God's Trilateral Fingerprint

The Creator's inscription of the number 37 into His written Word, His living Word, and His living creatures.

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Abstract

This article asks if God purposefully designed the number 37 into His spoken word (the first verse of the Bible, Genesis 1:1), into His created life (the genetic code) and into the names of His Son ("Jesus" and "Christ"). If so, the connections are profound. God creates through His word, and since the creation has a mathematical structure it shouldn't be surprising to find such structure also in the word. And since the Bible entitles Jesus as both God's word (Joh 1:1) and life (Joh 14:6), it is not far-fetched if similar patterns would also be found in the names of our Lord.

More specifically, we analyze divisibility patterns of alphanumeric coding schemes from Genesis 1:1 and the words Jesus Christ, as well as nucleon numbers of amino acid groups, derived from the genetic code. We introduce a null hypothesis that these patterns are generated by chance, and estimate the p-value, i.e. the probability for the observed structures to occur under this null hypothesis. It is found that the p-value of Genesis 1:1, the genetic code and the words Jesus Christ, after a generous correction for multiple testing, are 1.7×10^{-3}, $3.0 \cdot 10^{-14}$, and 3.7×10^{-3} respectively, whereas the combined p-value for all three divisibility patterns is at most $4.6 \cdot 10^{-11}$ after multiple testing correction.

Due to the objective and inerrant nature of mathematics, we argue that the abovementioned structural patterns are difficult to deny. And since both the Bible and the creation are branded by the same number 37, it seems reasonable to conclude that it is the same Intelligence behind both.

1 Introduction

In his now classical paper from 1960 - The Unreasonable Effectiveness of Mathematics in the Natural Sciences - Nobel laureate Eugene Wigner pondered over the fact that nature is mirrored in mathematical formalism (Wigner, 1960). He found the bond so profound that he even associated it to a miracle: "The miracle of the appropriateness of the language of mathematics for the formulation of the laws of physics is a wonderful gift which we neither understand nor deserve."

In this article we investigate if what Wigner referred to as a miracle may be taken one step further. We examine the possibility that in the same way as natural law contains a mathematical structure, so does God's word. Even if this sounds unfamiliar, it should not come as a surprise since God uses His word to create the very same laws. *"By faith we understand that the world was created by the word of God."* (Hebr 11:3, RSV)

We also investigate if the patterns in God's word may also be found in God's creation. The pinnacle of the creation is life, and therefore we investigate if life (as defined by the genetic code) also contains mathematical patterns. And since Jesus Christ is both God's Word (Joh 1:1) and God's Life (Joh 14:6) - even the Word of Life (1 Joh 1:1) - maybe also His names share the same pattern?

In this article we conclude that God's spoken word (specifically the "creation verse" Genesis 1:1), God's living Word (as the names of our Lord) and God's creation (specifically the genetic code) all contain mathematical patterns, and that these patterns ought to be a result of design. Not only this, but we also conclude that it is the same pattern, built on the number 37, in these three occurrences, probably demonstrating it is the same Designer behind them all. In statistical terms we find that the probability for the patterns to occur by chance is well below 10^{-10}.

2 What we do not claim

We are keenly aware that many fellow-Christians are dubious of exploring the Bible with the aim of detecting mathematical patterns. *And rightly so!* The area is loaded with unfounded speculation, wishful thinking, and outright errors. Therefore, we feel a need from start to stipulate what we do not claim:

2.1 We find no hidden messages in the Scriptures

The patterns in Scripture that we aim to show must not be confused with "codes" carrying secret messages or esoteric knowledge addressed to a select few with special insight. The Bible is written to be understood and applied to the Christian life, so why would its Author camouflage its teachings behind curtains of enigmatic mathematics? We reject all forms of mysticism, kabbalism and occultism.

However, we do believe that the possible patterns have another purpose than that of extending our knowledge from what is expressed in the plain text. We believe the structures are there to validate the text. They are deliberately incorporated in the Bible by God as His authenticity seal. The same is true for the genetic code. Its possible patterns based on the number 37 has nothing to do with its efficiency in coding for various lifeforms, but they uncover an intellect composing the code.

2.2 We do not search for ELS in the Scriptures

Equal Letter Sequences (ELS for short) is the idea that additional information may be extracted from a text by reading not every letter but every n:th letter, where n is a positive or negative integer which may be arbitrarily large (Witztum et al., 1994, McKay et al., 1999). Applied to the Bible, the method gives so many degrees of freedom that it is difficult to avoid observational bias: The text mass is large, n may be chosen freely, vowels may be inserted freely (since they are not part of the original text), and many possible "hits" are possible. For example, if searching for the holocaust, many words besides "holocaust" would fit the expected scheme, words such as "Hitler", "Göring", "Nazism", "Auschwitz", and "Jews".

In our opinion, these pitfalls are abundant in Michael Drosnin's bestselling book The Bible Code from 1997 and followed by two sequels from 2002 and 2010 respectively (Drosnin, 1997, 2002, 2010). Some argue that the drawbacks of the ELS-method are less obvious in Dr. Moshe Katz' Computorah from 1996 (Katz, 1996), but we do not make any claims whatsoever regarding the applicability of the method.

2.3 We do not attach any symbolic meaning to the numbers of Scriptures

The Scriptures seem to assign symbolic significance to certain numbers. For example, the Book of Revelation makes ample use of the number 7, probably representing spiritual excellence. In his classical book Number in Scripture from 1894, E.W. Bullinger exposes representational meaning to many numbers in the Bible, where the numbers are either expressively stated or found as the quantity of certain objects or concepts (Bullinger, 1894). He also gives significance to numeric values of Hebrew and Greek letters, identified through certain alphanumerical coding schemes, a concept that will be explained in Section 5.

Even if we do recognize symbolic meaning to some numbers in Scripture, this article makes minimal use of them. They are not part of the main flow of the argument, but on a few occasions, we use them to speculate why God has chosen specific numbers, and not others, in designing the codes.

2.4 We do not believe the detected patterns exist in other literature

Brendan McKay and others have found many ELS-codes in literature beside the Bible. As an example, McKay discovered many words connected to the murder of J.F. Kennedy in fictional pieces such as Moby Dick and War and Peace (McKay et al., 1999, Bronner, 2016, p. 50-51). The conclusion is that the degrees of freedom for an ELS-code, exemplified above, are so large that patterns may appear randomly in many texts that are extensive enough.

However, due to the extensive statistical method we are using in this article, we argue that there are patterns not explainable by chance.

3 What we do claim

Our aim is to expose similar mathematical patterns based on the number 37 both in the genetic code and in the Bible, mainly in its first verse and in the names of the Son of God, "Jesus" and "Christ". We believe this is a strong case for an intelligent Designer, but the fact that the Bible and the genetic code seem to contain analogous patterns take us even further: It would show that the patterns not only reveal an intellect far beyond human capacity, but also that it is the very same Intelligence behind both the Bible and the creation. And since we find the patterns of the Bible in both of its main languages (Hebrew and Greek), it may further be used as evidence for the same Author behind both the Old and the New testaments. By branding Scriptures with the number 37 we argue that God authenticates His word, and by imprinting the genetic code with the very same number, God verifies He is also the Creator of life.

Finding mathematical patterns in the Scriptures should not come as a total surprise. Creationists appropriately use mathematical regularities in natural law as evidence of a Legislator. This Lawmaker creates by speaking into existence (Hebr 11:3), and since the creation is mathematical so could God's word be. If the mathematical structure of the Bible astonishes us, we must not forget that also the mathematical structure of nature is a miracle. The difference maybe that we have become accustomed to the latter but not to the former.

4 Methods and results

In an unambiguously manner, our method assigns integers (called *counters*), to different constituents (called *words*) of the Bible text and of the genetic code, and then by combining these words in different predetermined sets (called *word groups*), we find that the groups' numeric values - obtained by adding the counters of the included words - are divisible by 37 far more frequently than would be expected if they were the result of chance. In our study, we analyze three different assemblies of word groups (called *word group collections*):

Genesis 1:1 The words are the 7 words of the Masoretic text, and the counters are their Hebrew gematria values (explained in Section 5). There are 127 word groups formed by permutating the words in all possible ways (excluding the trivial group with no words).

The genetic code The 21 words consist of the 20 standard amino acids derived from the genetic code together with the collection of atoms that these amino acids share (the standard block). The counters of these words are their nucleon numbers. There are 13 word groups formed in pre-defined ways, mainly by bi- and trisecting the code.

"Jesus" and "Christ" These names of our Lord constitute 2 words, and the counters are their Greek isopsephy values (explained in Section 5). There are 3 word groups formed by selecting all nonempty subsets of words.

