds are formed, but there is not a single example of forming a homochiral product from achiral substrates without some form of asymmetric induction. Therefore, when mathematicians Kondepudi and Nelson claimed that homochiral products might be prepared from achiral substrates after a symmetry breaking process based on conclusions obtained from their math equations, their claim caught the attention of many scientists (Jafarpour et. al., 2015, 2017; Michael Stich et al., 2016; Ribo et al., 2017).

Kondepudi and Nelson (1984) claim that symmetry breaking in non-equilibrium systems can occur in several ways, and the breaking of symmetrical states is extremely sensitive

to small interactions. Kondepudi and Nelson extended the general idea of symmetry breaking they saw in their system and applied it to a chemical system, and then compared the sensitivity of symmetry breaking leading to bifurcation with the selective formation of one chiral product being formed from a choice of two possible isomers. In order to extend symmetry breaking and bifurcation to a chemical system, they presented hypothetical chemical reactions and studied the kinetics of the derived rate equations in an effort to show that there was a very real mathematical possibility for creating new homochirality.

Kondepudi and Nelson (1984) further claim that when a chemical system is operated near equilibrium, the left- and right-handed molecules will be produced in equal amounts, but if the system is “far” from equilibrium, molecules of one kind could be produced in much larger quantity than the other, provided the kinetics have appropriate auto-catalytic steps. Because of the many claims that were made, it was necessary to determine if there was a possibility for new homochiral products to be formed in this way.

## Symmetry Breaking in a Physical System

The process of “symmetry breaking” described in Kondepudi and Nelson’s publications refers to a “system with symmetry” changing to a “system without symmetry.” Although one can imagine several ways in which symmetry can be broken, the system studied by Kondepudi and Nelson was not a simple system; it was a hypothetical system containing a bifurcation point where, because of bifurcation, there would be two possible outcomes after symmetry is broken. Kondepudi and Nelson further imagined that symmetry breaking initiated simultaneous bifurcation in their system, and once bifurcation occurred, only a single outcome would be possible because of the low energy required to break that symmetry.

Using all of the claims and descriptions made by Kondepudi and Nelson for what their system was supposed to do, their system can best be described as a spherical ball balanced on a fulcrum (see Figure 1).

Even though the ball-on-a-fulcrum description was not presented by Kondepudi and Nelson, this is a classic example of a system at symmetry taken from physics, and fully incorporates the description of the Kondepudi and Nelson system. When this system is balanced and symmetrical, there are two equally possible ways for the ball to fall. In order to understand the concept of “symmetry breaking,” consider

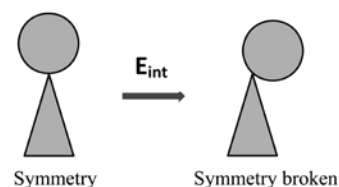


Figure 1. Ball on a fulcrum.

that balanced ball falling off of that fulcrum as shown in Figure 1. Once symmetry is broken by either internal or external forces, bifurcation simultaneously occurs. Although there are two possible outcomes before bifurcation, only one outcome is observed after symmetry was broken. When dealing with a symmetrical state as thus described, it would not take much energy to disturb (break) the symmetry of that ball balanced on a fulcrum. Thus, symmetry breaking leading to a single outcome is a reasonable conclusion in this model.

## Symmetry in Chemical Reactions

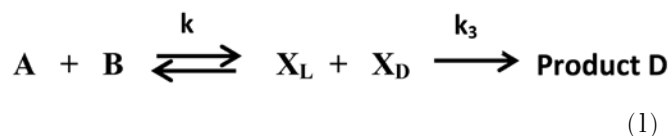
Believing that symmetry breaking can lead to a single outcome in their hypothetical system, Kondepudi and Nelson wanted to extend the concept of “symmetry breaking” to organic chemical reactions forming chirality with the expectation of forming a single homochiral product. The ball-on-a-fulcrum model described above may have many similarities with a chemical reaction forming chirality, and although not an exact representation of a chemical reaction, some organic reactions can possess symmetry and a bifurcation point. Among organic chemists, it is understood that symmetry can be created in a chemical reaction for example when a planar transition state is formed as in  $S_N1$  type reaction mechanisms. Furthermore, the planar transition state creates the opportunity for two possible products to be formed (bifurcation) and bifurcation occurs because reactions on this planar transition state must approach from either the top or the bottom of the plane of symmetry.

Kondepudi and Nelson took the assumptions and conclusions derived from study of their mathematical equations in physical systems, and proposed that symmetry breaking and bifurcation should be expected to occur in chemical reactions as well. It was further believed that since the energy required for breaking symmetry in a physical system is very low, the energy required to selectively form a single chiral product in a chemical system should be equally low. If these assumptions hold true in chemical systems forming chirality, those chemical reactions should be capable of forming only one chiral isomer, a result not expected from the chemical literature.

## The Kondepudi-Nelson Reactions

In order to show symmetry breaking and bifurcation in a chemical system, Kondepudi and Nelson created hypothetical chemical equations to prove their hypothesis. According to the Kondepudi and Nelson model, substrates A and B are the two starting materials, each having no chirality, and these substrates can combine chemically to produce a chiral product X at rate k. Product X, being chiral, is a mixture of the left-handed isomer ( $X_L$ ) and the right-handed isomer ( $X_D$ ), and since Kondepudi and Nelson expect to see these isomers

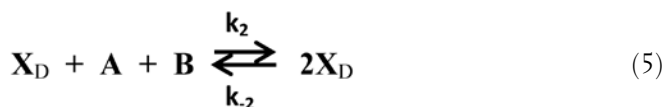
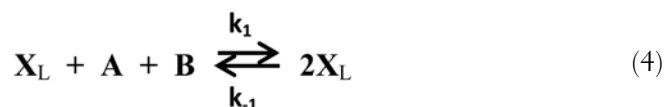
formed unequally, the individual rate constants are shown as  $k_L$  and  $k_D$  to represent the rate at which each chiral isomer is formed. Kondepudi and Nelson also show  $X_L$  and  $X_D$  as further reacting to form achiral product D at a rate of  $k_3$  according to the following chemical reaction:



Based on this chemical reaction, Kondepudi and Nelson derived the following rate equations:



Kondepudi and Nelson then assume that  $X_D$  and  $X_L$  can auto-catalytically reproduce more chiral product at different rates according to these reactions:



Then,  $X_L$  and  $X_D$  react to form D irreversibly.



From these chemical reactions, one can write the following rate equations:

$$\frac{dX_L}{dt} = k_{1L}AB - k_{-1L}X_L + k_{2L}ABX_L - k_{-2L}X_L^2 - k_3X_LX_D \quad (7)$$

$$\frac{dX_D}{dt} = k_{1D}AB - k_{-1D}X_D + k_{2D}ABX_D - k_{-2D}X_D^2 - k_3X_LX_D \quad (8)$$

If one assumes,

$$\alpha = (X_L - X_D)/2 \quad \text{and} \quad \beta = (X_L + X_D)/2$$

The appearance of asymmetric solutions for  $(AB) > (AB)_c$  will occur when:

$$(AB)_c = \frac{s + [s^2 - 4k_2^2k_1]^{1/2}}{2k_2^2}$$

$$\text{when } s = 2k_2k_1 + 4(k_2^2k_1)/(k_3 - k_2)$$

According to Kondepudi and Nelson, when the value of  $(AB)$  exceeds the critical value  $(AB)_c$  and if the supplemental solution  $(k_3 - k_2) \neq 0$  is satisfied, the following asymmetric steady states  $(\alpha_A, \beta_A)$  will appear:

$$\alpha_A = \pm[\beta_A^2 - K_1AB/(k_3 - k_2)]^{1/2} \quad (9)$$

$$\beta_A = (k_2AB - k_1)/2k_2 \quad (10)$$

According to these equations, there is a necessary condition requiring that  $k_3$  must be greater than  $k_2$  (Equation 9) so that  $\alpha_A$  and  $\beta_A$  can be real numbers. If this condition is met, there should be a set of reaction parameters where the concentration of  $X_D \neq X_L$ , and their conclusion of inducing new homochirality as the result of symmetry breaking will have been proved.

## Results and Discussion

The addition of hydrogen bromide to 2-butene is an excellent example of the formation of a chiral product from two achiral substrates when we assume 2-butene is substrate A and hydrogen bromide is substrate B (see Figure 2).

The expected product from this reaction would be an equal mixture of the left- and right-handed chiral isomers of 2-bromobutane, and if the Kondepudi and Nelson claims are correct, conditions could be found where symmetry breaking and bifurcation should form a different ratio of products.

In order for Kondepudi and Nelson to prove their claims, they would have to show the factors or conditions that must be met to form an unequal mixture of  $X_D$  and  $X_L$ . Unfortunately, *they made four bad assumptions and two major errors*, and consequently, they failed to realize that physical systems do not automatically correlate with chemical systems, that symmetry breaking is different than shifting the equilibrium,

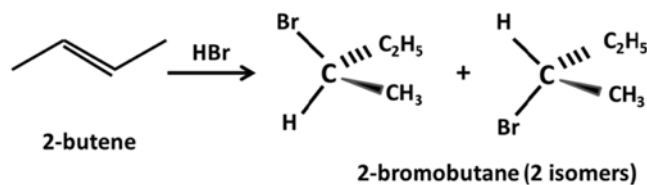


Figure 2. Reaction to form 2-bromobutane as two chiral isomers.

or that bifurcation can selectively choose one chiral isomer over another. Although symmetry and a bifurcation point are present because of the mechanism of the reaction that forms 2-bromobutane, we will learn that it is symmetry that creates the bifurcation point. We will also learn that the breaking of symmetry does not *cause* the reaction to proceed; symmetry is broken as the *result* of the reaction. As mentioned earlier, there are many similarities with Kondepudi and Nelson's physical system, but it was the non-similarities with the chemical reaction that Kondepudi and Nelson failed to consider as being a problem. This paper will show that chiral product formation has nothing to do with symmetry breaking, and un-aided bifurcation is the actual reason why one chiral isomer will never be formed in a chemical reaction.

## The Interaction Energy

In their earlier work, Kondepudi and Nelson (1981) claimed that systems that break symmetry are so sensitive that an interaction energy ( $E_{int}$ ) greater than  $10^{-15}$ – $10^{-17}$   $kT$ , where  $k$  is the Boltzmann constant and  $T$  is the temperature, is sufficient to break symmetry. According to Kondepudi and Nelson, such energies are within the range of parity violating weak-neutral-current interactions. Chiral interaction energies due to a combination of electric, magnetic, gravitational and centrifugal fields, even when high field strengths are considered, are found to be less than  $10^{-19}kT$ . Therefore, if the concept of symmetry breaking could be applied to a chemical system, that interaction energy should be more than enough to promote strong chiral selectivity.

Unfortunately, the energy requirements of the Kondepudi and Nelson system and a chemical reaction are very different. In a chemical reaction, the required symmetry must be created in the transition state, and the creation of the symmetrical transition state requires additional activation energy for such a reaction to proceed. In the Kondepudi and Nelson system, symmetry is already present with no mention of the energy required to get the system to a point of symmetry, and they assume that their estimated interaction energy ( $E_{int}$ ) is enough

to initiate and complete any chemical reaction. *This is their first bad assumption.* In the Kondepudi and Nelson model, the sequential process of symmetry breaking, bifurcation and single outcome formation was a domino effect aided by the ball's initial potential energy and the downward force of gravity; none of which would be present in a chemical reaction. The Kondepudi and Nelson system may have provided the results they wanted to achieve, but there is no reason to believe that results from their physical system will correlate with a chemical system.

## Shifting the Equilibrium

To achieve their goal, Kondepudi and Nelson say that symmetry breaking must occur under non-equilibrium conditions, and when the equilibrium is shifted "far" from equilibrium, bifurcation will occur in a physical system. To claim symmetry breaking in a chemical system, they must be assuming that a ball balanced symmetrically on a fulcrum is analogous to a chemical reaction at equilibrium, and by analogy, they must be assuming that symmetry breaking is the result of shifting that equilibrium. However, *this is their second bad assumption.* A chemical reaction at equilibrium means that there is a forward reaction converting starting materials into product, and there is a backwards reaction converting products back into starting materials. When a reaction is at equilibrium, there is a steady state concentration of starting materials and product and that concentration does not change. In chemistry, it is well known that pressure, volume, temperature, and concentration changes can shift the equilibrium of a reaction, but not to a point of bifurcation. Plus, the shifting of the equilibrium cannot be shifted to a point where the reaction is no longer non-reversible, and the shifting of equilibrium never breaks any symmetry if symmetry is present. The idea of shifting equilibrium to a point of bifurcation may be a theoretical exercise in math, but it is not a practical exercise in chemistry.

In a chemical system, the reaction is either at equilibrium or it is not, and it is the reaction mechanism that determines whether or not a reaction is at equilibrium. Furthermore, the ability to create new homochirality can *only* occur when the chemical reaction is NOT at equilibrium. Kondepudi and Nelson created their own problem when they wrote Reactions 2 and 3 as being at equilibrium, a fact not consistent with their original assumption of needing to be "far from equilibrium." By including the reverse reactions in the kinetic equations, Kondepudi and Nelson unnecessarily complicated the reaction equations they were trying to solve. By writing the reactions in this manner, they failed to realize that there is *not* a single example of homochiral products being formed by a reaction at equilibrium, and their math equations have done nothing to suggest otherwise.

## Formation of Product D

The stated objective of the Kondepudi and Nelson paper (1984) was to show that symmetry breaking and bifurcation can lead to a homochiral product, and to accomplish this purpose, Kondepudi and Nelson (1984) wrote a hypothetical chemical reaction to simulate symmetry breaking leading to bifurcation in a chemical system. However, since their reaction was not based on an actual chemical reaction, they failed to realize that the rate equations they wrote did not represent the chemical reaction they were trying to perform. According to the written chemical reaction (Equation 1), the only product that will be formed by this reaction is achiral product D, especially if  $k_3$  is greater than the reverse reactions forming products  $X_D$  and  $X_L$ . *The inclusion of product D in the chemical reactions is their third bad assumption.* The reaction in Equation 6 shows  $X_D$  and  $X_L$  reacting equally and irreversibly to form product D, and as long as  $k_3$  is greater than  $k_2$  from Equation 9, product D will always be the final product, but what is product D? If the goal of the paper was to create new chirality, why would you want to include a reaction that would take away any new chirality after it has been formed? Kondepudi and Nelson show product D as a secondary product of the reaction between  $X_D$  and  $X_L$  and the only mention of product D in the Kondepudi and Nelson original paper (although not specifically mentioned as product D) was to incorporate an element of "competition" or "source of mutual destruction" into the kinetics. The fact that Reaction 6 is included in the reaction is a huge problem that will always prevent the formation of a homochiral product formation.

As the rate equations are written, components  $X_D$  and  $X_L$  will always be formed from their starting substrates A and B, but  $X_D$  and  $X_L$  are also being constantly removed by the reaction to form product D. Since product D is never removed by any reaction, the ONLY product that will accumulate is product D. Since product D was supposed to be a source of "competition" for  $X_D$  and  $X_L$ , it did its job so well that it completely negated the Kondepudi and Nelson's intention of forming one chiral isomer. And even if you consider the possibility that an unequal mixture of  $X_D$  and  $X_L$  might remain after formation of product D, the reverse reactions (in Equations 2 and 3) would quickly remove that inequality. This is an excellent example of what can happen when writing hypothetical chemical reactions or rate reactions not based on real chemical reactions. In chemistry, the written chemical reaction is supposed to be an exact representation of what is occurring within the chemical reaction, not in a math equation.

## Presence of Auto-Catalysis

Kondepudi and Nelson claim that the unequal formation of  $X_D$  and  $X_L$  can result when auto-catalysis is working. Auto-catalysis (or self-catalysis) is the idea that the product of a chemical reac-

tion can catalyze the formation of itself. Kondepudi and Nelson are assuming that since auto-catalysis is working in a chirality forming reaction, and as the left-handed chiral isomer is formed by the reaction, the presence of that left-handed isomer will catalyze the formation of new left-handed isomers beyond its uncatalyzed formation rate. Of course, the same would be true for the right-handed isomer. Kondepudi and Nelson incorrectly assume that when left- and right-handed isomers are present in the same reaction mixture, those chiral isomers will unequally catalyze the formation of their respective chiral products, even though no verifiable evidence was provided to support that claim. *This is their fourth bad assumption.*

In the Kondepudi and Nelson model, Equations 4 and 5 are trying to show the unequal formation of products  $X_D$  and  $X_L$  where each product catalyzes the formation of itself unequally by separate and different rates of catalysis. Unfortunately, there are problems with these equations. First of all, Kondepudi and Nelson are assuming that auto-catalysis is a well-established fact of chemistry and is presented as if it is universally accepted by all chemists, but neither statement is correct. Secondly, Equations 4 and 5 should not have been written to include the catalyst as a substrate of the reaction because the way those Reactions 4 and 5 are written shows  $X_D$  and  $X_L$  as reacting stoichiometrically with substrates A and B instead of catalytically. Besides making the rate equation unnecessarily complicated, there is another problem. Once you remove their so-called catalyst as a substrate, Equations 2 and 3 and Equations 4 and 5 become identical, and being identical, Equations 4 and 5 showing auto-catalysis become unnecessary. Kondepudi and Nelson failed to realize that the reactions in Equations 2 and 3 and reactions in Equations 4 and 5 cannot both be working at the same time. As quickly as components A and B react to form product  $X_D$  or  $X_L$  as in Equations 2 and 3, the reactions given in Equations 4 and 5 have already begun to take place. Although one might argue that both reactions were taking place at the same time, Kondepudi and Nelson failed to realize that the rate constants in Equations 2 and 3 and the rate constants in Equations 4 and 5 cannot both be working at the same time. The rate constant is defined as the “total” amount of product formed in a specified period of time, and for this reason, the rate constants  $k_1$  and  $k_2$  cannot be forming products “in addition to” the rates for  $k_D$  and  $k_L$ . Since only one set of rate constants can be working at one time, rate constants  $k_1$  and  $k_2$  are unnecessary making Equations 4 and 5 redundant, and these auto-catalytic reactions should not have been included in their analysis.

Although Kondepudi and Nelson claim that the uncatalyzed reaction (Equations 2 and 3) occurs with one set of rate constants and the catalyzed reaction (Equations 4 and 5) occurs with a second set of rate constants, there is still no reason to believe that two enantiomers could ever be formed unequally

in their reaction. Contrary to the Kondepudi and Nelson claims, the idea of auto-catalysis forming unequal mixtures of  $X_D$  and  $X_L$  is contradicted by every known chemical reaction that forms chiral products as equal mixtures. In the chemical literature, there are hundreds of examples where mirror image chiral isomers react with other substrates at exactly the same rate forming equal mixtures of chiral products. The Kondepudi and Nelson math equations has not provided any reason to accept their claims of auto-catalysis and to overlook the chemical literature, confirming again that the written chemical reactions are supposed to be an exact representation of what is occurring within the chemical reaction.