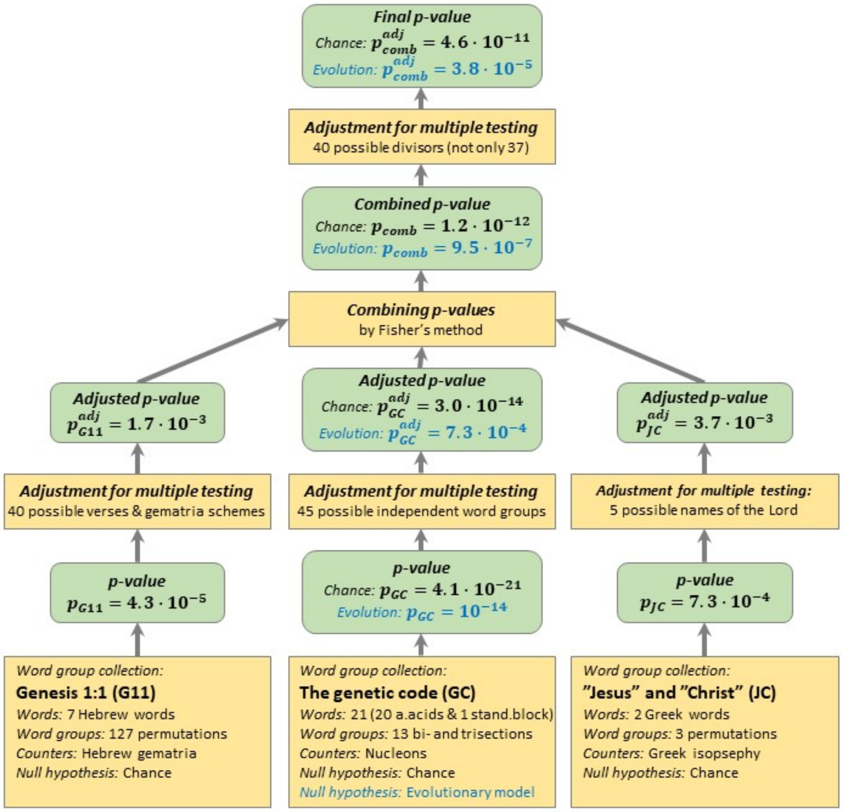


Figure 1: The method used in this article for computing the combined, adjusted p-value of Genesis 1:1, the genetic code and the words "Jesus Christ", together with its results.

Figure 1 gives an overview of the method used. At the bottom are the 3 word group collections with their respective words, word groups, and counters. Each box outputs a p-value (described in Sections 6, 7, and 8 respectively) which is the probability of obtaining the patterns of divisibility by 37 under the assumption that the null hypothesis is correct. Our null hypothesis is that the patterns are generated by chance meaning, in short, that a p-value gives the probability that the observed pattern appears by chance.

For an evolutionary biologist, another choice of null hypothesis for the genetic code may appear as more relevant, which is that the observed patterns may be a result of chemical evolutionary processes. We consider this possibility in Section A.7.3 of the appendix and include the resulting very conservative p-value estimate as blue text in Figure 1.

The p-values need to be safeguarded against observational bias, a concept which means that a hypothesis is tested only for an observed pattern while other patterns, with possibly as astonishing results, are disregarded. Therefore, in Section 9 we adjust for multiple testing, that is, the probability of randomly having at least one equally remarkable pattern as the one observed when certain factors are varied: for Genesis 1:1 we allow for other Bible verses and other Hebrew gematria schemes, for the genetic code we allow for other subgroups of codons, and for "Jesus" and "Christ" we allow for other names of the Lord.

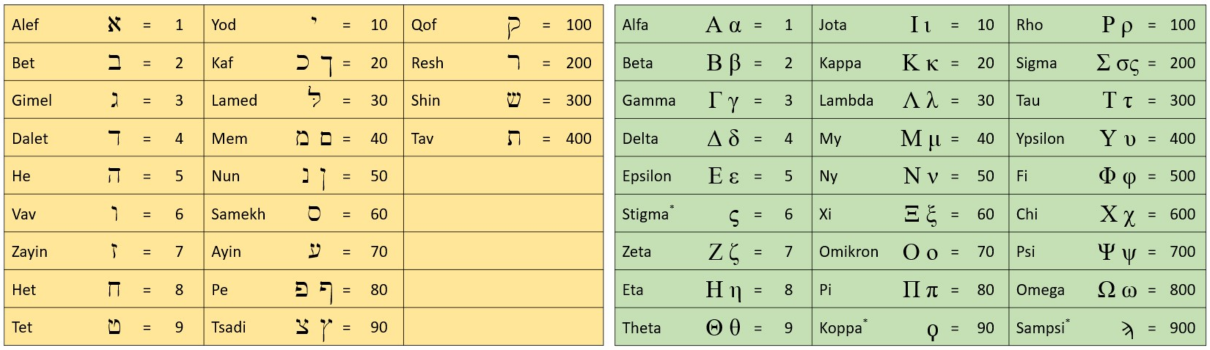
In Section 10 we merge the three p-values (adjusted for multiple testing) into one single p-value. The combined p-value is also adjusted for multiple testing because other divisors than 37 may give as remarkable results. The so constructed final p-value is low, 4.6×10^{-11}. A sensitivity analysis, with the combined p-values for other multiplte testing scenarios, is also provided in Section 10.

After showing (in Section 11) that all three word group collections contain other interlaced codes that further strengthen the conclusion, we conclude in Section 12 that the smallness of the final p-value suggests that there is something or Someone else at work besides randomness. We argue that there are mathematical patterns and that these are a result of fine-tuning.

All mathematical details are placed in an appendix (Sections A.1-A.7).

5 Alphanumerical coding schemes

Today we use dedicated symbols $(1, 2, 3, \ldots)$ to express integers, but in many ancient cultures, numeric values were instead assigned to the letters of the alphabets. Also words and phrases could be assigned values by simply adding the values of their constituent letters. This means that a written text not only conveyed semantic meanings on different levels but also numeric values that may be analyzed with arithmetic methods.



Alef	א	=	1	Yod	י	=	10	Qof	ק	=	100
Bet	ב	=	2	Kaf	כ ך	=	20	Resh	ר	=	200
Gimel	ג	=	3	Lamed	ל	=	30	Shin	ש	=	300
Dalet	ד	=	4	Mem	מ ם	=	40	Tav	ת	=	400
He	ה	=	5	Nun	נ ן	=	50				
Vav	ו	=	6	Samekh	ס	=	60				
Zayin	ז	=	7	Ayin	ע	=	70				
Het	ח	=	8	Pe	פ ף	=	80				
Tet	ט	=	9	Tsadi	צ ץ	=	90				

Hebrew: gematria scheme *mispar hechrachi*

Alfa	Α α	=	1	Jota	Ι ι	=	10	Rho	Ρ ρ	=	100
Beta	Β β	=	2	Kappa	Κ κ	=	20	Sigma	Σ σς	=	200
Gamma	Γ γ	=	3	Lambda	Λ λ	=	30	Tau	Τ τ	=	300
Delta	Δ δ	=	4	My	Μ μ	=	40	Ypsilon	Υ υ	=	400
Epsilon	Ε ε	=	5	Ny	Ν ν	=	50	Fi	Φ φ	=	500
Stigma*	ϛ	=	6	Xi	Ξ ξ	=	60	Chi	Χ χ	=	600
Zeta	Ζ ζ	=	7	Omikron	Ο ο	=	70	Psi	Ψ ψ	=	700
Eta	Η η	=	8	Pi	Π π	=	80	Omega	Ω ω	=	800
Theta	Θ θ	=	9	Koppa*	ϙ	=	90	Sampsi*	ϡ	=	900

Greek: isopsephy scheme

Figure 2: The Hebrew and Greek methods of assigning numbers to letters. In the Hebrew table, wherever two letters are given, the second one is used at the end of words. In the Greek table, the second lowercase letter for sigma is used at the end of words. Letters marked with an asterisk are extinct.

In Hebrew, the procedure of assigning values to letters is called gematria. (There is an extended application of the concept where each number is given a symbolic or mystic meaning, but as we have acknowledged in Section 2, we do not advocate such connections between gematria numbers and meanings.) The Jewish Encyclopedia lists a number of different gematria schemes (Skolnick et al., 2007), i.e. different ways of assigning numbers to letters, and we have employed the one called mispar hechrachi described in Figure 2. Our reason is threefold:

- It is the standard method and most commonly used.
- It is the most straightforward method in that the value of each letter is based on its position in the alphabet (Mispar hechrachi means “absolute value”).
- Its principle of assigning numbers to letters equates the principle of the corresponding Greek alphanumerical scheme. (Letters 1-9 give ones, 10-19 give tens, and $20-n$ give hundreds where $n = 22$ for Hebrew and $n = 28$ for Greek.)

In Greek, the corresponding practice is called isopsephy, and its cipher is also defined in Figure 2. Unlike Hebrew gematria with many possible alphanumerical conversion schemes, we have found only one used in isopsephy, and, as said, its principle corresponds to the Hebrew mispar hechrachi.

The Hebrews began using gematria after the Old Testament was written, which means that the key to decipher a possible code was discovered after the code was generated. In our opinion this excludes human interventions in creating both the code and the key. We believe that when God inspired the writers of the Scriptures, He led them to include mathematical patterns but had other men to discover them later. This is a form of progressive revelation, but not by adding to the Scriptures but by uncover what is already there.