In chiral organic synthesis, the only way to form the enantiomers unequally is by adding an additional catalyst; a technique called asymmetric induction (discussed later). It is likely that Kondepudi and Nelson are confusing auto-catalysis with asymmetric induction. In their paper, Kondepudi and Nelson (1984) tried to use the rhodium catalyzed hydrogenation with a chiral phosphine ligand as an example of auto-catalysis, but this is a perfect example of asymmetric induction. As a general rule, the expectation to form  $X_D$  and  $X_L$  unequally is only possible when one of the original substrates of the reaction is chirally enriched or when a third component is added to the mixture to influence product formation at the planar transition state, but Kondepudi and Nelson did neither. In the absence of chirally enriched substrates, Kondepudi and Nelson falsely assume that in Equations 4 and 5, the mere presence of  $X_D$  or  $X_L$  acts as its own catalyst unequally forming new chiral products from substrates A and B. As the Kondepudi and Nelson chemical reactions were written, no additional catalyst was ever present and therefore asymmetric induction cannot be working. Kondepudi and Nelson may have assumed that auto-catalysis was working in their reactions and they may have included it in their math equations as if it was a proven fact, but in reality, no such auto-catalysis was ever present or has ever been proved to be working in a chemical reaction.

## Problem of Bifurcation

Kondepudi and Nelson claim that the breaking of symmetry will cause the chemical reaction to reach a bifurcation point. A bifurcation point means that there will be a point where division occurs; a division point that provides the option for two possible outcomes. However, Kondepudi and Nelson are also assuming that at the exact instance the symmetry of a physical system is broken; the forces that cause symmetry to break also cause bifurcation to proceed in only one direction. This result may be true with a ball on a fulcrum because the ball is already balanced on the bifurcation point, but this is not true in a chemical reaction. *This is their first major error* because with a ball on a fulcrum, the energy required to break sym-

metry does not tell the ball which way to fall off the fulcrum. Kondepudi and Nelson may have thought that bifurcation created the final outcome, but in reality, it was only “chance” that provided that single outcome.

In the Kondepudi and Nelson model, symmetry is already present, but in a chemical reaction symmetry must be created in the intermediary transition state. In the Kondepudi and Nelson model, the bifurcation point (the fulcrum) is already present, but not so in a chemical reaction. Kondepudi and Nelson may want to believe that in a physical system the “breaking” of symmetry causes bifurcation to occur, but in a chemical reaction it is the “formation” of symmetry itself that causes bifurcation. Kondepudi and Nelson may observe bifurcation creating a single outcome in their model system, but bifurcation is the problem that “prevents” the creation of a single outcome in a chemical reaction. In a physical system, the fulcrum is the bifurcation point that creates the option for the ball to fall to one side or the other. Once symmetry was broken, it was only chance, not bifurcation, that determined to which side of the fulcrum the ball will fall.

In a chemical reaction forming chirality, symmetry must be created in an intermediate transition state, and bifurcation occurs at the plane of symmetry that is created in that transition state. Once a chemical reaction has reached its symmetrical transition state, it is this plane of symmetry that provides the option for two possible outcomes (the plane of the chiral carbon is the bifurcation point). As the fourth bond to a carbon is being formed, that new bond can only approach from the top or from the bottom of the plane created in the transition state, and the final outcome is only determined by chance (see Figure 3). Because of chance, the product will always be a 50/50 mixture of both isomers.

Kondepudi and Nelson are assuming that one instance of symmetry breaking in a physical system is equivalent to one chiral isomer being formed by a chemical reaction; this may sound logical, *but this is very wrong*. In chemistry, the chemical reaction describes what happens to the individual “molecules” as they react. Each “molecule” will go through that planar transition state and each “molecule” will have the option to form one of two possible outcomes. With only one instance of symmetry breaking of a ball on a fulcrum, it is easy to get a single outcome. However, there are  $6.023 \times 10^{23}$  molecules per mole of any chemical substance, and when all molecules have reacted, there will be a 50/50 mixture of the two possible outcomes. To expect a different result is to deny the legitimacy of the laws of probability.

## The Necessary Condition

Kondepudi and Nelson (1984) found two equations (Equations 9 and 10) where, if the rate constants and substrate concen-

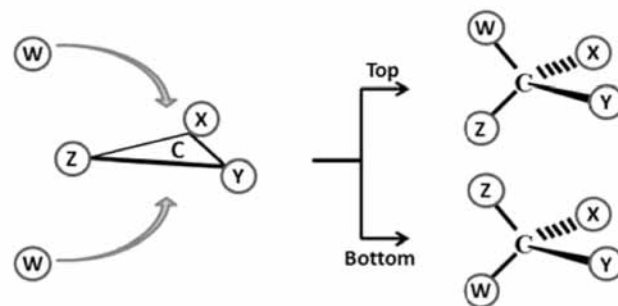


Figure 3. Bifurcation leading to chiral isomers.

trations are real and those values are attainable, there would be proof to suggest that symmetry breaking and bifurcation could induce new homochirality. Within Equation 9, we see the value  $(k_3 - k_2)$  in the denominator of the equation, and mathematically, this value cannot be negative or zero because of its location in the denominator of the equation under a radical. Mathematically, this condition must be met for  $\alpha_A$  of Equation 9 to be real, but there is another problem. Knowing that  $k_3$  is the rate of product D formation and  $k_2$  is the rate of the reverse auto-catalytic reaction, it is equally important to make sure that rate constants  $k_3$  and  $k_2$  also represent real rate values in a chemical reaction (this is their second major error). For this reason, *the condition that  $k_3$  must be greater than  $k_2$  poses the biggest problem of all* even if we assume all their other assumptions were correct. Since auto-catalysis does not exist in any reaction and the need for product D formation in their rate equations is certainly questionable, then the rate values for  $k_3$  and  $k_2$  are not real numbers. If  $k_3$  and  $k_2$  are not real numbers in Equation 9, then there are no parameters that would allow for unequal formation of  $X_D$  and  $X_L$ , and if true, there is no proof for their concept of symmetry breaking leading to bifurcation and the formation of a single chiral outcome.

## A Correct Understanding of Chirality Formation

In general, chemical reactions can only proceed to a product according to a mechanism, and it is this reaction mechanism that dictates how the substrates interact, combine, and proceed towards product formation. In a chemical reaction, it is the reaction mechanism that creates the symmetrical intermediate, and it is this symmetrical intermediate that becomes the bifurcation point. This is where the Kondepudi and Nelson logic fails because bifurcation (without asymmetric induction) does not ever form just one of two possible outcomes. And two, the determining factor for the existence of symmetry is

the reaction mechanism, not the shifting of the equilibrium. The reaction mechanism is what provides the opportunity for symmetry to be created, but there can be other geometric changes that can occur during a chemical reaction. It is also well known that a carbon atom will change its geometry in order to place the carbon atom in a favorable electronic state. This change of geometry will occur whenever there is a change in the number of other atoms attached to the central carbon atom. The change in geometry occurs because the bonds around carbon want to be as far from each other as possible. The geometry will be “linear” if a carbon atom has two other attached atoms; it will be “planar” if there are three other attached atoms, and “tetrahedral” if there are four other attached atoms to that carbon.

In the reaction of 2-butene with hydrogen bromide, after the proton from hydrogen bromide ( $H^+$ ) adds across the double bond of 2-butene, the circled carbon in the reaction intermediate below has only three other attached bonds and therefore that carbon will have planar geometry regardless of the number of bonds present in the original substrate. Once the reaction with the bromide ion is complete, the product now has four attached bonds and the circled carbon becomes tetrahedral in shape (see Figure 4).

Because the intermediate transition state has planar geometry, the bromide ion (analogous to element W in Figure 3) must approach from either the top side of plane or the bottom side of plane. In a chemical system, the plane of the carbon atom is the bifurcation point that forces the fourth bond to approach from one side or the other. In the absence of an outside influencing force, there is an equal probability of approach from the top or from the bottom of the plane by the bromide ion. Therefore, the product will always be an equal mixture of two chiral products.

In order to create new homochirality, the chemical reaction must NOT proceed through a bifurcation point. In the chemical literature, there are many reactions capable of introducing new homochirality into an organic molecule, but in every one of those reactions, the mechanism did not proceed through a planar intermediate. Without a planar intermediate, there is no

bifurcation. When there is no bifurcation, only one product is possible from the reaction, which is the desired outcome when creating new homochirality. However, when planar symmetry is present, there will always be a bifurcation point. It is the process of bifurcation that provides the opportunity for multiple outcomes in a chemical system. Whenever the reaction proceeds through a planar intermediate, the equal formation of  $X_D$  and  $X_L$  is the only possible result. Even if one started with a homochiral substrate ( $A^*$  or  $B^*$ ), as long as the chemical reaction proceeded through a symmetrical intermediate, the product will never contain any new homochirality because all pre-existing homochirality would be lost because of the symmetry of the planar intermediate. These are the facts that Kondepudi and Nelson were trying to overcome by the use of symmetry breaking. Symmetry breaking leading to bifurcation may be a valid observation in the system they imagined, but in chemical reactions, the breaking of symmetry does not occur and it is the symmetry that is created that forces a bifurcation point preventing the actual formation of new homochirality.

### Asymmetric Induction

In the system by Kondepudi and Nelson, a single outcome was achieved by the design of the system, but when chemical reactions proceed through a planar transition state, the product will always be an equal mixture of chiral isomers. In the absence of chiral substrates  $A^*$  or  $B^*$ , the only way for an unequal mixture of chiral isomers to be formed (meaning  $k_L \neq k_D$ ) is by the addition of a third optically active component to the reaction mixture; this process is called asymmetric induction. This third component either by incorporation, complexation or steric hindrance causes unequal access to the plane of the carbon, and unequal access means unequal mixture of products. In certain types of reactions, asymmetric induction can be accomplished by the addition of an optically active catalyst Z because that catalyst forms the product at a rate catalytically faster than those products can be produced naturally (meaning  $k_{cat} > k_D$  or  $k_L$ ). The rhodium catalyst with a chiral phosphine ligand mentioned by Kondepudi and Nelson is an excellent

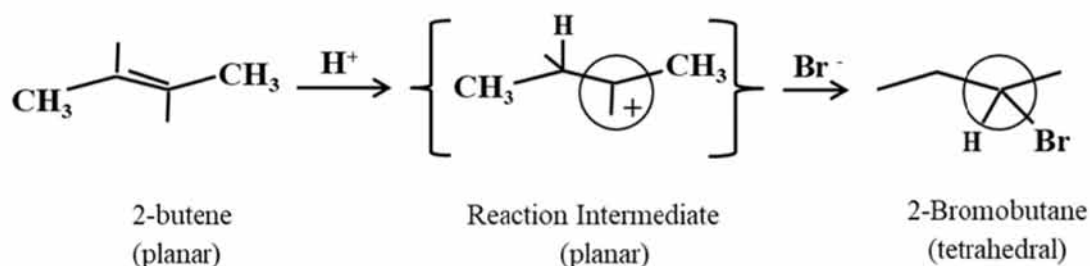
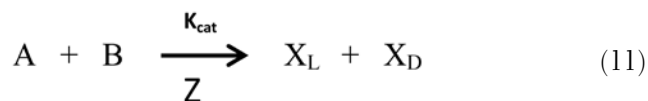


Figure 4. Symmetry changes due to geometric changes.

example of such a catalyst. It is the unequal catalytic effect provided by catalyst Z that allows for the unequal formation of  $X_D$  and  $X_L$  in the product as shown in Equation 11.



If asymmetric induction is present,  $X_L \neq X_D$   
 If not present,  $X_L = X_D$

Yes, there are two possible outcomes, but it was the catalyst Z that provided the mechanism for unequal formation of  $X_D$  and  $X_L$ , not bifurcation. Without an additional substrate like catalyst Z, the products  $X_D$  and  $X_L$  can only be formed in equal proportions due to the equal probability of approaching a two-sided plane of symmetry.

## The Correct Chemical Reactions

Since the chemical reactions need to be written in such a way that the actual products of those reactions are the products we desire to see and study, we need to remove the reaction-forming product D, the reactions showing auto-catalysis and all reverse reactions from the Kondepudi and Nelson equations. By removing these reactions, we are left with Equations 12 and 13 below. Consequently, there are only two equations that need to be evaluated, and coincidentally, these two equations are totally consistent with equations known from the chemical literature and they are the exact equations that a scientist would write for the formation of  $X_L$  and  $X_D$  as products of this reaction (see Figure 5).

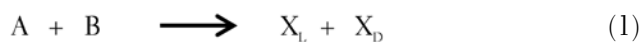


Figure 5. Correct rate equations from chemical reaction.

These new equations show the formation of  $X_L$  and  $X_D$  at rates  $k_L$  and  $k_D$  using much simpler rate equations. In order to show that an unequal mixture of  $X_L$  and  $X_D$  can be formed, one only needs to show that  $X_L$  and  $X_D$  are formed at different rates (meaning  $k_L \neq k_D$ ), but this is exactly the same problem that

Kondepudi and Nelson set forth to solve by incorporating symmetry breaking and bifurcation in the first place. Unfortunately, these reactions still confirm what was already known; that new homochirality cannot be created without some form of asymmetric induction (pre-existing homochirality). By removing those unnecessary reactions, the final reaction equations were greatly simplified, but even after simplifying these equations, it was still impossible to create new homochirality without some form of pre-existing homochirality (catalyst Z) already present. Contrary to their expectations, Kondepudi and Nelson were unable to solve the problem of creating new homochirality, which not surprisingly, explains why evolutionists cannot solve the mystery of homochirality; life and homochirality are not the result of chemical reactions.

## Conclusions

Although the original intent of Kondepudi and Nelson was to show that new homochirality could be formed by a process of symmetry breaking leading to bifurcation, that result was only assumed theoretically and never proven practically. Kondepudi and Nelson may see bifurcation leading to only one outcome in a physical system, but in chiral organic synthesis, bifurcation is the reason why one chiral isomer will never form. Their conclusions are totally contrary to the chemical literature, and nothing was presented to suggest that symmetry breaking leading to bifurcation could ever form just one chiral isomer in a chemical reaction. Kondepudi and Nelson want to believe that their mathematical analysis and more specifically their derived necessary condition proved the possibility of their claim, but unfortunately, a proper analysis of their “necessary condition” does more to prove the impossibility of creating new homochirality than the possibility of forming a single homochiral isomer.

There is a very good reason why the homochirality found in our bodies and life in general was never formed from chemical reactions as evolutionists suggest. The homochirality found in our bodies is there because the homochiral chemical molecules found in our bodies were supernaturally created to have that homochiral structure; they were created to be the way they are found. In chemistry, the formation of new homochirality always requires the pre-existence of another homochiral molecule. This is not just a statement of fact; it also means that existing homochirality, whenever observed, was never formed by a natural chemical reaction. The fact that homochirality exists anywhere means that chemical reactions did not form those homochiral molecules. This is why the origin of life and the subject of homochirality is a mystery to the evolutionists. It is a huge mystery because they have no answer to the question... How did that “first” homochiral molecule get into the “first” living organism if there is no God who created homochirality? To a Bible believer, it is easy. God created those molecules to

be the way they exist because there is no process capable of doing it naturally. Questions like these are easy to answer when you have God's Word telling us that...*all things were created by Him*, and because of the homochirality found in our bodies, we can believe that we are not the product of a chemical reaction, i.e., we are not an accident of nature; *we are fearfully and wonderfully made* in the image of our Creator.

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# The Distribution of Genetic Variants in the Human Genome Reflects Created Diversity

Marshall Jordan\*

## Abstract

Those who believe the record of Genesis account for genetic differences by two mechanisms: created diversity and mutations. For the Y chromosome, mutations appear to be sufficient to explain worldwide Y chromosome diversity. Also, for rare autosomal variants, mutations appear to explain their origins within a few thousand years. However, for common autosomal variants, creationists have proposed that common genetic variants represent created diversity which God put into Adam's genome. Evolutionists oppose this view, insisting that all genetic variation is due to mutations accumulated over millions of years. To test these opposing interpretations of the origin of genetic variation, the pattern of distribution of genetic variants across the human genome was determined to see whether the variants on Y chromosome and the autosomes have different mechanisms of origin. This investigation finds that the concentration of common genetic variants found on the Y chromosomes in the 1000 Genome database is 183 per million bases versus a mean of 2,958 per million bases found on the autosomes, indicating that the Y chromosomes lack created variants. The common variants on the X chromosome fall in an intermediate position of 1,890 per million bases, an indication that some created variants are carried on the X chromosome. Consistent with a mutational origin for all of the Y chromosome common variants and a created origin for most of the autosomal common variants, these findings provide an independent line of evidence supporting recent created diversity as the explanation for most human genetic variation.

## Introduction

In the 1000 Genome Project database (1000 Genomes Project Consortium, 2015), the typical human genome

differs from the reference genome at 4.1 to 5 million positions. The vast majority of these are common genetic variants (CGVs), which have minor

allele frequencies (AF) of 5% to 50%. Rare variants (AF < 0.5%) are 40,000 to 200,000 per genome. Have these genetic variants all come from mutations accumulated over millions of years, or are they explained by created diversity and recent mutation accumulation? Analysis of the 1000 Genome Project database

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Accepted for publication July 15, 2020

was performed in an attempt to answer this question.

Creationists have proposed that most human traits, and the CGVs which cause them, are due to created diversity (Sanford et al., 2018), whereas rare variants are mutations that are responsible for many genetic diseases (Venkataraman and Rivas, 2019; Horton and Lucassen, 2019; Wright et al., 2018). The Created Heterozygosity and Natural Processes Model of human variation explains current human genetic variation consistent with the historical record of Genesis (Jeanson and Lisle, 2016). The model assigns most CGVs (AF > 5%) to the category of created diversity and most rare variants (AF < 0.5%) to the category of acquired diversity, or mutation. Thus, according to this model, most of the 4.1 to 5 million CGVs found in the typical human genome are the result of God's design, and mutations have produced only a small fraction of the variants in a typical human genome.

God may have created about 1% of the nucleotide pairs in Adam's genomes as heterozygous (Carter and Lightner, 2016). This would mean that about 30 million variants were designed, not only in Adam, but also in Eve, if she were a clone of Adam with respect to her autosomes. These variants would have been passed down to their descendants as CGVs distributed on their chromosomes. Computer models by Carter and Powell (2016) show that most of these CGVs would have survived the Flood in the 8 people on the Ark. Mutations have added a few rare variants to these large numbers of created CGVs to produce the genetic variants found on human genomes today.

To understand the implications of the created diversity argument, one should consider the chromosomes of those who survived the Flood. Noah's family contained 10 unique copies of each autosomal chromosome, if the wives of Noah's three sons (which ac-

count for six of the 10) were not closely related. The autosomes of Noah's three sons are combinations of those found in Noah and his wife (the other four copies), and so are not unique. There would also have been nine unique copies of the X chromosome, if Noah and his wife were also not close relatives, two in each daughter-in-law, two in Noah's wife, and one in Noah (which would not get passed to his sons). But there would only have been one Y chromosome, which Noah passed down to his three sons and from which all Y chromosomes on Earth today have descended. Noah's one Y chromosome, by definition, cannot contain any diversity because genetic diversity is due to different bases residing on paired chromosomes. This means that all of the Y chromosome variants in the world today have resulted from the mutations which have accumulated onto the Y chromosomes as they have descended from Noah. As such, there should be few common variants on the individual Y chromosomes of the world, when compared to the autosomes. The total number of variants on a typical man's Y chromosome should be few and should reflect the mutation rate and the years since Noah.

The origin of variants on the X chromosome requires special consideration given the unique history of this chromosome. Adam had only one X chromosome. If Eve's two X chromosomes were clones of Adam's one X, then there should be no created diversity on the X chromosomes today, and only the few mutations accumulated since Creation. In that case, the pattern and concentration of variants on the X chromosomes in the 1000 Genome database should closely resemble the pattern and concentration of variants on the Y chromosomes in the database, both having accumulated all their variants by mutation in a few thousand years. On the other hand, if there is created variation between the two copies of Eve's X chromosome, this created diversity should be found today

as many CGVs on the X chromosomes in the 1000 Genome database.

Based on these considerations, the concentrations of variants on all of the chromosomes in 1000 Genome database was determined to test the hypothesis that human genetic diversity is mostly due to created variation with a few added mutations.

## Methods

The following will be described: the 1000 Genome database, the Python scripts written to analyze the database, the determination of the adjusted sequence length of the chromosomes, the computation of variant concentrations, and the determination of the number of individual Y chromosome variants per male.

The variant call files (VCF) of the 1000 Genome database for each chromosome were downloaded from the International Genome Sample Resource (IGSR) website ([www.internationalgenome.org/Data/Variant Calls/EBI FTP site](http://www.internationalgenome.org/Data/Variant%20Calls/EBI%20FTP%20site)). These files contain the variants from the genomes of 2,504 people from 26 populations from around the world. Each individual contributed variants from two copies each of the 22 autosomes, each female contributed variants from two copies of the X chromosome, and each male contributed variants from one copy of the X and one copy of the Y chromosome.

Custom Python scripts (available at <https://github.com/marshalljordanmd/Big-Data>) were written to count the variants on the chromosome files of the 1000 Genome database and to classify them according to their allele frequencies (AF) into three groups, the rare variants (AF less than 0.5%), the uncommon variants (AF between 0.5 and 5%), and the common variants (AF greater than 5%). Each variant with a listed AF greater than 50% was converted to the minor allele frequency by subtracting from 100%. A Python script ("big\_data.py")

extracted the AF values from the INFO column for each listed variant of each chromosome file.

To compare the Y chromosome variants to the autosomal variants derived from men only, another Python script (“male\_var.py”) was written to compute the AF for each male variant by counting the individual genotypes listed in the columns for the male samples of each chromosome file. A similar script (“genotype.py”) was written to count all of the genotypes, both male and female, and compute the AF for each variant listed in the 1000 Genome files for the autosomes 18–22, the X chromosome, and the Y chromosome. Due to the complexity of the X chromosome, three custom Python scripts were required to count the X chromosome genotypes for the whole sample, male-only samples, and female-only samples. The major difficulty with genotype counting on the X was due to male variants being recorded as haploid, except on the “pseudoautosomal” regions on the tips of the X chromosome, where male variants are recorded as diploid variants.

To compute the concentrations of variants found in each chromosome file, in order to normalize the variant counts to length of bases, a determination was needed of the length of DNA that was sequenced for each chromosome. The chromosome lengths were listed on the 1000 Genome Browser on the website of the National Center for Biotechnology Information ([www.ncbi.nlm.gov](http://www.ncbi.nlm.gov)). Inspection of the chromosomes on this browser showed that there was a large variation in the amount of DNA actually sequenced compared to the listed length due to the various amounts of heterochromatin and the size of unsequenced centromeres. For the five “acrocentric” chromosomes (13, 14, 15, 21, 22), variant data only from the long chromosome arm was given, the short arm being entirely heterochromatin. On other chromosomes, the centromere gap was much larger than the average

of about 3 million bases (MB) of unsequenced DNA found in most of the chromosomes. For these reasons, and to have a uniform criteria for determination of the length of DNA sequenced for each autosome and the X chromosome, a Python script (“std\_dev.py”) was written to measure the distance between each variant and compute the mean distance and standard deviation. This script was used to determine an adjusted sequence length by excluding lengths of heterochromatin, the centromeres, and gaps between variants larger than 1MB. This adjusted sequence length was used to normalize the variant counts for each autosome file and the X chromosome file to give the concentration of variants in units of variants per MB.

The Y chromosome presented unique difficulties in arriving at an adjusted sequence length. The length of DNA sequenced was considerably less than that of the other chromosomes, being about one third of its length, as determined by the above inspection routine used for the other chromosomes. The complexity of the Y chromosome and the difficulty of sequencing in regions of high X chromosome homology, found in the “ampliconic” and “X-transposed” regions, rendered half of the sequenced length to be unreliable for variant calls, according to Poznik et al (2013). Therefore, the 1000 Genome Project 10.4 MB inclusion mask, suggested for the Y chromosome by Poznik et al (2016), was used when computing the variant concentrations. The segments of the Y chromosome making up this 10.4 MB mask were downloaded from the technical page of the IGSB ([ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/supporting/chrY](http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/supporting/chrY)). The Python scripts were altered to count only the variants in this 10.4 MB region, and 10.4 MB was used as the adjusted sequence length.

To determine the average number of Y chromosome variants for each individual male, an allele count (AC) dictionary

was made with 616 keys, representing the minor AC bins, and with the number of variants for each AC as values. Then the key was multiplied by the value for each AC bin, and these were summed and divided by 1,233 to get the average total number of Y chromosome variants per individual male.

## Results

Based on the adjusted sequence lengths, the mean distance between variant positions ranged between 29 bases (SD 124) in the chromosome 16 file and 35 bases (SD 237) in the chromosome 1 file. For the X chromosome file, the mean distance between variant positions was 43 and the standard deviation was 221. For the Y chromosome file, using the 10.4 MB mask as the adjusted sequence length, the mean distance between variant positions was 168 and the standard deviation was 182 (see Table I).

For each of the chromosome files, the adjusted sequence lengths and the variant counts are listed on Table II with the counts divided into the three groups—rare, uncommon, and common. The variant concentrations in each frequency group, computed by dividing the variant counts by the adjusted sequence lengths, are listed on Table III. The autosome common variant concentrations per MB ranged from 2,676 for chromosome 1 to 3,374 for chromosome 19. The X chromosome common variant concentration was 1,890 and the Y chromosome common variant concentration was 183. The mean of the autosome common variant concentrations was 2,958 with a standard deviation of the mean of 172.58. The concentration of common variants on the Y was 6.19% of the mean for the autosomes. The variant concentrations for the three frequency groups for both the X and the Y chromosomes were significantly below the mean of the concentrations on the autosomes at  $p < 0.0001$ . The results for the common

**Table I.** *The distances between variants in bases, expressed as mean and standard deviation, with total variant counts and variants per bp for the 24 chromosome files of the 1000 Genome database.* Mean and SD for autosomes and the X chromosome were obtained using the Python script “std\_dev.py” which had been adjusted to exclude heterochromatin and gaps larger than 1 MB between variants. Mean and SD were obtained for the Y chromosome from the Python script “y\_variant\_dist.py,” using the 10.4 MB mask. “CHR” is the chromosome, “LEN” is the adjusted sequence length, “DIST” is the mean of the distances between variants, “SD” is the standard deviation of the mean, “VAR” is the total number of variants in the chromosome file, and “VAR / BP” is the variants divided by the adjusted sequence length.

| CHR | LEN   | DIST   | SD     | VAR     | VAR / BP |
|-----|-------|--------|--------|---------|----------|
| 1   | 228.2 | 35.28  | 237.36 | 6467979 | 0.0283   |
| 2   | 239.1 | 33.77  | 146.13 | 7081503 | 0.0296   |
| 3   | 194.9 | 33.42  | 56.39  | 5832220 | 0.0299   |
| 4   | 187.5 | 32.80  | 86.48  | 5736878 | 0.0306   |
| 5   | 177.9 | 33.78  | 87.92  | 5265703 | 0.0296   |
| 6   | 167.9 | 33.42  | 103.86 | 5024045 | 0.0299   |
| 7   | 156.1 | 33.99  | 114.99 | 4716660 | 0.0302   |
| 8   | 143.3 | 31.17  | 110.69 | 4597039 | 0.0321   |
| 9   | 123.0 | 34.54  | 340.04 | 3560643 | 0.0290   |
| 10  | 132.3 | 33.13  | 164.75 | 3992142 | 0.0302   |
| 11  | 131.8 | 32.57  | 183.41 | 4045566 | 0.0307   |
| 12  | 130.8 | 33.81  | 85.30  | 3868362 | 0.0296   |
| 13  | 96.1  | 33.62  | 155.46 | 2857873 | 0.0297   |
| 14  | 88.3  | 33.25  | 39.80  | 2655038 | 0.0301   |
| 15  | 82.5  | 34.03  | 339.30 | 2424665 | 0.0294   |
| 16  | 79.1  | 29.33  | 124.23 | 2697907 | 0.0341   |
| 17  | 78.2  | 33.57  | 126.17 | 2329260 | 0.0298   |
| 18  | 74.9  | 33.04  | 115.97 | 2267139 | 0.0303   |
| 19  | 56.0  | 30.54  | 80.05  | 1832467 | 0.0327   |
| 20  | 59.8  | 32.99  | 135.11 | 1812814 | 0.0303   |
| 21  | 35.6  | 32.16  | 196.13 | 1105518 | 0.0311   |
| 22  | 34.3  | 34.48  | 290.32 | 1073411 | 0.0313   |
| X   | 152.1 | 43.86  | 221.60 | 3467421 | 0.0228   |
| Y   | 10.45 | 168.33 | 182.37 | 61956   | 0.0059   |

variant concentrations, the CGVs, are displayed on Figure 1.

The results of genotype counting of the whole sample (males and females)

versus males-only for autosomes 18–22 and X and Y are listed in Table IV. By comparison of the males-only to the whole sample counts, it can be seen

that the variant counts in the common and uncommon groups are not much changed, whereas the rare variant counts are reduced when counting males-only. This is easily explained by the fact that, when counting singleton variants (those with only one person in the whole sample carrying the variant), if half the sample is female, then half of these singleton variants will not be counted in the male-only counts. Also, for doubletons, one expects that, on average, 25% of them would also not be counted since they would belong to only two females in the whole sample. Conversely, the common variant count is not much changed by counting of male-only genotypes, since, while the AC may be cut in half by only counting males, the AF remains unchanged since the sample size, the denominator, is also cut in half by only counting males. Therefore, counting male-only genotypes did not alter the finding that common variant counts are reduced on the Y chromosomes and the X chromosomes.

The average number of variants per male on the Y chromosomes in the 1000 Genome database was obtained by multiplying the AC bin number by the number of variants in the bin and adding them together. A total count of 732,415 was obtained. Dividing this total count by the sample size of 1,233 males, one finds that the average male in the database carries on his Y chromosome 594 variants: 68 rare, 178 uncommon, and 348 common. Assuming 200 generations since Noah, these mutations would have accumulated at a rate of 2.97 per generation. A result consistent with the Y chromosome mutation rate reported by Jeanson (2019) and Jeanson and Holland (2019).

## Discussion

The concentration of CGVs is significantly reduced on the Y chromosomes as compared to the autosomes of the 1000 Genome database, consistent with

the Created Diversity Model. This result overturns the notion that all variants on the autosomes are solely due to accumulated mutations. If the source of genetic variation on both the Y chromosomes and the autosomes were due only to mutations, one would expect them to have similar concentrations of CGVs. The mechanism of genetic variation must differ between the autosomes and the Y chromosomes. Interpretation of these results based on the historical record of Genesis offers an explanation for these remarkable findings, namely that the autosomes are replete with created diversity, while the Y chromosomes lack created diversity and only have the few mutations that have accumulated since Noah.

The variant concentrations for the X chromosomes are intermediate to those of the autosomes and the Y chromosomes. This suggests that the X chromosomes differ from the Y chromosomes by having some created diversity, but not as much as the autosomes. The implications of these findings are that Eve's two X chromosomes were seeded with created variant positions, and are not an identical clone of Adam's.

The concentration of rare variants is also reduced on the Y chromosomes. This can be explained by the fact that only 1,233 men contributed one copy each of the Y chromosome to the database, whereas these 1,233 men contributed two copies each of the autosomes to the database. The whole sample of 2,504 people thus contribute 5,008 chromosomes to each of the autosomal files. So the Y chromosome rare variants were found on 1,233 chromosomes, whereas the whole sample autosomal rare variants were found on 5,008 chromosomes. The fewer chromosomes sequenced will result in fewer rare variants recorded for the Y chromosomes due to the effect of sample size on the probability of discovery of low-frequency variants in the population.

**Table II. Chromosome lengths and variant counts.** “CHR” is the chromosome name. “SIZE” is the chromosome length in millions of bases (MB) on the NCBI 1000 Genome Browser. “SEQ” is the sequenced length covered in the file, minus gaps over 1MB (aka “the adjusted sequence length”). “<0.5%,” “0.5–5%,” “>5%” are variants counts for the rare, uncommon, and common allele frequency groups. “TOTAL” is the sum of the three groups, which is all the variants in the chromosome file.

| CHR | SIZE (MB) | SEQ.  | <0.5%   | 0.5–5% | >5%    | TOTAL   |
|-----|-----------|-------|---------|--------|--------|---------|
| 1   | 249.3     | 228.2 | 5111842 | 745512 | 610625 | 6467979 |
| 2   | 243.2     | 239.1 | 5634777 | 797577 | 649149 | 7081503 |
| 3   | 198.0     | 194.9 | 4607628 | 662904 | 561688 | 5832220 |
| 4   | 191.2     | 187.5 | 4484322 | 673473 | 579083 | 5736878 |
| 5   | 180.9     | 177.9 | 4169319 | 604297 | 492087 | 5265703 |
| 6   | 171.1     | 167.9 | 3900585 | 593941 | 529519 | 5204045 |
| 7   | 159.1     | 156.1 | 3700430 | 552416 | 463814 | 4716660 |
| 8   | 146.4     | 143.3 | 3644484 | 523788 | 428767 | 4597039 |
| 9   | 141.2     | 123.0 | 2812347 | 405938 | 342358 | 3560643 |
| 10  | 135.5     | 132.3 | 3130071 | 461441 | 400630 | 3992142 |
| 11  | 135.0     | 131.8 | 3193629 | 466650 | 385287 | 4045566 |
| 12  | 133.9     | 130.8 | 3037436 | 452868 | 378058 | 3868362 |
| 13  | 115.2     | 96.1  | 2236056 | 334631 | 287186 | 2857873 |
| 14  | 107.3     | 88.3  | 2090083 | 307965 | 256990 | 2655038 |
| 15  | 102.5     | 82.5  | 1914145 | 279164 | 231356 | 2424665 |
| 16  | 90.4      | 79.1  | 2156250 | 296673 | 244984 | 2697907 |
| 17  | 81.2      | 78.2  | 1852509 | 258608 | 218143 | 2329260 |
| 18  | 78.1      | 74.9  | 1779090 | 264493 | 223556 | 2267139 |
| 19  | 59.1      | 56.0  | 1430530 | 212992 | 188945 | 1832467 |
| 20  | 63.0      | 59.8  | 1434105 | 207606 | 171103 | 1812814 |
| 21  | 48.1      | 35.6  | 863351  | 127201 | 114966 | 1105518 |
| 22  | 51.3      | 34.3  | 836746  | 127937 | 108728 | 1073411 |
| X   | 155.3     | 152.1 | 2781668 | 398336 | 287417 | 3467421 |
| Y   | 59.4      | 10.4  | 50842   | 9216   | 1898   | 61956   |

### The Effect of Sample Size on Variant Discovery

To see how sample size affects variant discovery, consider a variant of AF = 0.1 in a large population. The probability that

a randomly selected genome from that population does not contain the variant is  $1 - 0.1 = 0.9$ . The probability, P, that a series of n randomly selected samples from the population does NOT contain

**Table III.** Chromosome variant concentrations, in variants per MB, obtained by dividing the variant count of each frequency group by the adjusted sequence length in MB. “CHR” is the chromosome name. “SEQ” is the adjusted sequence length in millions of bases (MB), “RARE,” “UNC,” “COMMON” are the concentrations of variants per MB for the three groups of rare, uncommon, and common variants, corresponding to Allele Frequencies (AF) <0.5%, 0.5–5%, and >5%, respectively. The concentration means and standard deviations (SD) are given for the autosomes, and the concentrations for the X and Y chromosomes are compared to them for statistical significance. The \* indicates statistical significance at  $p < 0.0001$  comparing X and Y concentrations to the means of the autosomal concentrations.

| CHR                       | SEQ   | RARE               | UNC              | COMMON           |
|---------------------------|-------|--------------------|------------------|------------------|
| 1                         | 228.2 | 22401              | 3267             | 2676             |
| 2                         | 239.1 | 23567              | 3336             | 2715             |
| 3                         | 194.9 | 23641              | 3401             | 2882             |
| 4                         | 187.5 | 23916              | 3592             | 3088             |
| 5                         | 177.9 | 23436              | 3397             | 2766             |
| 6                         | 167.9 | 23232              | 3537             | 3154             |
| 7                         | 156.1 | 23706              | 3539             | 2971             |
| 8                         | 143.3 | 25433              | 3655             | 2992             |
| 9                         | 123.0 | 22865              | 3300             | 2783             |
| 10                        | 132.3 | 23659              | 3488             | 3028             |
| 11                        | 131.8 | 24231              | 3541             | 2923             |
| 12                        | 130.8 | 23222              | 3462             | 2890             |
| 13                        | 96.1  | 23268              | 3482             | 2988             |
| 14                        | 88.3  | 23670              | 3488             | 2910             |
| 15                        | 82.5  | 23202              | 3384             | 2804             |
| 16                        | 79.1  | 27260              | 3751             | 3097             |
| 17                        | 78.2  | 23689              | 3307             | 2790             |
| 18                        | 74.9  | 23753              | 3531             | 2985             |
| 19                        | 56.0  | 25545              | 3803             | 3374             |
| 20                        | 59.8  | 23982              | 3472             | 2861             |
| 21                        | 35.6  | 24251              | 3573             | 3229             |
| 22                        | 34.3  | 24395              | 3730             | 3170             |
| Mean (SD)<br>of autosomes |       | 23680<br>(1012.13) | 3502<br>(142.40) | 2958<br>(172.58) |
| X                         | 152.1 | 18288*             | 2619*            | 1890*            |
| Y                         | 10.4  | 4887*              | 886*             | 183*             |

\* indicates  $p < 0.0001$  compared to the autosomal means for each group

the variant with allele frequency, AF, is given in Equation 1.\*

$$P = (1 - AF)^n \quad \text{Equation 1}$$

Equation 1 shows that, for a given sample size  $n$ , increasing AF reduces the probability that the variant will be missed. Figure 2 is a plot of  $P$ , the probability of missing the variant, versus  $n$ , the sample size, for variants of several different AF. This plot has the sample size scale ranging up to 1000, a sample size approaching that of the 1000 Genome database for the Y chromosomes, which are from 1,233 males. The three AFs on Figure 2 are 5%, the value separating common from uncommon variants, 0.5%, the value separating uncommon from rare variants, and 0.02%, the value for the “singletons” of the database, which are variants found in only one in 5,000. On Figure 2, note that 80% of variants of AF 0.02% in the population will be absent in a sample of 1,000. This difficulty in finding rare variants is acknowledged for Phase 3 of the 1000 Genome Project, where the power to detect variants of AF greater than 1% is estimated to be > 99%, but the power to detect variants of AF of 0.1% is only 75%. (The 1000 Genomes Project Consortium, 2015).