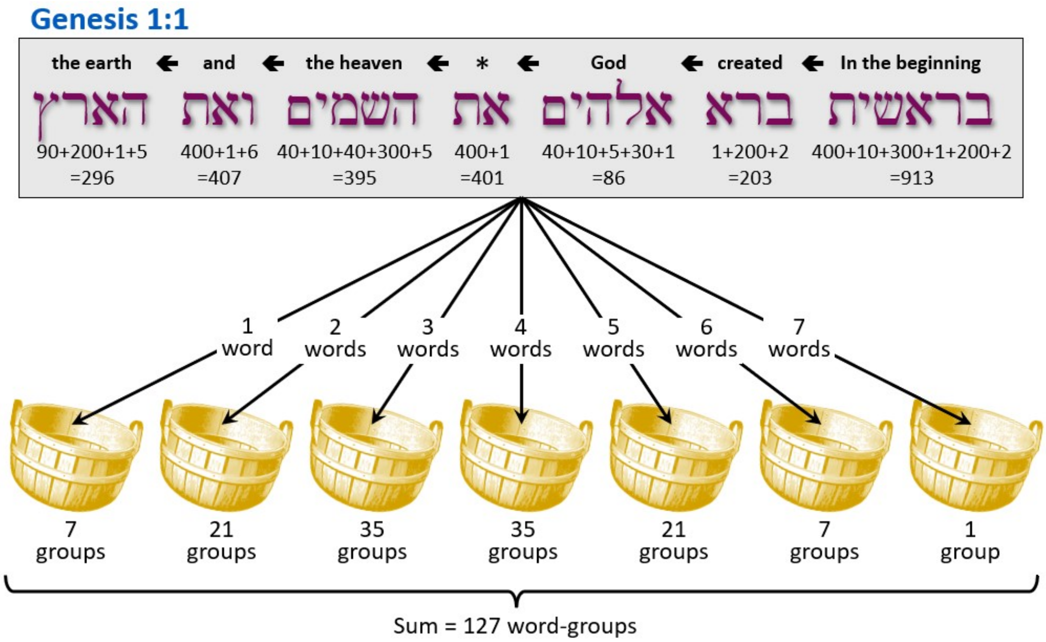


Figure 3: The gematria values associated with the letters and words of Genesis 1:1, and how the words are combined into 127 word groups. The middle word (marked with an asterisk) is a grammatical construction that cannot be translated. Note that in Hebrew the text is read from right to left.

6 37 in Genesis 1:1

We may now proceed to examine the first verse of the Bible with the intent of finding an alphanumeric pattern. We do this by forming all possible word groups and examining how many of these have gematria values divisible by 37. Figure 3 shows the numeric values associated with each letter and each word of this first verse of the Bible and how the words are combined into 127 possible groups.

Naturally, we will expect every m:th word group to be divisible by m from pure statistical reasons. For example, if we set $m = 5$, we would expect 25 or 26 word groups to be divisible by 5 since $127/5 = 25.4$. And in our case, 3 or 4 word groups ought to be divisible by 37 since $127/37 = 3.4$. In reality however, 23 of the word groups are divisible by 37 (see Table 3 in the appendix), which is far more often than may be expected from statistical reasons. In Figure 4 we display this fact intuitively, and in Section A.4.4 we calculate its p-value to $4.3 \cdot 10^{-5}$.

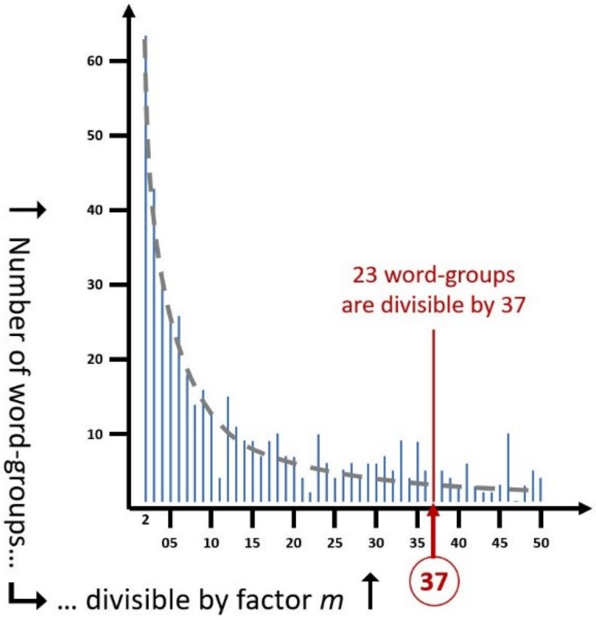


Figure 4: The bars show the *actual* number of word groups in Genesis 1:1 divisible by m, where m is displayed at the horizontal axis. The dashed line shows the *expected* number of such groups calculated as $127/m$. As shown by the red bar, $m = 37$ stands out.

We would like to give recognition to Vernon Jenkins (Jenkins, 2015) from whose website most of the information concerning 37 in Genesis 1:1 is derived.

7 37 in the genetic code

Vladimir Shcherbak (PhD) and Maxim Makukov (MS) have - evidently without any biblical ambitions - discovered arithmetic regularities based on the number 37 in the genetic code. This is explained in detail in Shcherbak (2003) and Shcherbak and Makukov (2013). In the latter paper the authors draw the conclusion: "Accurate and systematic, these underlying patterns appear as a product of precision logic and nontrivial computing rather than of stochastic processes (the null hypothesis that they are due to chance coupled with presumable evolutionary pathways is rejected with p-value 10^{-13})." They assert that the proposal that terrestrial life is intentionally seeded cannot be ruled out. We fully agree but want to extend their conclusion to identify the One who was doing the "seeding". Since the genetic code is hallmarked with the same number (37) as Genesis 1:1, in our view, its originator has introduced Himself as the God of the Bible.

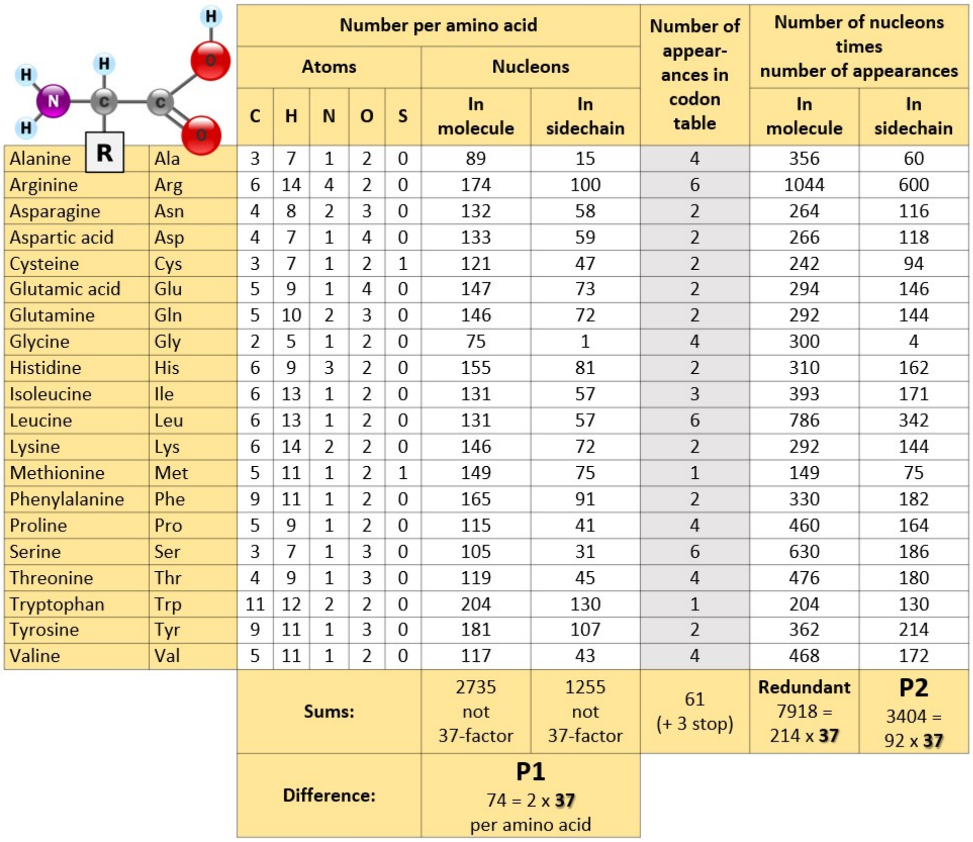
All our genetic patterns are from Shcherbak and Makukov. However, we will use a somewhat different approach. Their p-value does not incorporate divisibility by 37, while ours does, motivated by the fact that Genesis 1:1 has this number in its divisibility patterns. In their null hypothesis, the observed patterns are a result of random evolutionary processes, while in ours they are a result of chance in terms of random assignment of nucleon numbers. (However, in Section A.7 we also test a biologically motivated null hypothesis.)

A basic understanding of molecular biology is necessary to understand our method, and therefore we start by investigating some basics facts. The DNA-molecule stores its information as nitrogen bases which are transcribed into mRNA-molecules. When the genetic machinery translates this information into a sequence of amino acids that are about to become a protein, it reads the bases three and three. The bases may therefore be regarded as letters in a genetic language and the three-letter groups as words (called *codons*). There are 4 different letters/bases (denoted T, C, A and G), and therefore there are $4^3 = 64$ possible triplets which code for the 20 amino acids in the library of life (called *standard amino acids*). This means that different codons may code for the same amino acid or alternatively, the genetic language contains synonyms. Three of the codons do not code for any amino acid at all but constitute stop-codes to the translation machinery. (In RNA, T is replaced by U but that is irrelevant to our discussion here.)