From Equation 1 and Figure 2, while only 20% of singleton variants will be detected with a sample size of 1,000, all of the CGVs will be detected. A sample size exceeding 1,000 will lead to a greater detection rate of singleton variants, but will not change the detection rate of CGV. If any CGVs are missed, this would be due to sequencing errors and low coverage, not to low sample size.

Based on this statistical argument, the deficit in rare variants on the Y chromosomes compared to the autosomes can be explained by the smaller sample size for the Y chromosomes. But the deficit in CGVs is not due to this difference in sample size, but is due to the absence of created variants on the Y chromosomes.

## Data Quality Considerations

Data quality in the 1000 Genome database could impact these results. Low coverage of the Y chromosomes in the 1000 Genome database (the lack of repeat sequencing of variant positions to eliminate errors) could explain some of the deficit in Y chromosome variants. The error rate for variant discovery is thought to be greater for the rare variants. Increasing depth of coverage should reduce both the false discovery rate and the false negative rate.

The problem of low coverage affecting data quality is addressed by Ponzik, et al (2016) concerning the sequence reads of 1000 Genome Project used in his study. He states, “We applied stringent quality control to meet the Project’s requirement of false discovery rate (FDR) < 5% for SNVs (single nucleotide variants)... In our validation analysis with independent datasets, genotype concordance was greater than 99% for SNVs...” Table I in Ponzik’s paper shows that, in the 60,555 SNVs discovered in the Y chromosome 1000 Genome samples he studied, there was a false discovery rate of 3.9% and a concordance rate with the 1000 Genome database of 99.6%. Poznik et al (2016) then addressed the false negative rate of variant discovery by comparing the variable sites called on 143 high-coverage (80x) Complete Genomics (CG) Y chromosome samples to those found in the low-coverage data (4x) from the 1000 Genome database. They found 3,834 of 17,194 called sites on the high-coverage CG analysis were not called in the low-coverage 1000 Genome Y chromosome analysis, for a false negative rate of 22%. Most of the missed calls (87%) were for rare variants (Poznik et al., 2016, Supplemental Notes 1.3.1 and 1.3.2). High coverage of the CG samples found 22% more variants on the Y chromosome than the low coverage of the 1000 Genome Project. Most of the missed variants were rare variants.

The false negative rate of 22% does not alter the conclusion of this paper,

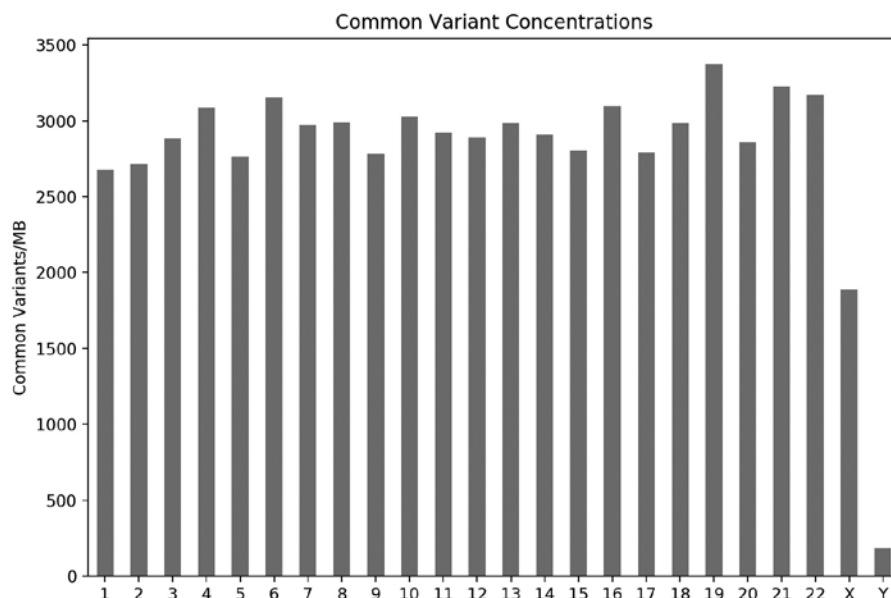


Figure 1. Common variant concentrations in variants per MB for the chromosome files from the 1000 Genome Project.

Table IV. Chromosome variant counts based on genotype counting from 1000 Genome database files obtained from International Genome Sequence Resources. The “WHOLE SAMPLE” counts (males and females) are from “genotype.py” and the “MALE ONLY” counts are from “male\_var.py.” X chromosome variants based on genotypes were counted by “new\_x.py” for the whole sample of males and females, and male-only variants based on genotypes were counted with “male\_var\_x.py.” These Python scripts are available on GitHub as noted in the text of the paper. Counts are displayed as [Rare, Uncommon, Common].

| CHR | WHOLE SAMPLE              | MALE ONLY                 |
|-----|---------------------------|---------------------------|
| 18  | [1772063, 264455, 223481] | [1204873, 265219, 223103] |
| 19  | [1425486, 212934, 188905] | [972048, 212861, 188197]  |
| 20  | [1428094, 207570, 171048] | [968455, 208136, 170923]  |
| 21  | [857935, 127026, 114844]  | [587414, 127333, 114526]  |
| 22  | [853657, 130811, 111404]  | [585829, 132065, 111228]  |
| X   | [2767440, 398236, 287277] | [1466272, 381575, 285758] |
| Y   |                           | [50580, 9241, 1858]       |

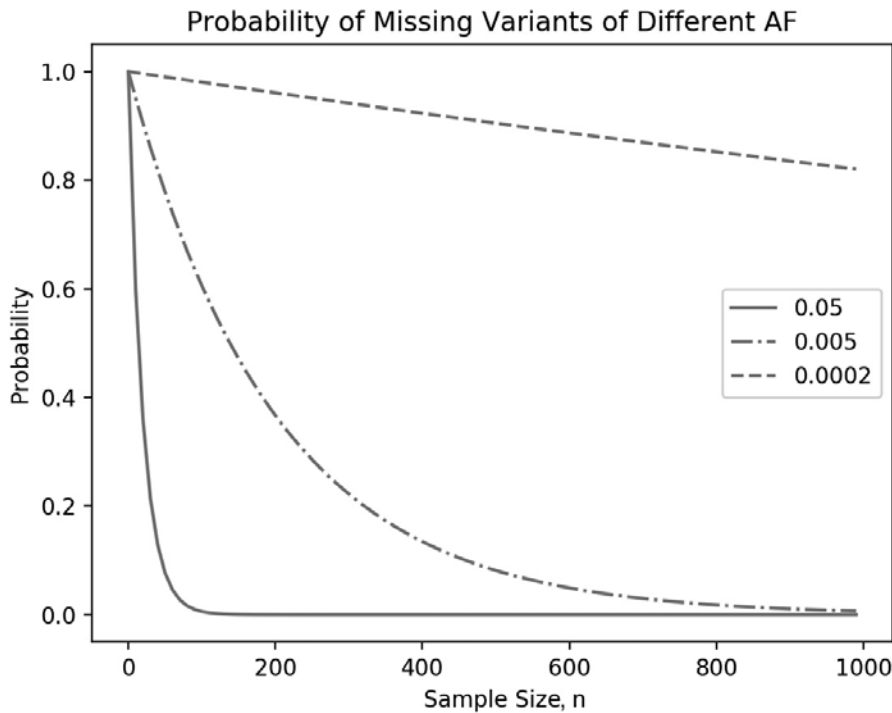


**Figure 2.** The probability of missing the variant after  $n$  samples selected, for variants of AF 0.05 (5%), 0.005 (0.5%), and 0.0002 (0.02%).  $P = (1 - AF)^n$ , where  $P$  is the probability the variant of allele frequency (AF) has not been found after  $n$  random selections from an infinitely large population; “ $n$ ” is the sample size.

since increasing the common variant counts on the Y chromosomes by 22% (a large over-correction), raising the concentration from 183 to 223 per MB, would still result in a statistically significant deficit, at the  $p < 0.01$  level, in CGVs on the Y chromosomes compared to the autosomes. The false negative rate of the 1000 Genome data due to low coverage does not explain the CGV deficit of the Y chromosomes. The lack of CGVs in the Y chromosomes of the 1000 Genome database is consistent with lack of created diversity on the world's Y chromosomes due to the descent of all men from Noah, as recorded in Genesis.

The 22% false negative rate does not completely explain the rare variant deficit of the Y chromosomes. A 22% increase in the number of rare

variants on the Y chromosome would raise the concentration from 4,887 per MB (Table III) to 5,962 per MB, which is 25% of the mean rare variant concentration found on the autosomes. The remaining rare variant deficit is explained by the lower sample size for the Y chromosomes.

### Predictions of Coalescent Theory

An ancestral tree can be drawn from one couple, with branching at each generation, as offspring descend to the current population. When the branches are followed back in time to the original couple, a coalescence process is seen to occur with branch points representing individuals who have produced multiple children. Such trees have been built

using genetic variant profiles, in which case the branch points represent common variants as the root of the tree is approached, going back in time. In other words, common variants are a marker of coalescence.

According to Coalescent Theory (Rosenberg and Norborg, 2002), the probability of coalescence of divergent sequences in the previous generation is inversely proportional to the number of samples ( $N$ ) as seen in the following equation:

$$P(\text{coalescence}) = n(n-1) / 4N$$

Equation 2

Here,  $P$  is the probability of coalescence in the previous generation,  $n$  is the number of variants under consideration, and  $N$  is the effective population size. The reciprocal of Equation 2 is the time to coalescence, which is proportional to  $N$ . When applied to DNA sequences, the value of  $N$  for autosomes is four times as large as  $N$  for the Y chromosomes since there are four copies of each autosome for every Y chromosome. Therefore, autosomes should coalesce 4 times slower than Y chromosomes. If both the autosomes and the Y chromosome descend from the same ancestral couple, and if all variants are due to mutations accumulating, the autosomes should have at least 4 times fewer variants than the Y chromosomes. Yet, in the 1000 Genome database, the autosomes contain many more variants than the Y chromosomes. According to the Created Diversity Model, this is due to created variation on the autosomes.

Coalescent Theory can be used to estimate the time to the most recent common ancestor (TMRCA) from the DNA sequence data of a population (Rosenberg and Feldman, 2001). The theory assumes that genetic variants derive from mutations that are inherited by successive generations down to the present, a condition applicable to the Y

chromosome according to both creationists and evolutionists.

After constructing a phylogenetic tree from the 1000 Genome Y chromosome variant data, and applying a mutation rate of  $0.76 \times 10^{-9}$  mutations per base pair per year, Poznik (2016) estimated the TMRCA to be 190,000 years. This mutation rate, derived using evolutionary assumptions, is two orders of magnitude lower than that measured from pedigree-based high coverage Y chromosome data. When the more accurate mutation rates are used, Coalescent Theory estimates a TMRCA based on the Y chromosome variants of about 4,500 years (Jeanson and Holland, 2019).

## Y Chromosome CGVs Are a Genetic Record of History

While all the variants on the Y chromosomes are due to mutations accumulated after Noah, the CGVs on the Y chromosome are due to mutations that occurred in the founders of the world's populations who spread out from Babel (Carter and Hardy, 2015; Sibley, 2017) and in men who fathered the large male lineages that persist in the world today. Historical events explain the survival of these lineages and the demise of others.

In contrast to the CGVs, the number of rare variants found on all the chromosomes in the database, is directly related to sample size. This is because mutations enter the population as rare variants, even as singletons. Every position in the genome is a potential variant site for a mutation. Among the 7.5 billion people in the world, variants are likely to exist today for every one of the 3.2 billion positions in the human genome, except for lethal variants. If all the genomes in the world were sequenced and variants recorded, the total variant concentrations in the database would approach 1 variant per base for all chromosomes as more and more rare variants were found. But the CGV deficit on the Y chromosomes compared to the autosomes

would remain a permanent feature of human genetic variation due to lack of created variants on the Y. This prediction of the Created Diversity Model can be tested as the databases expand with more Y chromosomes sequences.

\*[For a variant with  $AF = 0.1$ , the probability of randomly selecting a genome without this variant from a large population is  $1 - 0.1 = 0.9$ . The probability of missing the variant on two consecutive selections is  $0.9 \times 0.9 = 0.81$ . The probability of missing the variant on three selections is  $0.9^3 = 0.729$ . And so on. So the probability of missing the variant after  $n$  random selections is  $0.9^n$ . Thus,  $P = (1 - AF)^n$  is the probability of missing the variant of frequency  $AF$  after  $n$  selections.]

## Conclusion

The lack of common genetic variants found on the Y chromosomes versus the autosomes of the 1000 Genome database is consistent with most common variants on the autosomes being created diversity, which is absent from the Y chromosomes. The few variants found on the Y chromosome are due to mutations acquired with descent from Noah within the last 4,300 years. Human genetic variation is explained by two mechanisms: created diversity, which is the cause of most common variants, and mutations, which is the cause of most rare variants. Since common variants greatly outnumber rare variants in a typical human genome, created diversity, not mutations and natural selection, is the cause of most human genetic variation.

## Summary

The first two decades of the twenty-first century have witnessed a vast increase in knowledge in the science of genomics. Great controversy has attended the sequencing of the human genome as scientists with opposing worldviews give

conflicting interpretations of the data. Evolutionists have assumed that all human genetic variation has developed by mutation and natural selection over millions of years, while those who believe the biblical record of recent creation maintain that most human genetic variation is created diversity placed by God into the genomes of our original parents.

The pattern of human genetic variation found in the 1000 Genome Project database provides a way to resolve this controversy. Created variants should be absent from the Y chromosomes in the world, as all have descended from Noah's single Y chromosome. The investigation reported here finds that the concentrations of common genetic variants in the Y chromosomes of the 1000 Genome database is dramatically less than the concentrations found on the autosomes, consistent with the Created Diversity Model. The notion that all human genetic variation is due to mutation is thus overturned. The history of Creation and the Flood recorded in Genesis provides the basis for understanding the origin of human genetic variation.

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# A Computer Model of Mutation Accumulation on Y Chromosomes Suggests Events Recorded in Genesis Produced Common Variants

Marshall Jordan\*

## Abstract

Genetic variation on Y chromosomes is due to mutations accumulated as men have descended from Noah. Many of the Y chromosome common variants found today were produced by historical events causing large demographic changes when the world population was small. To gain understanding of how the ancient events described in Genesis following the Flood may have produced these common variants, a computer model was built. Output from this model suggests that this common variant pattern is the result of tragic demographic events, including the Babel dispersion and the Ice Age, resulting in population collapse and opportunistic male reproduction. High mutation rates in long-lived patriarchs may also have contributed to increasing common variants on Y chromosomes. The model most closely matches the common variant pattern when parameters are adjusted to reflect the historic record of Genesis. The population expands rapidly with few deaths until 560 men with their families disperse from Babel. The model further suggests that patriarch profiles of mutations might be found on the Y chromosomes of all men today.

## Introduction

It is generally understood that the Y chromosome bears a unique record of human history (Ponzik et al., 2016). Phylogenetic trees made from Y chro-

mosome variant data display a deep node structure indicating the unique phylogeny of the human Y chromosome (Bergstrom et al., 2020). Evolutionists assume that mutations producing this

record have accumulated on Y chromosomes over several 100,000 years of population stasis in Africa during the Pleistocene epoch (Harpending et al., 1998) followed by rapid expansion of lineages as humans migrated out of Africa, commensurate with technological developments, about 50,000 years ago (Ponzik et al., 2016). Creationists attribute the characteristic variant pattern to historical events recorded in Genesis

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Accepted for publication October 16, 2020

during and after the time of the Babel dispersion about 4300 years ago (Carter, 2009). Both sides agree that the rapid expansion of male lineages displayed in the Y chromosome phylogenetic tree is consistent with rapid population growth during recorded history. Rapid population growth, with associated growth in the number of male lineages, leads to the large numbers of rare variants found in Y chromosome databases. However, common variants are produced by long periods of population stasis, or by episodes of population collapse and recovery (Harpending et al., 1998). The challenge for creationists is to explain how the common variant pattern and deep-node structure was produced in a much shorter period of time, following the Flood during the early stages of rapid population growth. An answer may be found by computer modeling. Numerical simulation and computer modeling can help determine the demographic events that would cause the accumulated mutations to assume the pattern seen in the Y chromosome databases. Parameters of a model can be adjusted to produce output which can be compared to the real data, providing insight into real historical events. In this way, an explanation of the cause of the complex genetic pattern may be discerned where direct mathematic analysis is not possible (Baumgardner et al., 2008).

Here a computer model of Y chromosome mutation accumulation is presented to show that the characteristic common variant pattern found on Y chromosomes today could have been caused by a series of population collapses, or bottlenecks, corresponding to historical events recorded in Genesis. In this paper, the common variant pattern from the Y chromosome file of the 1000 Genome database is described. Based on the biology of Y chromosome inheritance and the initial conditions derived from Genesis, a computer model of mutation accumulation is presented and its parameters adjusted to produce output

resembling the real data. A discussion of the model's assumptions, main functions and justification of these functions then follows. Lastly, consideration is given to predictions regarding future discoveries from analysis of genomic databases.

### The 1000 Genome Data

Large databases of Y chromosome genomic sequences are available to the public on the internet. The 1000 Genomes Project (1000G) (1000 Genomes Project Consortium, 2015) and the Human Genome Diversity Project (Bergstrom et al., 2020) provide genetic sequences of Y chromosomes from around the world.