The letters/bases of DNA come in two different types: *purines* and *pyrimidines*. The main difference is that the nitrogen ring in purines is fused to an imidazole ring whereas in pyrimidines it is not. A and G are purines while T and C are pyrimidines. To reduce the burden of keeping track of which is which, from now on purines are simply called "A/G" and pyrimidines "T/C".

The standard *DNA codon table* defines which triplet of bases codes for which standard amino acid. This translation scheme is universal for the whole biosphere, although a few small variants are known (Knight et al., 2001). One way to put it is that all life forms "speak" the same genetic language. The table is depicted in Figure 6 where the first letter in each codon appears on the four main rows, the second letter in the four columns and the third letter within each square.

The divisibility patterns searched for are revealed by an analysis of the standard codon table. As numbering scheme for the amino acids, we use their numbers of nucleons, i.e. the protons and neutrons in their atomic nuclei. (Since STOP-codons do not code for any amino acid, their nucleon counts are set to zero.) This is appropriate since it well distinguishes the different amino acids, and it is a countable rather than a physically measurable parameter. In this way nucleon numbers become arithmetical units inside the genetic code that may be examined for divisibility patterns. We identify several unambiguously defined groups of amino acids, based on where and how many times these acids appear in the codon table, and then we investigate whether the groups' constituent amino acids have sums of nucleon numbers divisible by 37. If this occurs significantly more often than expected from statistical reasons, a purposeful signal in the code may be inferred. In total, we have identified 13 groups of amino acids which exhibit divisibility patterns based on 37, and we label these patterns P1-P13 below. It is crucial that these groups are formed from pre-defined criteria, since a freedom to form groups in arbitrary ways would greatly increase the probability of finding a searched-for pattern.



		Number per amino acid							Number of appearances in codon table	Number of nucleons times number of appearances	
		Atoms					Nucleons				
		C	H	N	O	S	In molecule	In sidechain		In molecule	In sidechain
Alanine	Ala	3	7	1	2	0	89	15	4	356	60
Arginine	Arg	6	14	4	2	0	174	100	6	1044	600
Asparagine	Asn	4	8	2	3	0	132	58	2	264	116
Aspartic acid	Asp	4	7	1	4	0	133	59	2	266	118
Cysteine	Cys	3	7	1	2	1	121	47	2	242	94
Glutamic acid	Glu	5	9	1	4	0	147	73	2	294	146
Glutamine	Gln	5	10	2	3	0	146	72	2	292	144
Glycine	Gly	2	5	1	2	0	75	1	4	300	4
Histidine	His	6	9	3	2	0	155	81	2	310	162
Isoleucine	Ile	6	13	1	2	0	131	57	3	393	171
Leucine	Leu	6	13	1	2	0	131	57	6	786	342
Lysine	Lys	6	14	2	2	0	146	72	2	292	144
Methionine	Met	5	11	1	2	1	149	75	1	149	75
Phenylalanine	Phe	9	11	1	2	0	165	91	2	330	182
Proline	Pro	5	9	1	2	0	115	41	4	460	164
Serine	Ser	3	7	1	3	0	105	31	6	630	186
Threonine	Thr	4	9	1	3	0	119	45	4	476	180
Tryptophan	Trp	11	12	2	2	0	204	130	1	204	130
Tyrosine	Tyr	9	11	1	3	0	181	107	2	362	214
Valine	Val	5	11	1	2	0	117	43	4	468	172
		Sums:					2735 not 37-factor	1255 not 37-factor	61 (+ 3 stop)	**Redundant** 7918 = 214 x **37**	**P2** 3404 = 92 x **37**
		Difference:					**P1** 74 = 2 x **37** per amino acid				

Figure 5: Numeric values for life's 20 amino acids. The most common isotope of carbon (C) has 12 nucleons, hydrogen (H) 1, nitrogen (N) 14, oxygen (O) 16, and sulfur (S) has 32 nucleons.

P1-P2: Nucleon counts for complete set of standard amino acids

Figure 5 gives some basic data for each standard amino acid. The graphic in the upper left corner illustrates a general amino acid which consists of a standard block, H2NCHCOOH (the same in all amino acids), and a side chain R (unique to each amino acid). The table lists the number of C-, H-, N-, O-, and S-atoms in each amino acid and the corresponding nucleon counts for both for the full amino acid molecules and for their side chains R.

(It should be noted that proline has a special chemical bound which causes one of the hydrogen atoms (one nucleon) in the standard block to chemically belong to the side chain. However, here it is considered as part of the standard block to make the structure uniform with the other amino acids. Shcherbak and Makukov call this the *activation key* of the code since there is no natural reason for such nucleon transfer. Instead it appears artificial, which is what seems to be its purpose. Since the discovered patterns in this way become virtual and not physical, they are protected from any natural explanation.)

P1 emerges as the nucleon count of the standard block of each amino acid, 74 ($= 2 \cdot 37$). In Figure 5, it appears as the difference between each amino acid's full molecule nucleon count and the nucleon count of its sidechain.

P2 emerges when multiplying the amino acids' nucleon counts by the number of times they appear in the codon table. The sum for all amino acids' sidechains is 3404 ($= 92 \cdot 37$), also divisible by 37. (Naturally, also the nucleon sum for the full molecules is divisible by 37, but this is redundant information since we have already concluded that each standard block is divisible by 37.)

P3-P9: Bi- and trisections of the full-sized genetic code table

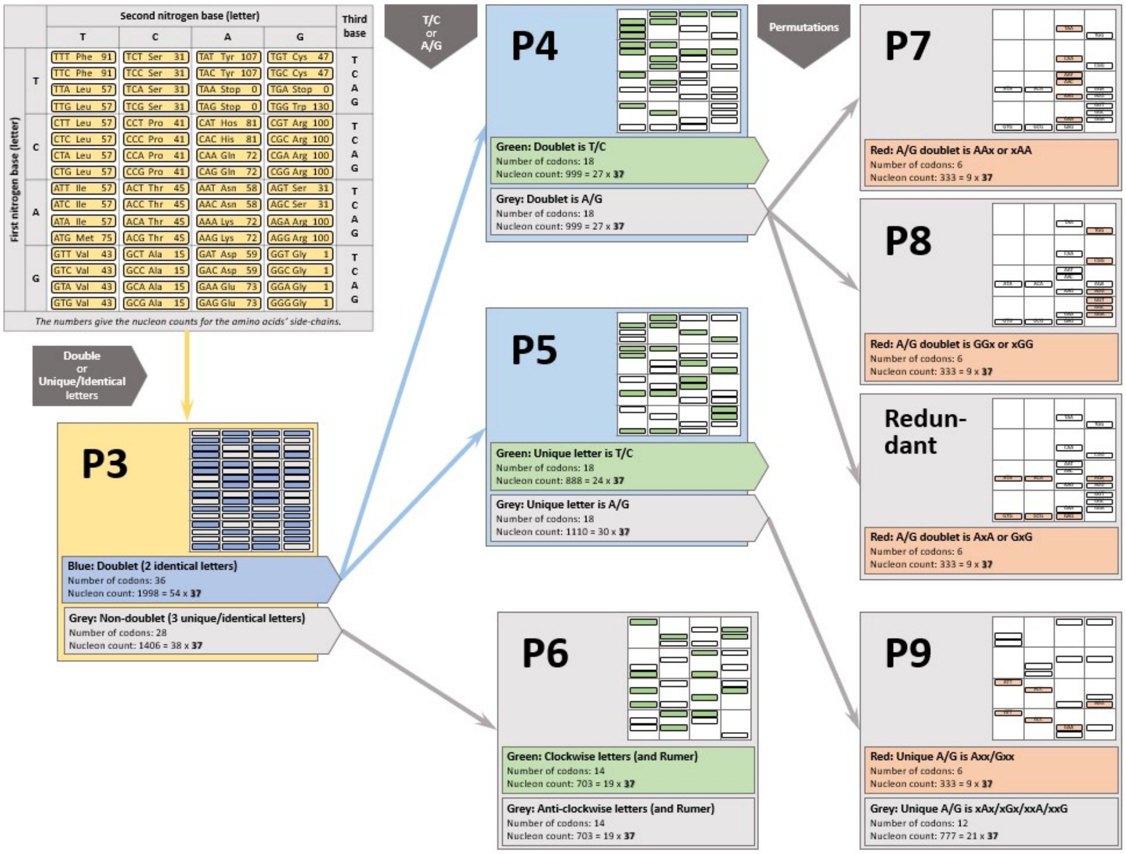
In P3-P9, the code table is divided into three levels according to certain well-defined rules. P3 is a bisection of the full code table, P4-P6 are bisections of the so obtained results, and P7-P9 are further subdivisions into still smaller fractions. For each so obtained group, divisibility by 37 is probed for the nucleon counts of its parts. The calculations are performed for the side chains of the amino acids, but since a standard block has 74 nucleons (which is divisible by 37), analogous results are obtained if the full amino acid molecules are considered. Figure 6 illustrates the procedures.

In **P3**, the codons of the full genetic table are grouped depending on whether they contain duplicate bases (blue in Figure 6) or not (grey). The first group contains 36 codons with a nucleon sum of 1998 ($= 54 \cdot 37$) and the second group 28 codons with a sum of 1406 ($= 38 \cdot 37$). Both are divisible by 37 but one of the groups is redundant since their sum is already accounted for through P2.