The 1000G database contains the mutations (variants) found on the Y chromosomes of 1,233 men of 26 populations from the Americas, Europe,

Africa, and Asia. These mutations are listed in a file in the "variant call format" (VCF). This VCF file was downloaded from the International Genome Sample Resource website and the allele frequencies (AF) of all the variants were extracted with a Python script. Figure 1 shows the minor allele frequency distribution for these variants which lie within the 10.4 million bases (MB) of Y chromosome sequence where most of the variant data in the file is found (Ponzik et al., 2016). The vast majority of variants are rare ( $AF < 0.5\%$ ) and would fall in the first bin, which has been reduced from 57,329 variants so that the other bins would appear on the plot. These rare variants are an indication of recent, rapid population expansion, well documented in historical records (Jeanson, 2019). All mutations enter the population as rare variants, each arising in a single person (Sanford et al., 2018, pp. 200–216). So

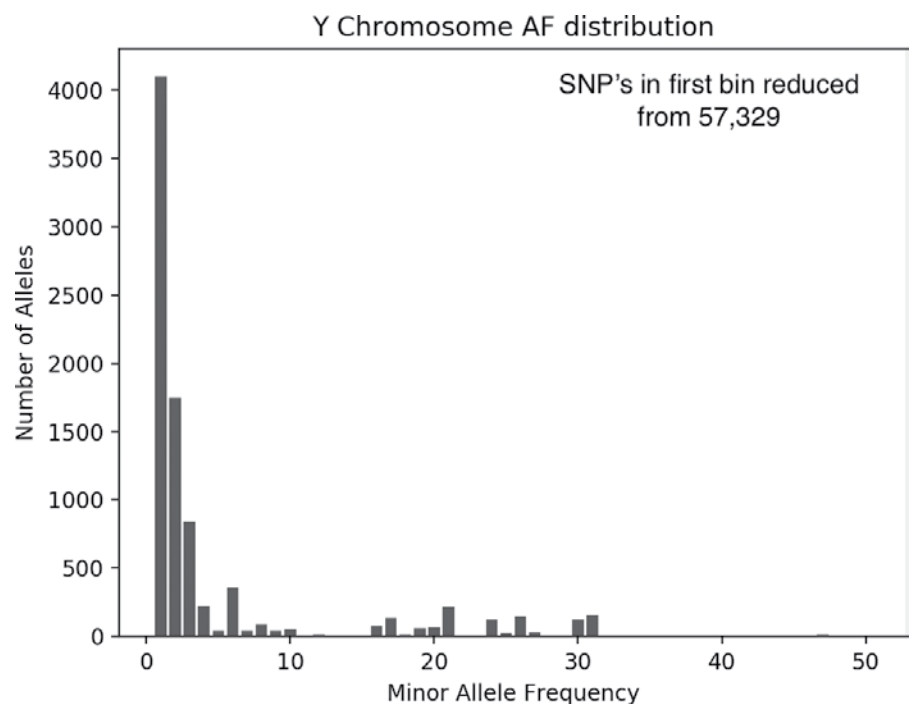


Figure 1. The minor allele frequency distribution for the variants of the 1000G data for the Y chromosome. The majority of the mutations, single nucleotide polymorphisms (SNP), in the first bin (57,329) are not shown.

rapid population expansion is characterized by accumulation of large numbers of rare variants. Since this study is concerned with ancient demographic events that produce common variants, these rare variants can be ignored as they are not the main concern of this paper.

Figure 2 shows only the common variants of Figure 1, those variants between AF 5% and 50%. On Figure 2 there are very few variants above AF 32%, but many variants are found between AF 16% and 32%. The largest bin, at AF 21%, has over 200 variants. Between AF 16% and 32% there are 10 bins with 10 variants or more. A total of 861 variants in the file have AF in this range. As will be seen in the description of Y chromosome inheritance below, these variants between AF 16% and 32% are mysterious because common variants in this range challenge the notion of simple clonal inheritance, yet they are the source of the deep-node structure of the phylogenetic tree. These are the variants that must be explained in a manner consistent with the record of Genesis and descent of all men from Noah.

## Y Chromosome Inheritance

Of the 46 human nuclear chromosomes, the Y presents the easiest case for modeling due to the fact that it is passed from father to son without chromosomal crossing over and without admixture from the maternal genome (Carter et al., 2018, pp. 133–151). As such, the Y chromosome, and any mutations in its sequence, is inherited in a clonal fashion. Today, the men of the world are more than 99.9% identical in their Y chromosome sequences, each man carrying only about 600–800 variants in the 10.4 MB part from which most of the variant data of the 1000G is obtained (Jordan, 2020). For these reasons, the model needs only to follow the accumulating mutations as the generations descend. The pedigree-based Y chromosome mutation rate has been measured to be about 3 mutations

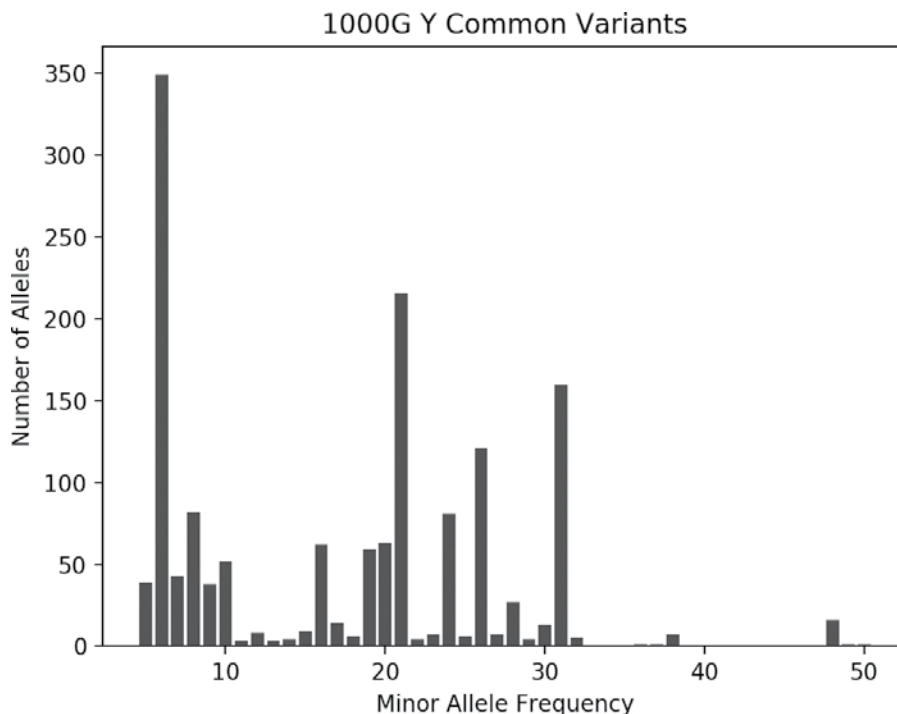


**Figure 2.** The allele frequency distribution of the common Y chromosome variants of the 1000G project. Minor allele frequency axis runs from 5% to 50%.

per man per generation (Jeanson and Holland, 2019). Thus, today, every male has about 3 more mutations on his Y chromosome than his father, 6 more than his grandfather, and 9 more than his great grandfather. His son will have about 3 more mutations on the Y chromosome than he has. In this way, the mutations are seen, today, to be accumulating in a clock-like fashion (Jeanson, 2020). Based on the average number of mutations found on Y chromosomes today this clock indicates that all men have descended from a last common male ancestor who lived about 200 generations ago. This would be Noah, who gave his Y chromosome to his three sons, presumably with unique mutations to each. Based on these considerations, each Y chromosome should have a genetic record of descent according to its lineage from one of Noah's three sons, assuming they each received a unique set of mutations on their Y chromosome.

## The Computer Model

Written in Python, the finished model (Y\_sim\_Pdrive.py) can be found at ["github.com/marshalljordanmd/Y-simulations."](https://github.com/marshalljordanmd/Y-simulations)

The model has three main functions, "Growth," "Mutation," and "Famine." The Growth function gives each male a number of sons in the next generation. Each son receives the unique Y chromosome mutations of his father. Once the males of the next generations are produced, the previous generation of males is allowed to die without producing any more sons. The first two generations are hard coded in the model. The first generation, "Gen\_0," consists of three men representing Shem, Ham and Japheth. "Gen\_1" consists of the 16 grandsons of Noah listed in Genesis 10 (5 sons of Shem, 4 sons of Ham, and 7 sons of Japheth). Subsequent generations grow at a rate set according to a parameter which randomly varies from 4 to 7 sons.

The Mutation function supplies new mutations to each of the males in the next generation. All these mutations are sequentially numbered so they can be followed and AF for each mutation computed at the end of each run of the program. To account for “patriarchal drive,” where the long-lived patriarchs described in Genesis are thought to have supplied many mutations to the Y chromosomes of their sons, a variable mutation rate function was devised based on the computer simulations of Carter (2019). Figure 9 of that paper shows the average number of new mutations per Y chromosome per year for 2000 simulated years following the Flood. The initial decay of this curve resembles a negative exponential out to 1000 simulation years, with the average number of new mutations decreasing from a maximum of 30 to 3. An equation was fitted to this simulation plot, and then converted from time in years to time in generations, with a generation assumed to be 30 years, resulting in Equation 1.

$$u(g) = C e^{-0.09g} \quad \text{Equation 1}$$

Here “ $u(g)$ ” is the number of new mutations per Y chromosome in generation “ $g$ .” The constant “ $C$ ” is the “Patriarchal Drive Coefficient.” In the program, the number of new mutations was caused to randomly vary up or down within 2 standard deviations of a Gaussian distribution with mean of  $u(g)$  mutations, providing realism by mirroring the stochastic process of mutation. Equation 1 provides a maximum number of mutations to Noah’s sons and falls to 3 per male per generation at 25 generations post-Flood. With this equation in the mutation function, the mutation rate is very high initially, reflecting patriarchal drive, and then decreases to the modern level as life spans decrease as recorded in Genesis.

When the populations grow to exceed the maximum, the Famine

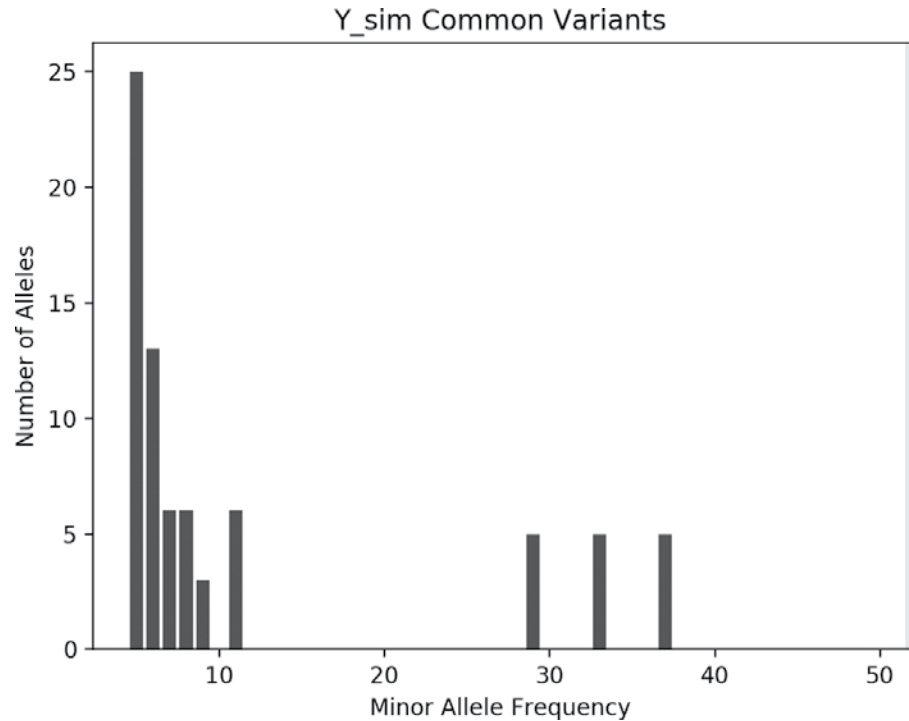


**Figure 3.** The allele frequency distribution of a run of the model `Y_sim.py` for 25 generations with no bottlenecks, no GK sons, and no patriarchal drive mutations.

function culls the populations back to the specified maximum by randomly eliminating men (and their unique mutations) from the population. Without this function, the populations rapidly expand to the point of overwhelming the computer’s memory. This function acts like a carrying capacity for each of the three subpopulations. The maximum populations were set to 400, 500, and 600 for the lineages of Shem, Ham and Japheth, respectively. These maximums were chosen based on assumptions of the relative numbers of these lineages in the 1000G data and to make the final population size to be about 1,200 men, which is the sample size of the 1000G data.

With these initial three main functions, the program was run for 25 generations. The AFs were computed for all mutations and common AF bins plotted, producing the common variant

distribution in Figure 3, which differed substantially from the 1000G common variant distribution in Figure 2. The simulation had only three common variant peaks, representing the three patriarch mutation profiles, above AF 16%, whereas the 1000G plot, Figure 2, has a dozen common variant peaks above AF 16%. To mimic the 1000G data, the model had to be improved to produce more common variants between AF 16% and 32%.

A moment’s consideration supplies an answer for how to improve the model. Consider the case of generation zero (Gen\_0) where Noah’s three sons each have one mutation on the Y chromosome inherited from their father. The AF of these Gen\_0 mutations would be 1/3, or 33% in Gen\_0. When passed to their sons in Gen\_1, these patriarch mutations (patriarch signatures or pro-

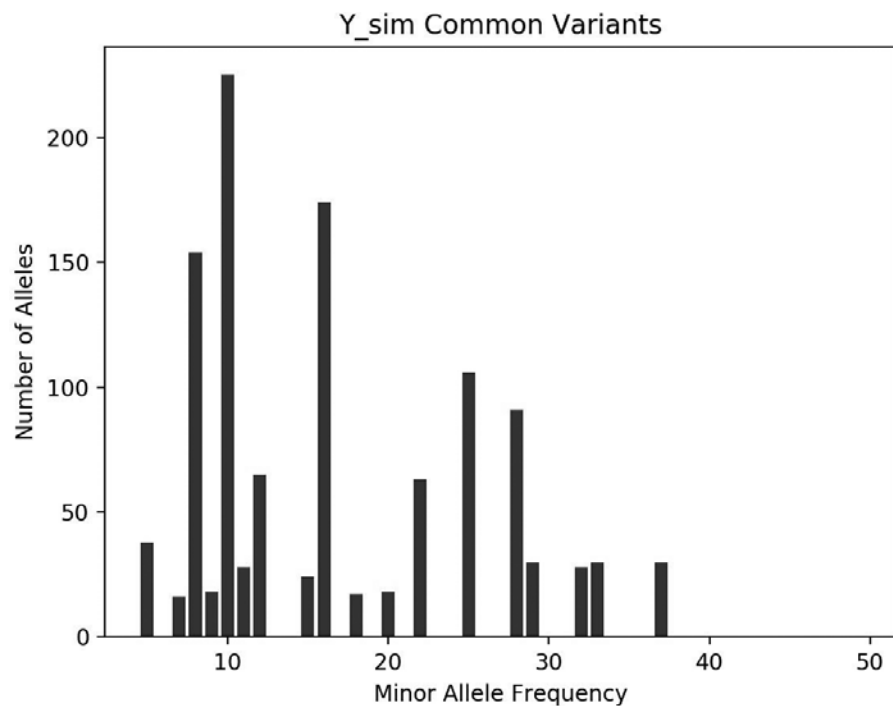


**Figure 4.** The allele frequency distribution for a run of the model `Y_sim_Pdrive.py` for 25 generations with Bottleneck Mortality 80%, GK sons 100, and Patriarchal Drive Coefficient 30.

files) would remain common variants in Gen\_1, with slight shifting of their AFs due to the changes in lineage numbers. Shem's signature would be in his 5 sons at AF of 5/16 (31%). Ham's signature would be in his 4 sons at 4/16 (25%). Japheth's signature would be in his 7 sons at 7/16 (44%). But the unique, new mutations in Gen\_1, received in these 16 grandsons of Noah, would each be at 1/16 (6%), a frequency just enough for them to be called common variants. For all subsequent generations, the patriarch signature mutations would remain common (unless a patriarch lineage fell below 5%), but no more new mutations would become common variants because those who carried these new mutations would be less than 5% of the population. From the third generation on, no new mutations could become common variants without major demo-

graphic changes. Such changes which occur when the population is very small are expected to increase common variant numbers since the future impact of new mutations is inversely related to population size (Carter, 2019). For this reason, the many common variants seen in the 1000G Y chromosome data is remarkable in that they indicate major demographic stirring in the first few generations that followed the Flood (Sanford et al, 2018, pp. 200–216).

What kind of demographic changes would produce more common variants in Gen\_2 and after? Many men would have to die without producing any sons, and a surviving man would then need to produce more than 5% of the sons in the next generation in order for his unique variants to become common variants in that generation. Turning on additional functions in the model caused this to

happen, producing output closer to the real data. A “Mortality” function causes each generation to lose 20–30% of the men at random before they produced any sons. A “Bottleneck” function causes the population to collapse by as much as 80% every few generations by randomly culling away men. Lastly, a function causes one randomly selected man in each generation to produce 50 to 150 sons, the exact number randomly selected. For lack of a better name, this function is called the “Genghis Khan” (GK) function.

Figure 4 shows a typical common allele frequency distribution from the model's output after the Mortality, Bottleneck, and GK functions are activated to produce demographic stirring. Each run of the model produces a unique picture due to the randomness programmed into the functions, so Figure 4 represents only one example, with close approximation to the real data. Notice that 10 variant peaks now have AF between 16% and 35% so this plot more closely resembles Figure 2.

## Modeling with Biblical Parameters

The model was set to reflect the historical record of Genesis 9–11 by setting the first two generations to Noah's three sons and 16 grandsons. Assuming that each of Noah's sons received many mutations on the Y chromosome inherited from their father, the patriarchal drive coefficient was set to 30. Bottleneck events were set to occur for the generations listed on Table 1, according to major historic events recorded in Genesis and Exodus (Austin, 2019; Whitcomb, 1993) and an assumed Ice Age (Snelling and Matthews, 2013). The Babel event was set to Gen\_4. The Ice Age was assumed to suppress population size in generations 5 and 6 so that the initial population bottleneck lasted 3 generations. With these settings, the population at Gen\_3, one generation before the Babel event,

Table I. Potential bottleneck (population collapse) events recorded in Genesis and Exodus. (Austin, 2019; Whitcomb, 1993; Snelling and Matthews, 2013)

| Event         | Reference     | Date      | Generation |
|---------------|---------------|-----------|------------|
| The Flood     | Gen. 6-9      | 2391 BC   | 0          |
| Babel         | Gen. 11       | 2250 BC   | 4          |
| Ice Age       | ? Job 38:22   | ? 2100 BC | 5–6        |
| Abram Famine  | Gen. 12:10    | 2000 BC   | 9          |
| Isaac Famine  | Gen. 26:1     | 1950 BC   | 10         |
| Joseph Famine | Gen. 41:29-30 | 1875 BC   | 12         |
| Moses's birth | Exodus 1      | 1525 BC   | 22         |

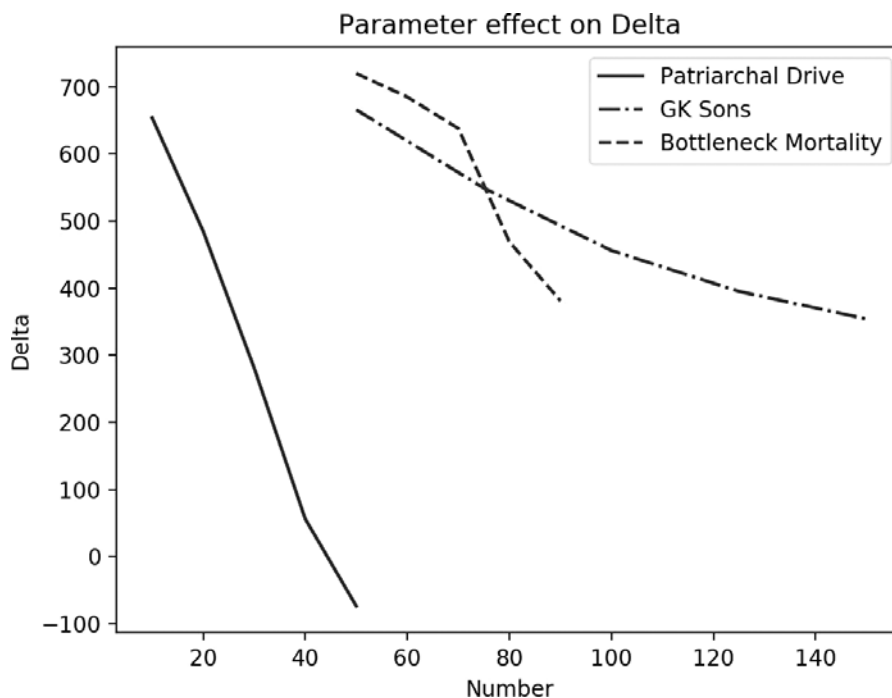


Figure 5. Parameter effect on Delta using program “Y\_sim\_Pdrive.py.” Patriarchal Drive Coefficient  $C$  (see Equation 1) varied from 10 to 50 mutations. GK sons varied 50 to 150 sons, Bottleneck Mortality varied 50% to 90%. Delta is the average of 861 minus the number of variants between AF 16–32% after 25 simulated generations.

averaged 560 men. These represent the fathers, with their wives and the children, who were scattered from Babel, alto-

gether several thousand people. Since the model does not cull the population (causing men to die) until the set maxi-

mums are exceeded, and these had not been exceeded by the time of the Babel event, the model includes Noah and his sons among those who dispersed from Babel (Carter and Lightner, 2016).