In **P4**, codons with two identical bases (blue in P3) are subdivided depending on whether these double bases are T/C or A/G. Both groups contain 18 codons with a nucleon sum of 999 ($= 27 \cdot 37$).

In **P5**, the same codons (i.e. blue in P3) are subdivided depending on whether the remaining unique base is T/C or A/G. The first group contains 18 codons with a nucleon sum of 888 ($= 24 \cdot 37$) and the second group 18 codons with a sum of 1110 ($= 30 \cdot 37$).

In **P6**, codons without duplets (grey in P3) are subdivided based on several rules, the details given in Figure 5a of Shcherbak and Makukov (2013). "And Rumer" in P6 in Figure 6 indicates that also the inversions T ↔ G and A ↔ C, the so-called Rumer's



First nitrogen base (letter)	Second nitrogen base (letter)				Third base
	T	C	A	G	
T	TTT Phe 91	TCT Ser 31	TAT Tyr 107	TGT Cys 47	T
	TTC Phe 91	TCC Ser 31	TAC Tyr 107	TGC Cys 47	C
	TTA Leu 57	TCA Ser 31	TAA Stop 0	TGA Stop 0	A
	TTG Leu 57	TCG Ser 31	TAG Stop 0	TGG Trp 130	G
C	CTT Leu 57	CCT Pro 41	CAT Hos 81	CGT Arg 100	T
	CTC Leu 57	CCC Pro 41	CAC His 81	CGC Arg 100	C
	CTA Leu 57	CCA Pro 41	CAA Gln 72	CGA Arg 100	A
	CTG Leu 57	CCG Pro 41	CAG Gln 72	CGG Arg 100	G
A	ATT Ile 57	ACT Thr 45	AAT Asn 58	AGT Ser 31	T
	ATC Ile 57	ACC Thr 45	AAC Asn 58	AGC Ser 31	C
	ATA Ile 57	ACA Thr 45	AAA Lys 72	AGA Arg 100	A
	ATG Met 75	ACG Thr 45	AAG Lys 72	AGG Arg 100	G
G	GTT Val 43	GCT Ala 15	GAT Asp 59	GGT Gly 1	T
	GTC Val 43	GCC Ala 15	GAC Asp 59	GGC Gly 1	C
	GTA Val 43	GCA Ala 15	GAA Glu 73	GGA Gly 1	A
	GTG Val 43	GCG Ala 15	GAG Glu 73	GGG Gly 1	G

The numbers give the nucleon counts for the amino acids' side-chains.

Figure 6: P3: The full-sized codon table (top left) is bisected into two groups resulting in nucleon counts divisible by 37. P4-P6: P3 is subdivided in three ways resulting in further divisibility by 37. P7-P9: Still further subdivisions result in new patterns with divisibility by 37. All details are given in the text. The nucleon counts for the amino acids' side chains are given in the codon table giving the reader an opportunity to control the calculations.

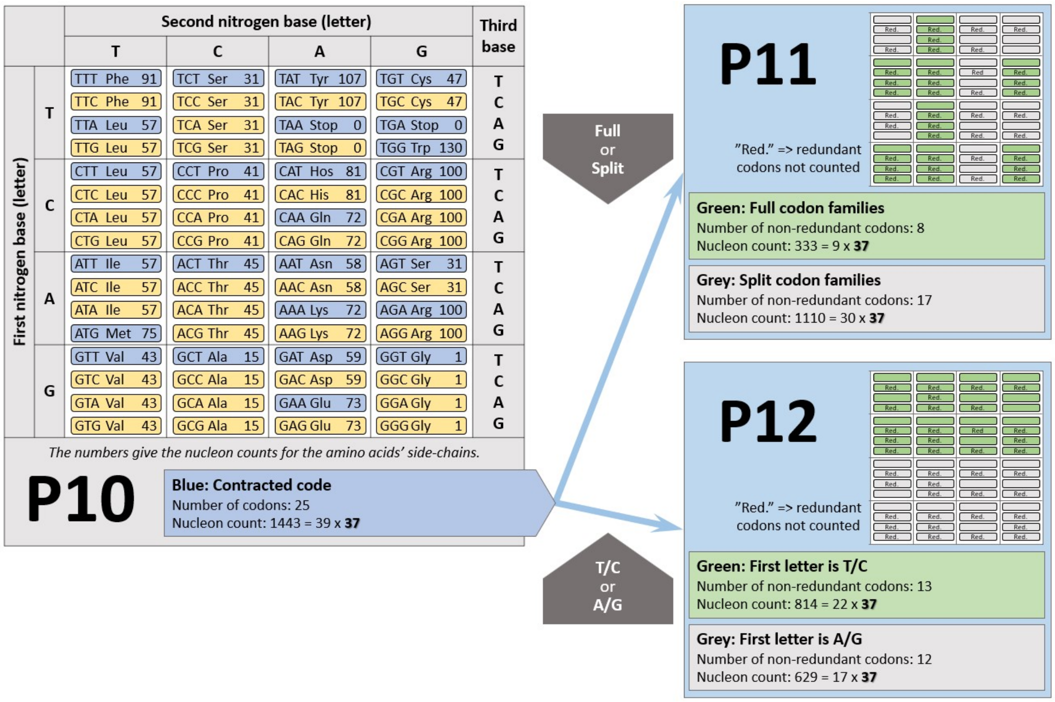
transformation (Rumer, 1966), are necessary for an unambiguous sorting into the two halves.

In **P7**-**P8**, the A/G doublets of P4 (grey) are trisected into three groups: AAx/xAA (P7), GGx/xGG (P8), and AxA/GxG (redundant), where x is the unique base of each codon. (The third group is redundant since the sum of all three groups' nucleon counts is already accounted for through P4.) All three groups contain 6 codons with nucleon sums of 333 $(= 9 \cdot 37)$.

In **P9**, the A/G unique letter group of P5 (grey) is bisected depending on whether the unique letter appears as Axx/Gxx or not (i.e. xAx/xGx/xxA/xxG). The first group contains 6 codons with a nucleon sum of 333 $(= 9 \cdot 37)$, and the second 12 codons with a sum of 777 $(= 21 \cdot 37)$.

P10-P12, Bisections of the contracted genetic code table

So far, the results have been based on the full-sized genetic code. In the so-called contracted code the redundancy has been eliminated, meaning that amino acids with synonymous codons are counted only once. Redundancy is defined per square in the codon table (called codon family) of Figure 7, implying for example that Leu is counted twice, once in family TTx (with redundancy 2) and once in CTx (with redundancy 4).



First nitrogen base (letter)	Second nitrogen base (letter): T	C	A	G	Third base
T	TTT Phe 91	TCT Ser 31	TAT Tyr 107	TGT Cys 47	T
	TTC Phe 91	TCC Ser 31	TAC Tyr 107	TGC Cys 47	C
	TTA Leu 57	TCA Ser 31	TAA Stop 0	TGA Stop 0	A
	TTG Leu 57	TCG Ser 31	TAG Stop 0	TGG Trp 130	G
C	CTT Leu 57	CCT Pro 41	CAT Hos 81	CGT Arg 100	T
	CTC Leu 57	CCC Pro 41	CAC His 81	CGC Arg 100	C
	CTA Leu 57	CCA Pro 41	CAA Gln 72	CGA Arg 100	A
	CTG Leu 57	CCG Pro 41	CAG Gln 72	CGG Arg 100	G
A	ATT Ile 57	ACT Thr 45	AAT Asn 58	AGT Ser 31	T
	ATC Ile 57	ACC Thr 45	AAC Asn 58	AGC Ser 31	C
	ATA Ile 57	ACA Thr 45	AAA Lys 72	AGA Arg 100	A
	ATG Met 75	ACG Thr 45	AAG Lys 72	AGG Arg 100	G
G	GTT Val 43	GCT Ala 15	GAT Asp 59	GGT Gly 1	T
	GTC Val 43	GCC Ala 15	GAC Asp 59	GGC Gly 1	C
	GTA Val 43	GCA Ala 15	GAA Glu 73	GGA Gly 1	A
	GTG Val 43	GCG Ala 15	GAG Glu 73	GGG Gly 1	G

The numbers give the nucleon counts for the amino acids' side-chains.

P10

Blue: Contracted code
Number of codons: 25
Nucleon count: 1443 = 39 x **37**

P11

"Red." => redundant codons not counted

Green: Full codon families
Number of non-redundant codons: 8
Nucleon count: 333 = 9 x **37**

Grey: Split codon families
Number of non-redundant codons: 17
Nucleon count: 1110 = 30 x **37**

P12

"Red." => redundant codons not counted

Green: First letter is T/C
Number of non-redundant codons: 13
Nucleon count: 814 = 22 x **37**

Grey: First letter is A/G
Number of non-redundant codons: 12
Nucleon count: 629 = 17 x **37**

Figure 7: The contracted codon table (identified by blue codons in the table) together with two of its bisections that result in nucleon counts divisible by 37. The details are given in the text. The nucleon counts for the amino acids' side chains are given in the codon table giving the reader an opportunity to control the calculations.