## Model Optimization

A target, Delta, was devised to compare the model's output to that of the 1000G data. Delta was the number of variants of AF between 16% and 32% in the 1000G data (861 variants fell in this range) minus the number in this range in the model's output at the end of each run of 25 generations. The more closely Delta came to zero, the more closely the model matched the 1000G data. The parameters were optimized one at a time with the model's other settings not changed. Using this method, it was found that the number of sons (GK function), the bottleneck mortality, and the Patriarchal Drive Coefficient had a major effect on Delta and could be adjusted to make the model's output resemble the 1000G data. Figure 5 shows the effect of these three parameters on Delta. Delta was most sensitive to the Patriarchal Drive Coefficient, which gave a slope of -18.2 as the maximum number of mutations,  $C$  in Equation 1, increased from 10 to 50. Figure 6 shows the average number of new mutations added per male per generation for various settings of the Patriarchal Drive Coefficient,  $C$ . Table II gives the model's parameters and their standard settings during the optimization procedure. Tables III–V show the data displayed in Figure 5. As the number of GK sons, bottleneck mortality, and Patriarchal Drive Coefficient increased, Delta decreased.

## Model Analysis

The program was analyzed in a Monte Carlo fashion by running it three hundred times with these optimized parameters: GK sons 100, Bottleneck mortality 75–85%, Patriarchal Drive

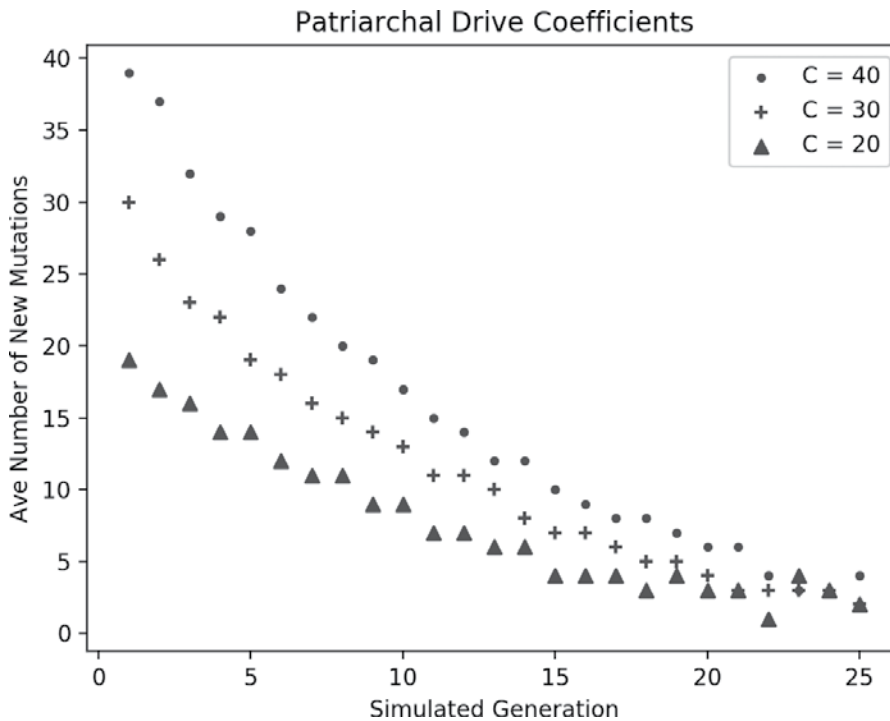


Figure 6. Model “Y\_sim\_Pdrive.py” output for various Patriarchal Drive Coefficients,  $C$ , showing average number of new mutations per male at each simulated generation. Based on Equation 1,  $u(g) = C e^{-0.09g}$ , with added random variation of 2 standard deviations around a Gaussian of mean  $u(g)$ .

Table II. Parameters of the model (Y\_sim\_Pdrive.py) and their standard settings during the optimization procedure.

| Parameter             | Setting                                                    |
|-----------------------|------------------------------------------------------------|
| growth rate           | random 4–7 per male per generation                         |
| mutation rate         | $u(g) = C e^{-0.09g}$ , $C = 30$ , $g = \text{generation}$ |
| annual mortality      | 20–30% per subpopulation                                   |
| subpopulation maximum | $S = 400$ , $H = 500$ , $J = 600$                          |
| GK sons               | random selection of 50–150 sons                            |
| Bottleneck events     | Gen. 4, 5, 6, 9, 10, 12, 22                                |
| Bottleneck mortality  | random between 65% and 85%                                 |

Coefficient 42. Figure 7 shows the distribution of Deltas produced. Figure 8 shows a Q-Q plot of the Deltas versus

a normal distribution. The mean Delta was 7.46, the SD was 188, and the 95% confidence interval was -18.9 to 33.9 ( $n$

= 200). Since a Delta of zero falls within the 95% confidence interval, the model run on these settings yields results closely matching the 1000G data.

The effect of population bottlenecks on mutation accumulation was analyzed by running the model for 25 generations with and without bottlenecks, other parameters being held constant. At 10 generations, the total number of mutations, number of extant mutations, and number lost to drift were 773162, 95023, 678139 for the run with no bottlenecks and 520002, 11683, 508319 for the run with bottlenecks. Total mutations were lower in the run with bottlenecks due to lineage losses caused by population collapses. Figure 9 shows the percent of mutations lost due to drift for the two scenarios. By generation 10 without bottlenecks, 88% of the total mutations had been lost due to drift. With bottlenecks included, 98% of total mutations had been lost due to drift by generation 10. Thus, the model demonstrates the effects of population bottlenecks, which increase the loss of mutations by drift (Carter, 2009), thus altering the allele frequency distribution. Since the most likely lost mutations are rare, the percentage of common variants is increased, consistent with the common variant pattern seen in the 1000G data.

## Patriarch Profiles

One interesting result supported by the model is the persistence and prominent location of AF bins containing the original mutations of the three sons of Noah. These “Patriarch Profiles” should exist on the Y chromosomes of all men, according to which of the three lineages they belong, due to the clonal inheritance of mutations on the Y chromosome. The model’s output, in the graphic form of the allele frequency distributions, always displays the three patriarch AF bins as the highest frequency variants for each lineage. When the number of men carrying each patriarch

Table III. Optimization of Number of Sons fathered by opportunistic reproducers (GK function). One man in each generation in each subpopulation fathered many sons. Delta = 861 minus average number of variants of AF 16–32% (100 iterations). S. D. = 1 standard deviation.

| Sons | Delta | S. D. |
|------|-------|-------|
| 50   | 666   | 92.5  |
| 75   | 549   | 117   |
| 100  | 456   | 127   |
| 125  | 395   | 137   |
| 150  | 354   | 143   |

Table IV. Optimization of Bottleneck Mortality. Average Delta over 100 runs of 25 generations with Mortality 50 to 90%. Delta = 861 minus average mutation count between AF 16–32% (100 iterations). S. D. = 1 standard deviation.

| Mortality % | Delta | S. D. |
|-------------|-------|-------|
| 50          | 720   | 57.5  |
| 60          | 685   | 76.7  |
| 70          | 638   | 99.2  |
| 80          | 469   | 124.0 |
| 90          | 381   | 119.0 |

Table V. Optimization of Patriarchal Drive Constant, C, in the mutation function where the number of new mutations per man per generations is  $u(g) = C e^{-0.09g}$  (equation 1). Delta = 861 minus average number of mutations between AF 16–32% (100 iterations). S. D. = 1 standard deviation.

| C  | Delta | S. D. |
|----|-------|-------|
| 10 | 654   | 127.0 |
| 20 | 485   | 96.4  |
| 30 | 281   | 106.7 |
| 40 | 56    | 167.9 |
| 50 | -74   | 213.9 |

signature are added, the sum is the total population at the end of the model run. The mutations that accumulate in the lineages that branch off and descend from the three patriarchs are always in AF bins of lower frequency than the patriarch bin. Some of these “descendant” bins become common AF bins due to demographic events, but most of them remain uncommon or rare.

## Discussion

A biblical model of human history requires an explanation of how the Y chromosome genetic diversity found in the world today has developed within the 4,500 years since the Flood. The large number of rare variants found on Y chromosomes today are due to rapid population expansion, which is amply detailed in historic records. These rare variants have accumulated as mutations were passed down in a clonal fashion to the rapidly increasing number of new male lineages. But simple clonal inheritance of mutations cannot explain the common variant pattern of the Y chromosomes found in large databases because new mutations in a rapidly expanding population produce rare variants. Major demographic events, such as population bottlenecks and the fathering of many sons by a few men, must have occurred while the population was small in order to produce these common variants. The historic events recorded in Genesis provide the basis of an explanation for the Y chromosome common variants. With this in mind, the computer model presented in this paper was calibrated to show how population collapses and opportunistic male reproduction, together with increased mutation rates in the early post-Flood world, could produce the common variant pattern.

At 25 generations, the model matches the real data when the optimized parameters are set according to the events recorded in Genesis and Exodus. But how realistic are these parameters?

## Population Collapses (Bottlenecks) Due to Historic Events

After the Flood, the next bottleneck in human population was the Babel event, where people scattered from a civilization into an uncharted wilderness. Some may argue that these people were primitive, bronze-age nomads used to survival in adverse circumstances. The biblical record says otherwise. The city of Babel was a civilized place, for they had a common language and culture (Genesis 11:1), a ceramic industry (Genesis 11:3), engineering and architecture (Genesis 11:4), a long term strategic plan (11:4), and they were organized with an administration or government (Genesis 11:3–4). The industries of the pre-Flood world were known to Noah and his sons, who lived until after the Babel event. For example, they knew how to build cities (Genesis 4:17), they knew about metallurgy in copper and iron (Genesis 4:22), and animal husbandry (Genesis 4:20). Furthermore, Noah and his sons had built the largest, ocean-going boat the world has ever seen until the advent of twentieth century supertankers and container ships. Such activities require mathematical and engineering knowledge as well as organization. These are the trappings of civilization.

However, the world into which the refugees of the Babel civilization were scattered was completely unknown and unpeopled. Recent historical examples of people leaving civilizations to live in unknown and under-populated areas give some measure of how much of a population collapse might accompany such a migration. The Pilgrims, who established the Plymouth Colony in AD 1620, lost 47 of the 102 passengers of the Mayflower by the end of their first winter in the New World, due to starvation and disease (Bradford, 1920, p. 85). The 121 of Roanoke Colony in AD 1518 completely vanished (Lawler, 2017). The Jamestown Colony of AD

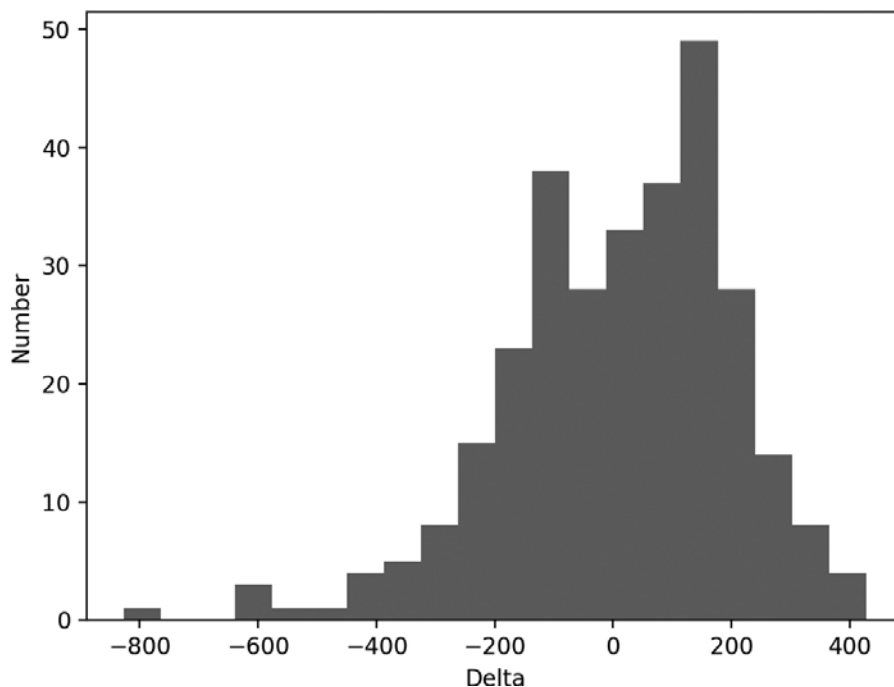


**Figure 7.** Distribution of Deltas from 300 runs of “Y\_sim\_Pdrive.py” with optimized parameters: GK sons 100, Bottleneck Mortality 75–85%, Patriarchal Drive Coefficient 42. Delta is the number of variants of AF 16–32% in the 1000G data (861 variants) minus the number in this range in the model’s output at the end of each run of 25 generations.

1607 was nearly wiped out, and so was abandoned after 3 years, when 80 to 90% of the original 100 settlers were dead (Stebbins, 2011). Starvation and disease played a big role in the failure of these colonies, but strife with the local American Indians was also a contributing factor. While those who left Babel had no natives to contend with, neither did they have help from friendly natives, as Squanto helped the Pilgrims (Bradford, 1920, p. 85). Also, the Ice Age was building up soon after the Babel event (Snelling and Matthews, 2013), which would cause crop failures and starvation to those who had settled in Europe and northern Asia. Given these historic events and considerations, it does not seem inappropriate to set the bottleneck collapses in the range of 80%.

For most of the recorded events, the Bible gives no hint regarding how much of a population collapse occurred (Carter and Lightner, 2016). The record is silent on the degree of population decline at Babel, the Ice Age, and the famines in Canaan during the days of Abraham and Isaac. However, the famine of Joseph’s day was said to be worldwide (Genesis 41:57), in which case a 50% or greater collapse does not seem unreasonable. “Worldwide” need not include the Americas or Oceania and Australia in 2000 BC, because the population then is estimated to have been only a few million (Jeanson, 2019). Likely, migration farther than Asia had not yet occurred, or only to a limited extent. Such a worldwide famine probably caused a population collapse similar to

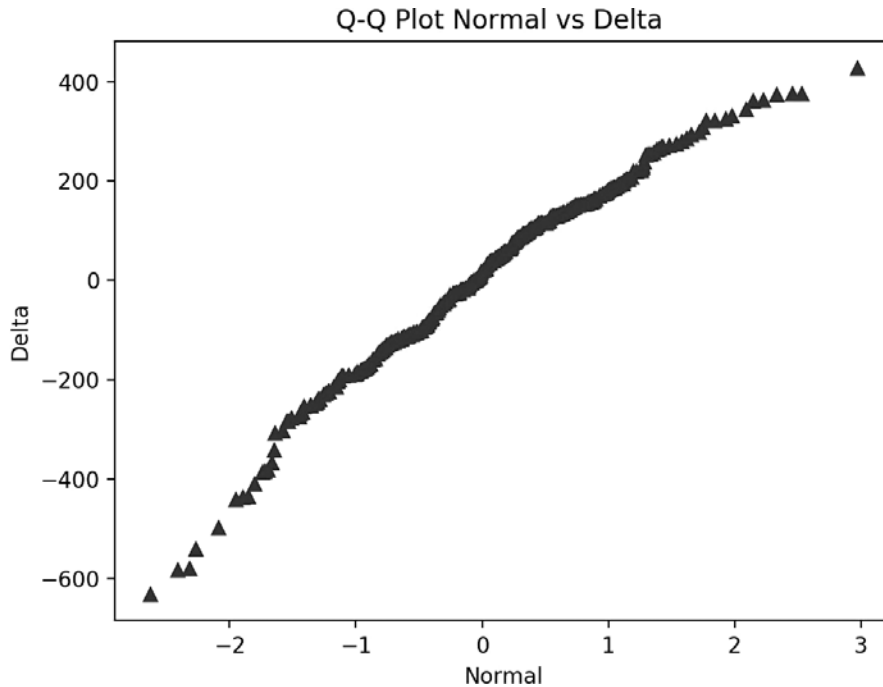


**Figure 8. Normal Q-Q Plot of Deltas vs Normal distribution from 300 runs of “Y\_sim\_Pdrive.py” with optimized parameters: 100 GK sons, Bottleneck Mortality 75–85%, Patriarchal Drive Coefficient 42. Delta is the number of variants of AF 16–32% in the 1000G data (861 variants) minus the number in this range in the model’s output at the end of each run of 25 generations.**

that of the Babel event. Regarding the population collapse of generation 22, since the children of Israel in Egypt were a large part of the population (Exodus 1:7), the genocide practiced by Pharaoh at the time of Moses’ birth, directed as it was against the male children, may have caused a loss of male lineages similar to that of major wars throughout history.

The high values of parameters required to match the 1000G data within 25 generations raises the question whether demographic events later in history, up to the present, have contributed to the common variant pattern. The program might generate the same common variant pattern with smaller parameter values if the simulation were extended to 100 or more generations with frequent

bottlenecks. The question then becomes whether population bottlenecks of 80% have occurred in recent times of larger world population.

The bottleneck events recorded in Genesis occurred when the world’s population was small, likely no more than a few thousand during the Ice Age. By the time of Moses, 22 generations post-Flood, the population had increased to several million, a 6-fold increase from Noah’s family (Jeanson, 2019). The demographic effects of bottlenecks on genetic data will be greater for small populations than for large and rapidly growing populations. Given the large population today, even the catastrophic losses of male lineages in the 20th century (White, 2016; Satter, 2017) would

not be expected to alter the common variant pattern of Y chromosome data drawn from the entire world of over 3 billion men. Simply put, population collapses of 80% have not occurred upon a worldwide basis in recent times. The loss of male lineages from the very large population of modern times would not affect genetic variant frequencies to the same degree as population collapses much earlier in history when the total population was only a few million or less (Carter, 2019).

Massive population bottlenecks are more likely to have occurred in the Middle Ages, when the total population was less than 200 million (Jeanson, 2019). In the 13th century bubonic plague may have wiped out a half of Europe (Benedictow, 2005). History does not record the mortality suffered in China, where the plague originated, but it may have been even greater. A case can be made for 50–80% population collapses during the Middle Ages. The effect of bubonic plague on the genetics of the Y chromosome have yet to be investigated.

Other than population collapses, demographic factors such as differential reproduction within subpopulations, have likely contributed to the production of some common variants by favoring some male lineages over others. This may explain the haplogroup of R1b3 found in Ireland in 20% of the men living there today. This variant originated from a man in Asia around AD 1000 (Moore et al., 2006). The R1b3 is denoted by SNP M269, which falls in minor AF bin 17% in the 1000G data. This mutation is an example of a recent demographic trend producing a common variant on the Y chromosome in the 1000G data. But on a worldwide scale, such more recent demographic events have less effect than similar events in ancient times. So, based on these theoretical considerations, the bottleneck events recorded in Genesis and Exodus are likely the major cause of the common variant pattern seen in the Y chromosome data.

## Opportunistic Male Reproduction

Adjusting the model to produce variant patterns similar to the 1000G data also required the advent of men who fathered 50 to 100 sons or more. These opportunistic breeders are well documented in the Bible and throughout history up to the present. A recent, notorious example is an NBA basketball star of the 1970's, who claimed to have had sexual relations with 20,000 different women during his life. If 1% of these women had given birth, he could have fathered 100 sons. Similar feats of male reproductive prowess stretch back to ancient times. Solomon had 700 wives and 300 concubines (I Kings 11:3). If half of these became pregnant, 250 sons may have been born. Like Solomon, Genghis Khan is thought to have had many wives and many sons (Zerjal et al., 2003; Carter, 2009). Unlike Solomon, Genghis Khan slaughtered many young men as his armies ranged over half the world (Zerjal et al., 2003). It is a sordid fact of human history that those who achieve great military victories and slaughter entire male populations tend to celebrate their victories by impregnating all the wives and daughters of the defeated. Thus, wars often have resulted in the extinction of large numbers of male lineages and repopulation by the sons of the conqueror. When this aspect of history was incorporated into the model, combining opportunistic male reproduction with population bottlenecks, the common variant pattern more closely resembled the 1000G data.

## Patriarchal Drive

Patriarchal drive may also have contributed to the formation of the common variant pattern. Patriarchal drive refers to the genetic effects of very old men fathering children in small populations. A mutational load builds up in the sperm of aging fathers as the germ cells continue to divide throughout the

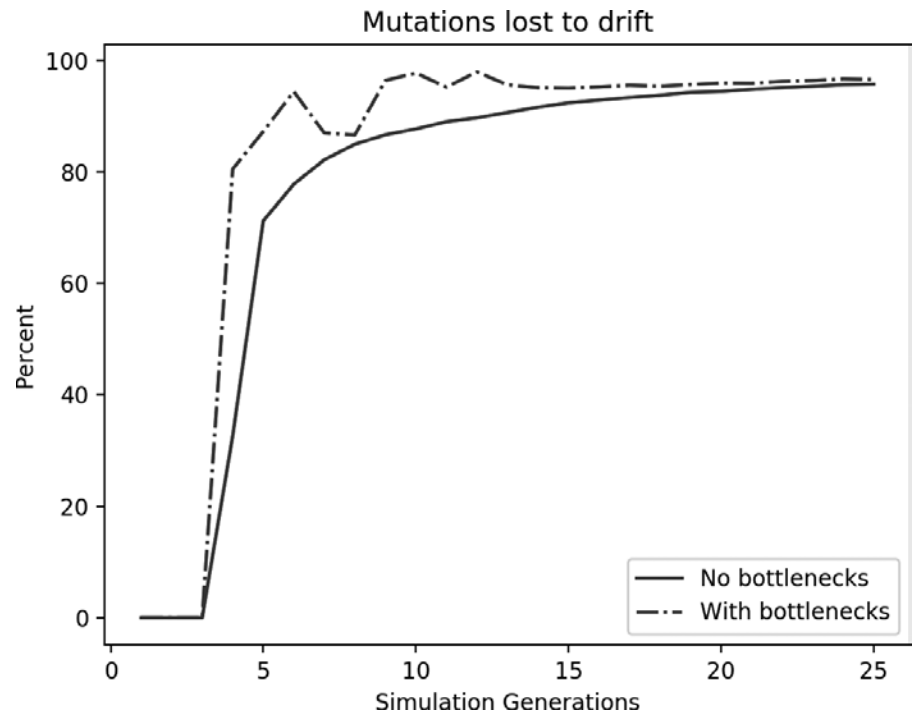


**Figure 9.** Mutations lost to drift over 25 simulated generations for the model “Y\_sim\_Pdrive.py” run with and without population bottlenecks at generations 4, 5, 6, 9, 10, 12, 22. All bottlenecks were 80% mortality. Percent = 100 X (number of mutations lost / total mutations).

man's life (Carter, 2019) so that older fathers pass on more mutations. Since Noah was 500 years old when his sons were born (Genesis 5:32), assigning 30 or more unique mutations to each of his sons is justified. The increased mutation rate of patriarchs is implicated as a cause of the deep-node structure of the Y chromosome phylogenetic tree, where the ancient branch lengths are much longer than recent branches. This explanation for the branch-length disparity is confirmed by Carter's computer model of patriarchal drive (Carter, 2019). Another explanation could be that the long branch lengths are due to population collapse, as implicated for the structure of the Native American phylogenetic tree analyzed by Jeanson

(2020). The loss of many male lineages due to population collapse also lengthens branches of the phylogenetic tree.

The Patriarchal Drive Coefficient had to be set to 42 to cause the model's output to approach a Delta of zero. Lower values of C would not allow the Delta to approach zero in 25 generations even with bottleneck mortality set to 90%. Extending the simulation to 180 generations and adding 80% bottlenecks every 5 generations caused the model to produce a Delta approaching zero with no patriarchal drive mutations added. Because these different sets of parameters were both able to force Delta to zero, the model alone does not allow conclusions regarding historically accurate parameter settings.

## Other Implications of the Model

The model's output suggests several conclusions about human population growth. The population at Babel was several thousand when the reproductive rates of Shem, Ham and Japheth are extended to Generation-4. The world's population would have reached billions before 1000 BC had not bottleneck events intervened to severely limit population growth. In the model, the population recovers rapidly following bottlenecks. This is consistent with historical records which indicate that, by 1000 BC, a 7-fold population increase had occurred from after the Flood (Jeanson, 2019).

Since the model does not account for the effects of mutations on individual fitness and reproductive success, and since the common variant pattern of the 1000G data can be modeled by demographic changes alone, natural selection of beneficial over deleterious mutations appears to be irrelevant. This is consistent with the observation that today a man's reproductive success has to do with survival from war and famine, and decisions regarding marriage and family, rather than any apparent fitness conferred by superior genes.

With each run of the model, the patriarch signatures of Noah's sons remain as prominent common AF peaks on the plot. If the model is an accurate representation of Y chromosome inheritance, the patriarch signatures of Noah's sons should be evident in the 1000G data, as the highest AF bins for each lineage. This idea is currently under investigation. However, if the model's assumptions are not true, then patriarchal variant signatures may not be discernible today. For example, the model assumes no crossing over, no gene conversion and no homoplasy (Carter, 2009). If these processes frequently occur for the

Y chromosome, then the Y chromosome common variants may not contain patriarchal signatures.

## Summary

Based on the historical events recorded in Genesis, the common variant pattern found on the Y chromosomes in the 1000 Genome database was reproduced by a computer model in 25 simulated generations post-Flood when population bottlenecks, opportunistic male reproduction, and high patriarchal mutation rates were added to the Growth, Mutation, and Famine functions. This indicates that major demographic disruptions, in the form of massive extinctions of male lineages, may have accompanied the Babel event, the Ice Age, and the famines and genocide recorded in Genesis and Exodus. The establishment of new male lineages by feats of reproductive prowess, is also implicated as a cause of the many common variants on the Y chromosomes of the world. Truly, this gives a dark picture of the character of the human male and his blood-stained history, yet this fallen character is well documented in the pages of the Bible. The reign of death due to sin described in Genesis has left a genetic record on the Y chromosome. Because mutations in the model were neutral with respect to survival and reproduction, it can be inferred from this study that natural selection, favoring beneficial mutations and eliminating unfavorable ones, has played a minor role, if any, in producing the current pattern of variants on the Y chromosomes of the 1000G database. Rather, high patriarchal mutation rates, the demographic events recorded in Genesis causing massive extinction of male lineages, and the advent of occasional men fathering hundreds of children, is the major cause of these patterns. The model indicates that the

patriarchal patterns of mutations should still be discernible in the Y chromosome databases, an area of ongoing study.

## Acknowledgments

Many thanks to Richard and Marilyn Pelosi for their assistance with the Monte Carlo simulation and statistical analysis.

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# 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.

## Coulson Response to Hebert Review

I am writing in response to a review by Jake Hebert, recently published by CRSQ, on my book, *Creation Unfolding: A New Perspective on Ex Nihilo* (CRSQ 56(4): 269). It seems that Hebert misunderstood my position, leading him to make interpretive errors which have unfortunately led to his misrepresenting both myself and the book. I would like to address some of these misunderstandings.

One misunderstood concept is my position on the ambiguity of creation. Hebert says this at the beginning of the review:

If the evidence for the creation is equivocal, then uniformitarians and evolutionists are in some sense being reasonable (p. 137) when they deny God, despite the fact that those who do so are “fools” (Ps. 14:1) and “without excuse” (Rom. 1:20). While God no doubt may withhold additional revelation in order to minimize future condemnation, this basic “natural revelation” is unambiguous, “for God has shown it to them” (Rom. 1:20).

It is true, I did make this statement on page 136 of my book, “I believe that this same kind of ambiguity has been purposefully built into the creation.” Using this statement *alone*, I could understand why Hebert makes these claims, but I clarify this statement in the very next sentence, “This concept contradicts a common, evangelical belief that presupposes God’s *creative strategy should be obvious* in the things that He has made” (emphasis mine). By “creative

strategy” the reader of my book will, by this stage, already know that I am talking about a creator God *who made the universe in six days, six thousand years ago*. It is this *strategy* that is ambiguous, *not* the creation. This is clarified several times throughout the book. This is stated on page 138:

This does not mean, of course, that the universe is devoid of evidence for God. It is *full of evidence and truly declares His power and His divine nature*. This can be seen at the macro-scale in the intricate, mathematically wondrous, and symmetrically consistent nature of the universe, as well as at the micro-scale in the complex, informationally perfect, and functionally intelligible nature of DNA (emphasis mine).

In what sense am I saying that “evidence for the creation is equivocal”? I also say this on page 133:

A great, powerful, eternal Creator *can surely be understood from nature*, but unless the gospel of Jesus Christ regenerates the heart of those witnessing that creation, they will consistently choose to rebel against the *true* God of creation, choosing rather to worship the creation (idolatry and false religion) (emphasis mine).

I make it very clear throughout the book that I am addressing the *hyper-evidentialism* of many young-Earth creationists, like Hebert, who suppose scientific evidence supporting a 6000-year-old universe is *overwhelmingly obvious*.

*THIS* is what I’m saying is ambiguous. Hebert should have included this incredibly pertinent information in his review. If Hebert had done this, it would have altered the theological implications to which I turn next.

Hebert references Romans 1:18–20 and correctly evaluates its purpose. Humans are without excuse because evidence for a creator God is *unambiguous*. Yet nowhere in Romans 1 or any other Bible passage are we told that humans are held accountable if they do not believe that our planet was made *in six days, six thousand years ago*, based on *scientific knowledge alone*. Romans 1, and, in fact, the entire Bible just doesn’t make that claim. It seems that Hebert wants Romans 1 to say more than it does. Romans 1 says that humans can derive a very *general* knowledge of God from nature—His existence, power, and Godhead, but that based *solely* on this *general knowledge*, they reject Him. That’s it. That’s all it says. This is important, because on more than one occasion, Hebert uses the theological purpose of Romans 1 to denigrate my theology as “dangerous” and “terrible.”

Regarding the Coconino Sandstone and Noah’s Flood, Hebert says, “Yet oddly, the author drops the subject with no attempt to present additional evidence that the Flood was global.” Yet this is not the case. I clearly make this obvious on page 157, “The Flood was universal.” Leaving my position on the Flood unclear, Hebert, unintentionally I hope, leaves the readers to question my position on the scope of the Flood.

I have a close, personal relationship with Dr. Brand and Dr. Whitmore, as well as with several others who are doing research on the Coconino Sandstone. Dr. Whitmore even reviewed this section of my book and said it was great! These people will be the first to affirm, based on the current state of creationist research, that we simply do not have a model showing *how* the Flood of Noah deposited the Coconino sandstone. We should not, therefore, say “the Flood did this” without being able to show “how” the Flood did this. Simplistically saying “the Flood did this” is neither scientifically accurate nor apologetically helpful. This comes from those young-Earth creationists doing the research on the Coconino, not myself!

Towards the end of the review, Hebert says that “Coulson acknowledges that his position stretches the bounds of what is considered orthodox.” In the context of the review, what is the reader to think of this statement? Without reference to the book, the reader *may* assume that I am not *theologically* orthodox. Yet this is what I said *in context*:

Having said all of this, I am fully aware that some of my *scientific and/or philosophical ideas* will not ally themselves with mainstream young-Earth creationism. These ideas are not a departure from the latter, but they certainly do seem to stretch the bounds of what is and what is not considered “orthodox.” *My deviation from mainstream young-Earth*

*creationism is, however, related only to science and philosophy, not theology* (emphasis mine).

It is surprising that Hebert would leave the question of my Christian convictions and theological commitment open to interpretation.

This review contains several other misrepresentations and even mistakes. I will direct the reader to my website for a detailed response: <https://www.creationunfolding.com/blog>. I hope that CRSQ’s readers will appreciate the full ramifications of this response and reserve their judgment until they read the book for themselves.

Sincerely,  
Ken Coulson

## Response to Colson Letter

First, let me apologize to you, Dr. Coulson, for using the epithet “young Earth evolutionist” in my criticisms of your book. Let me also state that I have no doubt that you truly believe in a recent six-day creation and a global Flood and that you sincerely want to honor the Lord Jesus Christ. However, I think you are under a serious misimpression about the state of the *evidence*. The whole premise of your book (in this discussion, page numbers are from the Kindle version) seems to be an attempt to “explain” why *evidence* is lacking for recent creation and the Flood.

However, the existence of a relatively thin veneer of fossil-containing, water-deposited rocks on the Earth’s surface is *prima facie* evidence for the Flood, as is the fact that more than seventy percent of the Earth’s surface is still underwater, not to mention the hundreds of Flood legends from around the globe. Why then are some creationists intent on acting as if evidence for the Flood doesn’t exist?

The Coconino Sandstone is a case in point. I believe you when you say Drs. Whitmore and Brand concur that we cannot use the Coconino sandstone as evidence for the Flood. Nevertheless, I am dumbfounded by this declaration. We can’t use a water-deposited layer of sand covering huge portions of the North American continent as Flood evidence until we can explain *exactly* how the Flood deposited it? *Really?* Uniformitarian geologists have no viable alternative explanation for such large-scale sedimentary deposits and Dr. John Baumgardner (2016) has demonstrated that giant tsunamis in the Flood could plausibly deposit thick layers of sediment on the continents. I find this reticence astonishing—especially compared to the eagerness with which some creationists are willing to confer plausibility on

dubious evolutionary arguments, such as whale “vestigial” appendages—even though these “vestigial” bones are *known* to be used in the reproductive process! Why acquiesce to such an obvious evidential double standard, one that is *ridiculously* slanted in favor of the evolutionist position?

Had you merely said scientific evidence alone was insufficient to prove an age of 6,000 years for the universe, I would not have objected. In fact, in my entire life I have never *once* heard *any* young-Earth creationist make such a claim. Yes, we think the preponderance of evidence strongly favors a young universe, but ‘young’ is a relative term. There are simply too many uncertainties to claim that science itself can prove a precise age of 6,000 years for the universe. The data are *consistent* with a young universe, although they cannot *prove* the universe to be young.

But you didn’t just say that the age of the universe is scientifically indeterminable; you said the universe really *does look old* (pp. 25, 31). Apparently, you think the data are *inconsistent* with recent creation. So, it isn’t too surprising that you implicitly or explicitly criticize nearly every single young-universe argument discussed in your book by saying it is inconsistent (p. 77) for creationists to use these arguments, because the ages contradict one another. But your claim of a contradiction is based on the misunderstanding that these estimates are *minimum*, rather than *maximum*, ages. If they are maximum ages, then they do not contradict one another, and creationists are *not* being inconsistent in using them.

Yes, you did briefly affirm design in nature on p. 113, but your claim that God *purposely* built ambiguity into the creation as an act of mercy to the rebellious (p. 133) undermines the design

argument. While your intent may have been merely to say that the *date* of creation is ambiguous, one of the examples you use clearly extends to the *fact of creation itself*, not merely the *date* of creation (p. 137):

As I suggested earlier, God could just as well have created a universe where every newborn baby came with the words “Made in Heaven by the God of Israel” stamped on their buttocks. Could He not have done this? This would have made things *unambiguous*, right? But this is not how He did it.

This is a clear reference to the fact of creation, not just the date of creation. So, despite your brief affirmation of design, I stand by my contention that your book, *as a whole*, undermines rather than affirms the design argument.

No one is denying that there are “problem” areas in creation science that still need to be addressed, but I absolutely reject the suggestion that evidence for a recent creation and a global Flood is lacking or is weak or equivocal.

Please understand that I am not trying to be harsh or needlessly critical, but I’m genuinely *alarmed* about the logical implications coming from your book’s thesis. I hope I’m over-reacting, but I don’t think I am. CRSQ readers can read it and decide for themselves. I think most will concur with my negative review.