In **P10**, all 25 codons in the contracted code are included, giving a nucleon sum of 1443 $(= 39 \cdot 37)$.

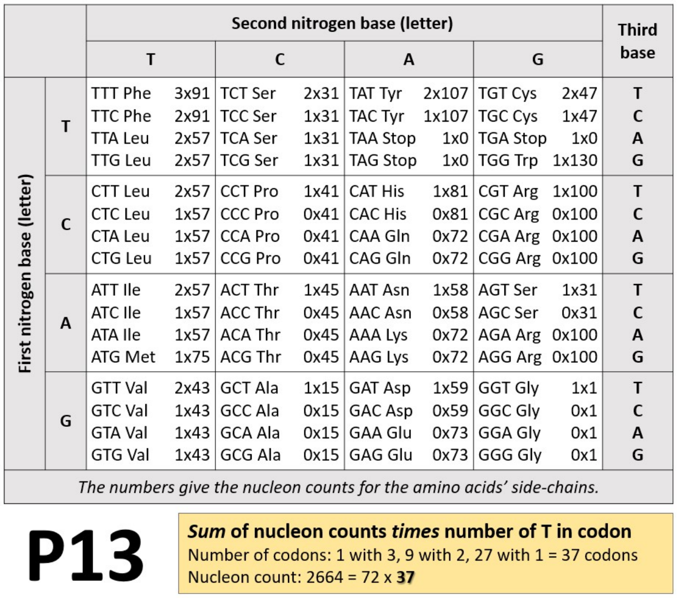
In **P11**, the codons of the contracted codon table are grouped depending on whether they belong to a full codon family (i.e. the last letter is insignificant) or a split codon family (i.e. the last letter is significant). The first group is green in Figure 7 and contains 8 codons with a nucleon sum of 333 $(= 9 \cdot 37)$, and the second group is grey and contains 17 codons with a sum of 1110 $(= 30 \cdot 37)$.

In **P12**, the codons of the contracted codon table are grouped depending on whether the first letter is T/C or A/G. The first group is green in Figure 7 and contains 13 codons with a nucleon sum of 814 $(= 22 \cdot 37)$, and the second group is grey and contains 12 codons with a sum of 629 $(= 17 \cdot 37)$.

P13, Decomposition of the codon table into all its bases

In the final pattern we decompose the codons of the standard code table into $64 \cdot 3 = 192$ separate bases/letters. Each base attains the nucleon count of the amino acid of the codon it is part of. Since the sum of all amino acids' sidechain nucleons is 3404 (pattern P2), and since each codon contains 3 bases, the total nucleon count for the decomposed codons is $3 \cdot 3404 = 10,212$.

In **P13**, we split the decomposed bases into two groups, T and A/C/G (Figure 8). The first group contains 1 codon with 3 Ts (TTT), 9 codons with 2 Ts, and 27 codons with 1 T, giving a nucleon count of 2664 ($= 72 \cdot 37$). The second group is redundant since the sum of the nucleon counts of both groups is accounted for in P2.



First nitrogen base (letter)	Second nitrogen base (letter)				Third base
	T	C	A	G	
T	TTT Phe 3x91	TCT Ser 2x31	TAT Tyr 2x107	TGT Cys 2x47	T
	TTC Phe 2x91	TCC Ser 1x31	TAC Tyr 1x107	TGC Cys 1x47	C
	TTA Leu 2x57	TCA Ser 1x31	TAA Stop 1x0	TGA Stop 1x0	A
	TTG Leu 2x57	TCG Ser 1x31	TAG Stop 1x0	TGG Trp 1x130	G
C	CTT Leu 2x57	CCT Pro 1x41	CAT His 1x81	CGT Arg 1x100	T
	CTC Leu 1x57	CCC Pro 0x41	CAC His 0x81	CGC Arg 0x100	C
	CTA Leu 1x57	CCA Pro 0x41	CAA Gln 0x72	CGA Arg 0x100	A
	CTG Leu 1x57	CCG Pro 0x41	CAG Gln 0x72	CGG Arg 0x100	G
A	ATT Ile 2x57	ACT Thr 1x45	AAT Asn 1x58	AGT Ser 1x31	T
	ATC Ile 1x57	ACC Thr 0x45	AAC Asn 0x58	AGC Ser 0x31	C
	ATA Ile 1x57	ACA Thr 0x45	AAA Lys 0x72	AGA Arg 0x100	A
	ATG Met 1x75	ACG Thr 0x45	AAG Lys 0x72	AGG Arg 0x100	G
G	GTT Val 2x43	GCT Ala 1x15	GAT Asp 1x59	GGT Gly 1x1	T
	GTC Val 1x43	GCC Ala 0x15	GAC Asp 0x59	GGC Gly 0x1	C
	GTA Val 1x43	GCA Ala 0x15	GAA Glu 0x73	GGA Gly 0x1	A
	GTG Val 1x43	GCG Ala 0x15	GAG Glu 0x73	GGG Gly 0x1	G

The numbers give the nucleon counts for the amino acids' side-chains.

P13

***Sum* of nucleon counts *times* number of T in codon**
Number of codons: 1 with 3, 9 with 2, 27 with 1 = 37 codons
Nucleon count: 2664 = 72 x **37**

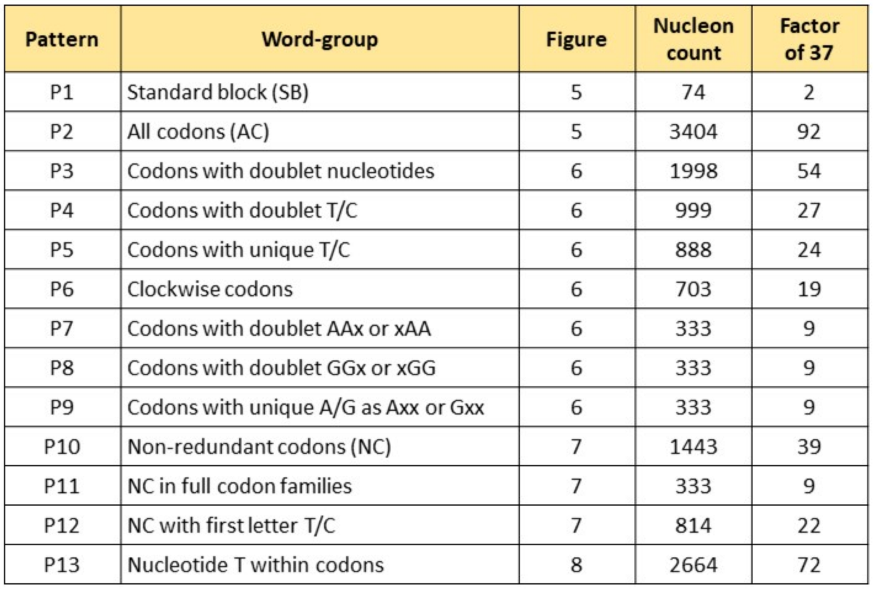
Figure 8: Pattern P13.

Summary of all patterns P1-P13

Figure 9 summarizes the thirteen appearances of 37 that are extracted from the genetic code. In Section A.3 we calculate the probability that this is due to chance to $4.1 \cdot 10^{-21}$.

8 37 in Jesus Christ

With the Greek isopsephy scheme (in Figure 2), the numeric values of "Jesus" and "Christ" are 888 ($= 24 \cdot 37$) and 1480 ($= 40 \cdot 37$) respectively (see Figure 10). Both are divisible by 37, which gives us two new independent occurrences of 37. In Section A.4.3, we calculate the probability for this to happen by chance to $7.3 \cdot 10^{-4}$.



Pattern	Word-group	Figure	Nucleon count	Factor of 37
P1	Standard block (SB)	5	74	2
P2	All codons (AC)	5	3404	92
P3	Codons with doublet nucleotides	6	1998	54
P4	Codons with doublet T/C	6	999	27
P5	Codons with unique T/C	6	888	24
P6	Clockwise codons	6	703	19
P7	Codons with doublet AAx or xAA	6	333	9
P8	Codons with doublet GGx or xGG	6	333	9
P9	Codons with unique A/G as Axx or Gxx	6	333	9
P10	Non-redundant codons (NC)	7	1443	39
P11	NC in full codon families	7	333	9
P12	NC with first letter T/C	7	814	22
P13	Nucleotide T within codons	8	2664	72

Figure 9: Summary of the thirteen patterns (P1-P13, referred to as word groups) in the genetic code that show divisibility by 37. P1 is based on the nucleon count for the standard block while P2-P13 are based on the nucleon counts for the sidechains.

9 Multiple testing

The probabilities (p-values) we have calculated so far have not been safeguarded against observational bias, which means we run the risk of testing only for patterns that confirm our hypothesis while overlooking other patterns which may surprise us as much. To limit this risk, in this section we perform multiple tests of other potential and similar types of patterns and adjust our p-values accordingly. The resulting p-values give the probability of by chance having at least one equally remarkable divisibility pattern as the one observed. Section A.6 gives the details.