Jake Hebert, Ph.D.  
Irving, Texas

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## Thoughts on the Creation Model Controversy

I became involved in the CRS (Creation Research Society) shortly after the organization was founded in 1964. Since then I have seen several major changes in the focus of the Creation Movement. One of the most radical is the shift from responding to evolution claims to pushing to develop creation models. This shift occurred about 30 years ago. In no way do I want to discourage research, but we should not lose sight of the importance of responding to evolutionary claims. One reason for my concern has to do with the results of my several decades study of why people reared in the Young-Earth Creation (YEC) movement leave and become evolutionists, often atheists. My research resulted in a full-length book on the topic (Bergman, 2019). Other researchers have come to the same conclusion as I have (Babinski, 1995). In short, YEC creationists come to reject YEC and accept the evolutionary account of the origin of life, which often goes like this:

In the beginning the Big Bang banged. What existed before this is unknown, but scientists will surely in time fill in this God of the Gaps, continuing to negate the God explanation. Soon after the Big Bang began, hydrogen atoms formed, eventually producing stars as effectively explained by the laws of physics, specifically accretion theory. Then, after billions of years, the heavy elements were formed by exploding stars called supernovae. Next, the planets formed, also by accretion, from the remnants of the supernovae explosions. On some planets, including Earth, simple molecules formed which, after a billion years or so, formed simple life. The details have not been worked out yet, but once life began the basic outline of the evolution of life has now been largely been filled in by science research. Single-celled life

evolved into multi-celled life, such as amoebae, which evolved into fish, then reptiles, then mammals, next primates and, lastly mankind. The details are now being meticulously filled in by science successfully negating the need for a creator God.

This story is very compelling to many college students, many who tend to uncritically accept it and are unaware of the enormous evidence against this worldview; consequently, the importance of presenting the evidence against it. Thus, I had more than enough cases of ex-YEC supporters who became well-known scientists to more than fill my 334-page book on the subject.

One of many examples of the problem the shift from responding to the arguments of evolution to the development of creation models caused was the 2018 ICC peer-reviewing process. I know of four excellent papers that were rejected, and the main reasons given in writing were as follows:

1. As editors, we feel that papers need to build the creationist model, not just attack the evolutionary one. We feel that as proposed, your submissions do not accomplish that important goal of ICC.
2. This proposal in its current form is inadequate for the ICC. It does not build the creation model as per instructions.

Another reason given for their rejection is that certain reviewers did not approve of critiquing Darwinism, which they called “evolution bashing.” As a result, some creationists did not attend the last ICC. The referees’ focus was on building *the* creation model. The problem is, there are many creation models, and they did not say *which one* of the many creation models that exist they support. *The* creation model was never defined, as many contradictory creation models exist. Some common competing creation models include

the residual catastrophism model, the Catastrophic Plate Tectonics (CPT) model, the Larry Vardiman hypercane model, the biogeographic rafting (or floating mat) model, the Canopy model, the neo-Canopy model, J.W. Smith’s Noah’s Upheaval (NU) Flood Theory, and the Pan Noah Flood theory, to name a few of the more popular models. The Trollingers effectively show that none of these models are empirical science but actually historical science which Ken Ham and others document is problematic (Trollinger and Trollinger, 2016, p. 81). Most of the papers rejected for ICC have now been peer-reviewed and, after very favorable feedback, were published elsewhere.

Creation models rarely even cover the central issues of creation, such as how life, and especially mankind, were created. Nor do they cover the origin of life in general except some life was created with the appearance of age [aka appearance of history]. Examples include Adam and Eve were created appearing as adults and the fruit trees were created bearing mature fruit. What is *the* creation model for the origin of the cell, the heart, the brain, and every other body part? How the animals knew when and where to travel to the Ark location has never been covered by any creation model. The development of creation models often amounts to attempting to remove the supernatural element from creation. Some events require faith and, to some degree, creation models appear to be primarily an attempt to explain what we see as miracles by naturalism. This goal is what led to the complete replacement of supernaturalism by naturalism, as C.S. Lewis has eloquently warned (Bergman, 2017). It is true that some creation models are based on empirical evidence, such as oil-well and seismic data of rock strata, to reveal the Earth’s physical past (Clarey, 2020). Unfortunately, though, many creation

models contain far more speculation than evidence.

Creation models cover primarily three areas: the age-of-the-Earth/Universe question, the details of Noah's Ark, and the Genesis Flood, by taking the existing scant scriptural skeleton and, using much speculation, embellishing it. What is *the* creation model for the origin of lightning, the Earth, the Solar System, and plants? What about the creation of photons, protons, positrons, neutrinos, and electrons and all of the other subatomic particles (if they all truly exist)? And the Sun and stars and just about everything else including time, space, matter and energy? All the Scriptures say is that, in six literal solar days, God created the fundamental

entities by fiat, then afterward made, formed, and established everything else, nothing more.

Both the Flood and the Ark are important topics that should be covered, but so should the rest of creation, as well as the major problems with Darwinism in explaining creation. In short, in contrast to the long history of the Creation Movement (Morris, 1984) as the 2018 ICC conference illustrated, outright censorship against refutation of the claims of evolutionists exists in some quarters of the modern Creation Movement (Bergman, 2018). Refuting the claims of Darwinists should continue to be a major focus of the Creation Movement today.

Jerry R. Bergman

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# Media Reviews



## *For the Love of Lakes*

by Darby Nelson

Michigan State University Press,  
East Lansing, MI, 2012,  
255 pages, \$25.00

As a non-biologist I enjoy classics in life science, especially concerning earth stewardship. This book qualifies and is similar to Henry David Thoreau's *Walden* (1854) and also Aldo Leopold's *A Sand County Almanac* (1949).

Author Nelson is a retired professor of limnology and an active conservationist in Minnesota. The book reads like a field guide to many North American lakes. Also included are descriptions of ice age evidence including the glacial "ghost" Lake Agassiz. The author explains the opposition of naturalist Louis Agassiz (1807–1873) to Darwinian evolution, although in a negative sense.

Some of the lakes that Nelson explores via canoe excursions follow:

- Fox Lake, Illinois, a model for lake ecology studies following the work of pioneer Stephen Forbes 150 years ago.

- Lake Mendota, Wisconsin, another birthplace of aquatic ecology research.
- Cedar Bog Lake, Minnesota, a classic ice age kettle lake.
- Ryan Lake, Minnesota, within Voyageurs National Park. Northern pike in this lake have the state's highest mercury concentration, even though located far from industry. Surrounding wetlands and mercury-loving bacteria are contributors (p. 180).
- Mirror Lake, New Hampshire, thoroughly studied decades ago. It was found that a major portion of the lake's phosphorous, nitrogen and acidity come from precipitation rather than surface infiltration.
- Lake Winnipeg, Canada, described as a last surviving remnant of former Lake Agassiz (p. 102).
- Walden Pond, Massachusetts, 65 acres of water made famous by the writings of Thoreau.

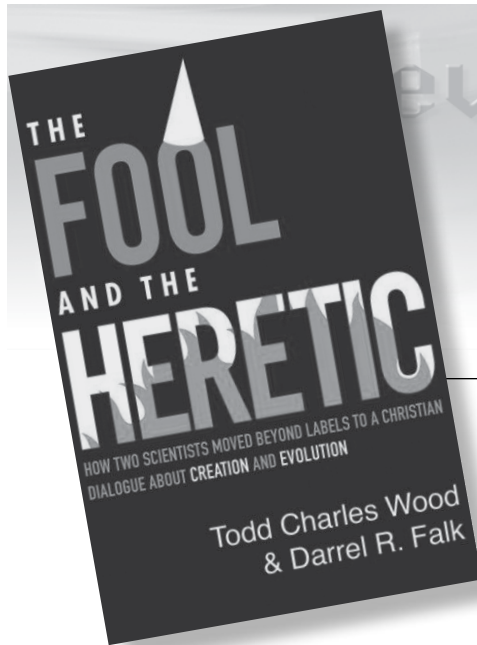
The author is an expert on aquatic vegetation and the book's helpful illustrations are plentiful. Evolution is not emphasized although assumed throughout. At one point, our large brain size is

attributed to a historic diet of fatty acids from fish (p. 26).

Author Nelson is an excellent teacher and writer, and clearly has a heart for the beauty of lake ecosystems. Still, the book is missing something very basic. The approach to earth stewardship is entirely horizontal, maintaining the perceived health of lakes. Nelson laments agricultural erosion, pollution, invasive species, shore development, removal of native vegetation and natural lake eutrophication. Why, he asks, do we love lakes but tend to degrade them? His long-range outlook for North American lakes is not positive. Meanwhile, the book does not give recognition of a higher purpose for the study and protection of lake systems. This purpose is found in Genesis 1:28, which gives mankind's "marching orders" to subdue the earth, that is, to understand and manage God's amazing world including the lakes.

The paperback book has an extensive bibliography. Unfortunately, no index is provided.

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## *The Fool and the Heretic*

by Todd Wood and  
Darrel Falk, edited by  
Rob Barrett

Zondervan, Grand Rapids,  
2019, 202 pages, \$10.00

This book tells the story of two Christians, one who accepts the Genesis creation account, while the other accepts evolutionary creation, which as far as I can tell is evolution with a thin veneer of theism. Evolutionary creation teaches that evolution creates everything, but exactly how God is behind creation is not explained. It is a popular view. The Pew Research Center finds “nearly all scientists (ninety-seven percent)” believe that humans and all other living things evolved from a common ancestor over time (p. 20).

Wood and Falk have one major event in common. Both were reared in loving Christian families and became born-again Christians at a very young age. Both had to struggle with their faith as a result of their exposure to evolution in school. And both acknowledged, as Falk admits, that the

...unpleasant reality is that evolution itself is dangerous. It is not unusual for young people who have been taught creation in their churches to go off to a Christian college, become influenced by evolution, and ultimately abandon their faith

[in Christianity]. Unfortunately, I have seen the same thing happen with students who left the Christian college where I used to teach. They went to a secular university to pursue a postgraduate degree, accepted evolution, and left their faith (p. 35).

Falk mentions one of his own students, a gifted young-earth creationist who came to his college, Point Loma Nazarene College, on a scholarship. She went on to become a neurosurgeon and now is an evolutionist and atheist (pp. 142–143). Unfortunately, “the majority of evangelical Christian colleges teach evolutionary creation” (p. 20).

Editor Rob Barrett correctly observes that, “despite Todd’s credentials, he likely would not be hired to teach science in the majority of Christian colleges” because of his creation worldview (p. 23). Of note for CRSQ readers is that, when Todd was a student at Liberty University, he discovered in the library the *Creation Research Society Quarterly*, remarking, “I never knew such a thing existed. That’s how I entered the world of young earth creationism” (p. 58).

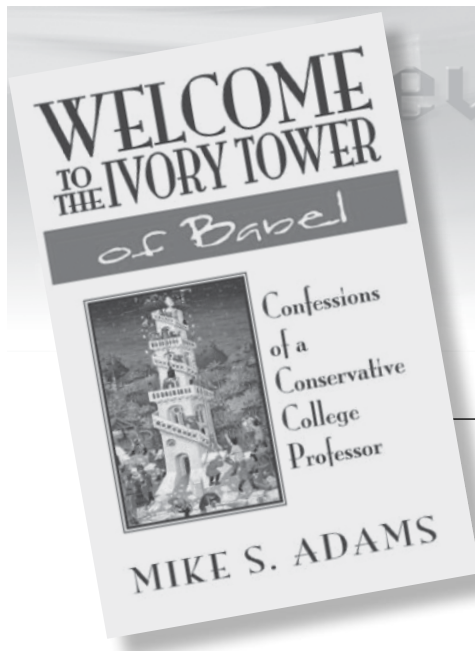
In view of the claim that rejection of evolution alienates many Christians, Falk supports Bio-Logos’ efforts to get churches to accept Darwinism. Falk states, “It’s not just that Todd is wrong, but I believe he is harming the church by promoting his view of origins.” Yet as Wood correctly observes, “I haven’t seen any evidence that mainstream scientists

are becoming Christians in droves because Darrel and others accept the theory of evolution” (pp. 35, 44). Falk admits that, while in graduate school “I never met any other biologist whom I knew to be a Christian” (p. 72).

One bothersome point about Falk is his repeated statement that “the evidence for evolution is vastly overwhelming,” and there are “few things about which I am more certain than I am about evolution.” He stresses the “overwhelming support for evolutionary theory” (pp. 43, 48, 134, 141, 148). He also repeats the now-disputed Out-of-Africa theory of human evolution.

In the chapter titled *Overwhelming Evidence*, Falk repeats the usual evolution stories, even *Tiktaalik*, now considered an evolutionary dead-end. Falk also makes far-reaching and dogmatic claims, for example, “We do know from genetics that there was never a time when just two members of our species were present on earth” (p. 116). Falk writes that “Chimpanzees and humans descended from a common ancestral species that existed about five or six million years ago” (p. 140). If true, the known genetic mutation load in humans would have resulted in the extinction of these humans eons ago. In conclusion, this book is one more example that evolution is the doorway to atheism.

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## Welcome to the Ivory Tower of Babel: Confessions of a Conservative College Professor

by Mike Adams

Harbor House, Boyne City, MI,  
2004, 200 pages, \$29.95

I read this book in remembrance of my recently-deceased author friend Mike Adams. The book is 16 years old and remains relevant. The concern of the book is that universities are focused not only on favoring skin-color diversity, which I support, but also on opposing mind diversity, to which I object.

At Adam's university (North Carolina Wilmington), creationists, Christians, Republicans, and conservatives of all types are rare (pp. 144–145). Fortunately, some schools realize this is a problem and advertise that they do not focus on teaching *what* to think, but rather *how* to think.

In court, due to discrimination he faced because of conservative Christian beliefs, Adams prevailed in a landmark First Amendment case (*Adams v. Trustees*, 2011). Decided in 2011, the court held that professors have the full protection of the First Amendment when discussing matters of public concern. Hence, for annual review, tenure, or promotion materials, the university does not have license to discriminate on the basis of a professor's views. The case was widely regarded as

a major victory for academic freedom (Bonilla, 2019).

Fully 40 percent of Americans accept the view that humans did not evolve from an ape ancestor, but rather God created mankind in his present form about 10,000 years ago. Of biology professors, only 0.02 percent fully accept this view. Furthermore, “over 150 years after *On the Origin of Species*, less than 20 percent of Americans accept that humans evolved by natural and unguided processes... It's hard to think of any other discipline at odds with the mainstream scientific consensus” (Lang and Rice, 2019).

The creation issue often occurs in this book. Adams devotes an entire chapter responding to Texas Tech biology professor Michael Dini who notes that medicine was “first rooted in the practice of magic ... until it was replaced by science” (pp. 90–91). Dini writes that biology is the “science most important to the study of medicine” adding that “evolution as the ‘central, unifying principal of biology,’ ... includes both micro- and macro-evolution and that applies to all species,” including humans (p. 91). Dini opines, without citing evidence, that someone who rejects “the most important theory in biology cannot properly practice medicine,” and physicians who ignore “Darwinism are prone to making bad clinical decisions.” This rationale is given as his reason for refusing to write a

letter of recommendation for a pre-med honor student. Dini admits that all of the details of human evolution are not yet known, but that human evolution from some evolutionary ape ancestor is a proven fact (p. 93).

Adams responds to Dini by demanding proof for the assertion that the origin of all species can be traced back to some primordial soup (p. 94). The response was silence. Adams concludes that biology “has been hampered by the widespread and uncritical acceptance of Darwinian principles” (p. 94).

After Adams wrote a column criticizing the theory of evolution, he received a note saying, “God is only a theory and evolution is a fact,” to which he responded by noting that Darwin himself called his idea, not fact, but “my theory” (Adams, 2003, p. 171). This response, instead of humbling the note writer, only generated anger.

In spite of glowing student evaluations, the school administration disliked Adams, leading to his recent tragic demise. That is, Adams took his own life on July 23, 2020. Assuming the events he relates in the book are true, and I have no reason to believe otherwise, colleges are in deep trouble. As University of Michigan's Marvin Olasky earlier writes, “Mike Adams is a rarity at a secular university—an outspoken Christian and a conservative with tenure” (Olasky, 2009). As a colleague told

me years ago, a professor's goal is to make students as much *unlike* their parents as possible. As I read this book, I thought about Professor Michael Scott Adams (1964–2020), who will be missed by me and many others.

**Jerry Bergman**  
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# 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](http://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](mailto: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 abbrevi-

ated 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. Following this period, individuals who desire to write additional responses/comments (particularly critical comments) regarding a specific *Quarterly* article are encouraged to submit their own articles to the *Quarterly* for review and publication.

### 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.

# 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](http://creationresearch.org).



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† **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.

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## 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 Chino Valley, 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.

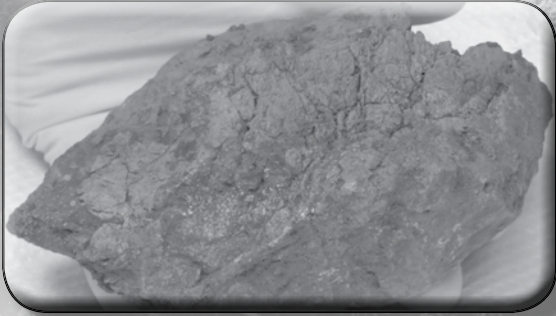
2. All basic types of living things, including humans, were made by direct creative acts of God during the Creation Week described in Genesis. Whatever biological changes have occurred since Creation Week have accomplished only changes within the original created kinds.

3. The Great Flood described in Genesis, commonly referred to as the Noachian Flood, was a historical event worldwide in its extent and effect.

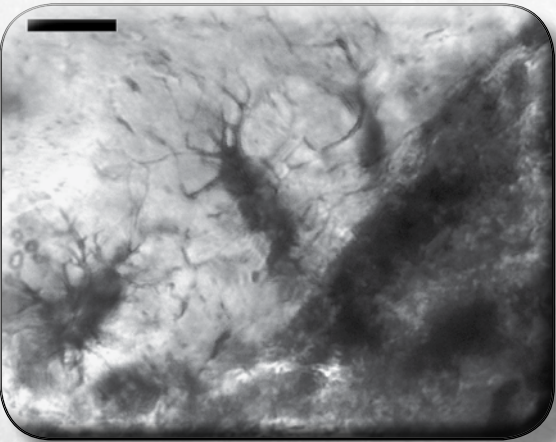
4. We are an organization of Christian men and women of science who accept Jesus Christ as our Lord and Savior. The act of the special creation of Adam and Eve as one man and woman and their subsequent fall into sin is the basis for our belief in the necessity of a Savior for all people. Therefore, salvation can come only through accepting Jesus Christ as our Savior.

# iDINO II

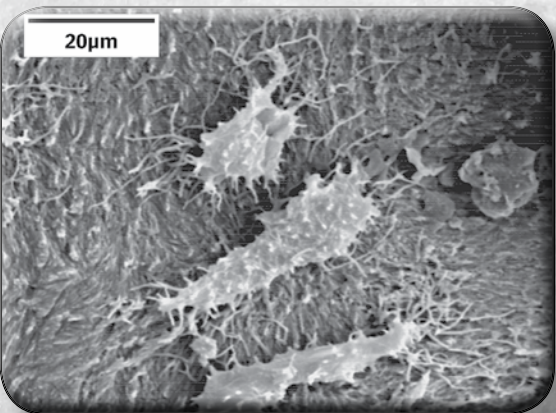
## Investigation of Dinosaur Intact Natural Osteo-tissue



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](mailto:crsvarc@crsvarc.com).

Also visit <http://tinyurl.com/nphm2c4> for project updates and details.



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