We perform multiple tests for the p-values of G11, GC, and JC, as illustrated in Figure 1. These tests are carried out even though we argue that external factors make our selection

Figure 10: The Greek way of assigning numbers to letters applied to the two names of the Lord from Matt 1:1. Both “Jesus” and “Christ” are divisible by 37.

of word group collections straightforward and "natural", implying our observational bias is small. We motivate our choice of parameters for each of the p-values as follows:

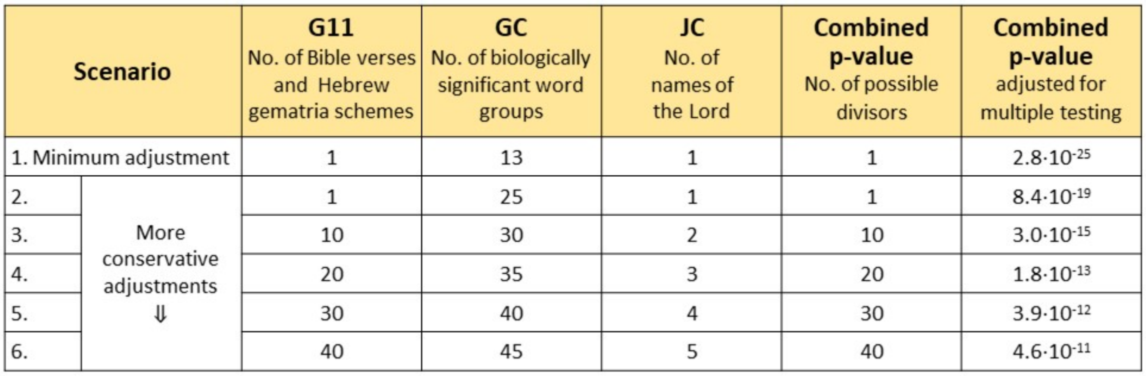
- For the mathematical pattern of **Genesis 1:1 (G11)**, we test for alternative Bible verses and other gematria schemes that may display similar patterns. However, we believe the selection of the first verse of the Bible is firmly established by the fact that it proclaims God's creation and is in some sense the theological counterpart of the genetic code which forms the basis of life. Since it also connects to Jesus Christ as Creator and Giver of life, it seems that no other verse of the Hebrew Bible could replace it. And our reasons for selection mispar hechrachi as the Hebrew gematria scheme are given in Section 5.
- For the **genetic code (GC)**, we adjust the p-value for other possible and biologically significant word groups (than those of Figure 9) that may give divisible patterns based on 37. In Section A.6, we identify 12 other (than P1-P13) "non-hit" word groups that are formed in similar ways but do not display such divisibility patterns. This means that our multiple testing must include at least these 12 groups (plus others that we possibly have not envisioned).
- For **"Jesus" and "Christ" (JC)**, we test for other Greek names of the Lord such as "Lord", "Logos", and "Emmanuel". However, this may be overcautious since by far the most used names in the New Testament are "Jesus" and "Christ", by themselves or together. ("Lord" is also used many times, but it is not a name but a title and not used exclusively for Jesus.)

10 Combined p-value

In Sections 6-8, we found that divisibility patterns based on the number 37 frequently appear in the numerical schemes of Genesis 1:1 (G11), the genetic code (GC), and Jesus Christ (JC) respectively. We derived probabilities (p-values) for the appearance of these patters, assuming the word- and nucleon-numbers were randomly generated (the null hypothesis). Then in Section 9 we adjusted the p-values of G11, GC, and JC for the multiple testing scenario of Figure 1. These three probabilities are still small after such an adjustment, but of course the combined probability that all three word group collections (G11, GC, and JC) show the same numerical pattern, is even smaller. Therefore, in Sections A.5-A.6 we merge the three individual p-values (after adjustments for multiple testing) into a single combined p-value, which strengthens the conclusion that the three number schemes are not formed by chance. The combined p-value is shown to be $1.2 \cdot 10^{-12}$ (see Figure 1).

We also adjust the combined p-value for multiple testing because other divisors than 37 may give as remarkable results. For the multiple testing scenario of Figure 1, such a correction gives a combined p-value of $4.6 \cdot 10^{-11}$. However, once again we believe our choice of divisor is the most straightforward one based on external factors. The number 3 stands for what is real, substantial, and complete, while 7 is the number of spiritual perfection (Bullinger, 1894). The number may also be interpreted as “three sevens” which is 777, a number sometimes used to symbolize God, His character, and His works.

Figure 11 shows the adjusted p-values for 6 different multiple testing scenarios with different choices of parameters. The first row corresponds to a scenario with no adjustment for multiple testing (including only the 13 word groups P1-P13 for GC), the second row corresponds to a mimimal amount of adjustment for multiple testing (including 12 additional word groups for GC, which are the 12 “non-hit” groups that we identified), and the rest give more and more conservative estimates. The most conservative multiple testing Scenario 6 is the one depicted in Figure 1. As may be seen, the combined p-value remains staggering low even for the most conservative adjustments for multiple testing. Therefore, we conclude that the word and nucleon counts of G11, GC, and JC are fine-tuned, and that the observed patterns point towards an Intelligent Designer.



Scenario		**G11** No. of Bible verses and Hebrew gematria schemes	**GC** No. of biologically significant word groups	**JC** No. of names of the Lord	**Combined p-value** No. of possible divisors	**Combined p-value** adjusted for multiple testing
1. Minimum adjustment		1	13	1	1	$2.8\cdot10^{-25}$
2.	More conservative adjustments ⇓	1	25	1	1	$8.4\cdot10^{-19}$
3.		10	30	2	10	$3.0\cdot10^{-15}$
4.		20	35	3	20	$1.8\cdot10^{-13}$
5.		30	40	4	30	$3.9\cdot10^{-12}$
6.		40	45	5	40	$4.6\cdot10^{-11}$

Figure 11: The combined p-value adjusted for six scenarios of multiple testing.

11 Further evidence

Besides patterns divisible by 37, G11, GC, and JC contain other features that indicate they are nonrandom and the result of design. We present some of this evidence in this section, and although we do not quantify it, we suggest it strengthens the inference of an intellect behind both the Bible and the genetic code.

11.1 Genesis 1.1

Besides the divisibility pattern based on 37, G11 shows other divisibility patterns based on the number 7. (All below numbers may be verified through Figure 3.)

- Genesis 1:1 has 7 words.
- The verse has 28 (4 × 7) letters.

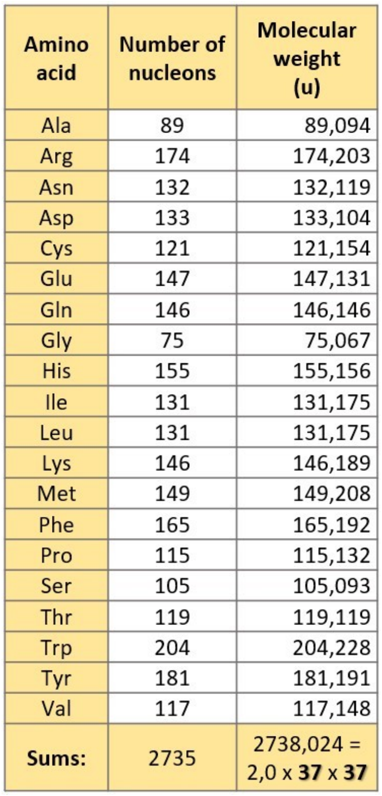
- The 3 first words (from right to left) have 14 (2×7) letters, and the 4 last words have 14 (2×7) letters.
- The 3 main words (God, the heaven, the earth) have 14 (2×7) letters altogether, and the remaining part of the verse has 14 (2×7) letters.
- The middle word with its left neighbor has 7 letters, and so does the middle word with its right neighbor.
- The 3 main words (God, the heaven, the earth) have a numeric value of 777 (111×7).
- The sum of the numeric values of the first and the last letters in each word (14 letters) is 1393 (199×7).
- The sum of the numeric values of the first, the two middle and the last letters (4 letters) is 133 (19×7).

It should be noted that since both 7 and 37 are prime numbers, the two divisibility patterns are independent of one another. This in turn means that the two code systems are *superimposed*. Like in a crossword puzzle, one letter cannot be changed to fit an intended pattern without simultaneously changing another, leading to an exponentially increasing complexity. The semantic meaning of the letters is a third superimposed code, and since the divisibility patterns based on 7 are applicable to both the number of letters/words and their gematria values, we may count a fourth superimposed code. Although a quantitative analysis of these superimposed codes must account for multiple testing, it is still reasonable to conclude that the complexity of such a multiple code system is beyond human ability.

11.2 The genetic code

Besides the patterns based on the nucleon counts, GC seems to contain another trace of design that is based on the molecular weights of the constituent amino acids. A particular chemical element comes as different isotopes which differ in neutron number and therefore in nucleon number. The nucleon counts we have used so far are integers applied to the most common isotopes in nature which are also radioactively stable (1H, 12C, 14N, 16O and 32S). In contrast, molecular weights are real numbers applied to ordinary mix of isotopes present in nature. These weights are given in the *atomic mass unit*, u, where 1 u is equal to the weight of one nucleon, or to be exact, it is defined as 1/12 of the weight of a carbon isotope with 6 protons and 6 neutrons. Figure 12 gives the molecular weights of the 20 standard amino acids of life with the normal mix of C-, H-, N-, O-, and S-atoms in nature. Remarkably, the sum of the molecular weights of all standard amino acids is divisible by 37, not only once but twice. The precision is high. With molecular weights from Wikipedia (as in the figure), an accuracy of one decimal is achieved. Since the natural abundance of isotopes varies both in space and time, an enhanced accuracy would probably be meaningless.

As for Genesis 1:1, the genetic code is "multiple" in that it is composed of several superimposed codes. Molecular biologists have discovered that a certain sequence of DNA may



Amino acid	Number of nucleons	Molecular weight (u)
Ala	89	89,094
Arg	174	174,203
Asn	132	132,119
Asp	133	133,104
Cys	121	121,154
Glu	147	147,131
Gln	146	146,146
Gly	75	75,067
His	155	155,156
Ile	131	131,175
Leu	131	131,175
Lys	146	146,189
Met	149	149,208
Phe	165	165,192
Pro	115	115,132
Ser	105	105,093
Thr	119	119,119
Trp	204	204,228
Tyr	181	181,191
Val	117	117,148
Sums:	2735	2738,024 = 2,0 x **37** x **37**

Figure 12: Molecular weights and their sum for the 20 standard amino acids.

be used in different ways for different needs by starting the decoding from different places along the molecular string or by reading it from different directions, see for instance Sanford (2008) and references discussed in Section A.7. We believe that such superimposed codes are correctly used by creationists to verify the supernatural origin of life. We now suggest it is time to do the same for the Bible, at least for its opening verse.

11.3 "Jesus" and "Christ"

These two names of our Lord share another dividend besides 37, namely 8. "Jesus" has a Greek isopsephy numeric value of 888 ($= 111 \cdot 8$), and "Christ" has a value of 1480 ($= 185 \cdot 8$). Again, since 8 is not of factor of 37, these two code systems are independent, i.e. superimposed on one another. Bullinger ascribes the meaning "the first of a new series" to the number 8 (Bullinger, 1894), and indeed, Jesus is a new beginning. He rose from the dead on the eighth day. (Other instances where 8 symbolizes a new beginning are the 8 persons that disembarked the ark and circumcision which should be performed on the 8th day.)

12 Conclusions

Our conclusions are:

- The first verse of the Bible (G11), the genetic code (GC), and the names "Jesus" and "Christ" (JC) contain mathematical patterns that reveal an intelligent origin. The probability that those patterns are randomly generated (the p-value) is demonstrated to be less than $4.6 \cdot 10^{-11}$, after a correction for multiple testing.
- These patterns share the same internal structure (divisibility by 37) which reveals that it is the same Intelligence behind God's Word (the Bible), God's Life (the genetic code), even the Word of Life (Jesus). This Originator is the God of the Bible.
- Beside these divisibility patterns (with 37 as divisor), there are other superimposed codes in G11, GC, and JC which reduces the possibility of an origin by chance even further.
- God has not been silent but uses the mathematical patterns of this article (and probably other patterns) as a signature to reveal Himself.

In our opinion, arithmetic patterns like these make it impossible to continue denying the Creator on intellectual grounds. They constitute God's Trilateral Fingerprint.

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A Appendix: Statistical analysis of divisibility patterns from the Bible and the genetic code

In this appendix we analyze in more detail how likely it is that the frequent divisibility by 37 of numeric values of word groups (WGs) in Genesis 1:1 (G11, Section 6), the genetic code (GC, Section 7) and the words Jesus Christ (JC, Section 8), is a chance phenomenon. We start by introducing a general framework for word groups in Section A.1. More specifically, we demonstrate that G11, GC, and JC are *word group collections* (WGCs). Assuming that numerical values have been assigned to all words and word groups, the *divisibility count* is the number of word groups within the word group collection that are divisible by a pre-specified number m. Although $m = 37$ is of major concern, our methodology is applicable for any prime number m. In Section A.2 we introduce a statistical model for the numerical values of words, under a null hypothesis that these have been generated randomly. This makes it possible to rigorously define how likely it is that the observed divisibility counts of G11, GC, and JC occurred by change (their p-values), as well as how many standard deviations away from the mean these divisibility counts are. Then in Section A.3 we demonstrate how to calculate p-values of word group collections with independent numerical values of its word groups, and apply this to finding the p-value of GC. In Section A.4 we treat the more general case of word group collections whose word groups have numerical values that are not independent, and apply this framework for finding the p-values of JC and G11. The p-values of G11, GC, and JC are merged into one single p-value in Section A.5. An adjustment for multiple testing and observational bias is provided in Section A.6, whereas alternative choices of null hypotheses are discussed in Section A.7. A summary of notation can be found in Table 1.

Some parts of this appendix require knowledge of undergraduate courses in probability theory and statistical inference. The contents of Gut (2009) and Held and Bové (2020), for instance, is an as appropriate background.

A.1 General framework

In this section we provide a unified framework for analyzing the divisibility patterns of the numeric schemes of word group collections. This general framework is illustrated in Table 2 for the three word group collections we study; the first verse of the Bible (G11, Section 6), the genetic code (GC, Section 7) and Jesus Christ (JC, Section 8).

We start by considering a set of n words, labeled $i = 1, \ldots, n$. It is assumed that a numeric scheme is used to assign non-negative integers $Y_1, Y_2, \ldots, Y_n$ to each of these words. For G11 words have their usual meaning, with the first sentence of the Bible containing $n = 7$ words, and likewise JC contains the $n = 2$ words with labels 1=Jesus and 2=Christ. The numerical values of these words rely on Hebrew gematria and Greek isopsephy schemes respectively, as explained in Sections 5, 6, and 8.

The definition of words, and the assignment of numbers to these words, is a bit more complicated for GC. This word group has $n = 21$ words, and in line with Appendix E of

Table 1: Symbols and abbreviations used in the appendix. They are sorted into the four categories general, words, word groups (WGs), and word group collections (WGCs), separated by horisontal lines.

General	Meaning
m	Positive integer larger than 1 (typically a prime number).
π	Probability ($= 1/m$) that a randomly chosen number is divisible by m.
π'	Probability ($= 1/(m-1)$) that a randomly chosen number *not* divisible by m, has a prescribed remainder modulo m.
Words	Meaning
n	Number of words.
i	Word, identified by its order number ($\in \{1, \ldots, n\}$) among all words.
Y_i	Numerical value of word i.
$\boldsymbol{Y}$	Column vector $(Y_1, \ldots, Y_n)^T$ of length n with the numerical values of all words.
X_i	Numerical value of word i modulo m.
$\boldsymbol{X}$	Column vector $(X_1, \ldots, X_n)^T$ of length n with the numerical values modulo m of all words.
R_n	Number of words, among n words, whose numerical values are divisible by m.
Q_n	Number of words, among n words, whose numerical values are *not* divisible by m ($= n - R_n$).
q	Observed value of Q_n, the nr. of words among n, with numerical values *not* divisible by m.
H_0	Null hypothesis that the numerical values of all words have a remainder modulo m that is uniformly distributed on $0, 1, \ldots, m-1$.
H_1	Alternative hypothesis that word groups are divisible by m more often than expected under H_0.
H_0'	Modified null hypothesis that no words are divisible by m, with numerical values modulo m that are uniformly distributed on $1, \ldots, m-1$.
WGs	Meaning
I, J	A word group, possibly with multiple occurrences of words, like $\{1, 1, 2, 3\}$. If at most one copy of each word occurs in this word group, then I (or J) is a subset of $\{1, \ldots, n\}$.
Y_I	Total numerical value of all the words in word group I.
X_I	Total numerical value of all the words in word group I modulo m.
K_I	Divisibility indicator that equals 1 if the total numerical value of the words in word group I is divisible by m, and otherwise it equals 0.
WGCs	Meaning
$\mathcal{I}, \mathcal{J}$	A word group collection, i.e. a set word groups. It is assumed that $\mathcal{I}$ is a smaller word group collection than $\mathcal{J}$, so that $\mathcal{I}$ is a subset of $\mathcal{J}$.
$\boldsymbol{Y}_{\mathcal{J}}$	Column vector $(Y_I;\, I \in \mathcal{J})^T$ of length $\lvert\mathcal{J}\rvert$ with the numerical values of all word groups.
$\boldsymbol{X}_{\mathcal{J}}$	Column vector $(X_I;\, I \in \mathcal{J})^T$ of length $\lvert\mathcal{J}\rvert$ with the numerical values modulo m of all word groups.
$\boldsymbol{A}_{\mathcal{J}}$	A matrix (a_{ji}) of dimension $\lvert\mathcal{J}\rvert \times n$ that summarizes $\mathcal{J}$, with a_{ji} the number of times word i occurs in word group j.
$r_{\mathcal{J}}$	Rank of matrix $\boldsymbol{A}_{\mathcal{J}}$, i.e. the number of linearly independent word groups of $\mathcal{J}$.
N_{nsr}	Number of word group collections $\mathcal{I} \subset \mathcal{J}_{\text{all}}$ constructed from n words such that $\mathcal{I}$ has s word groups, and $r_{\mathcal{I}} = r$.
$K_{\mathcal{I}}$	Divisibility indicator that equals 1 if all word groups I in $\mathcal{I}$ are such that the total numerical values of the words in I are divisible by m.
$\mathcal{J}_{\text{all}}$	When word groups contain at most one copy of each word, this is the word group collection that consists of all word groups, i.e. all $2^n - 1$ non-empty subsets of $\{1, \ldots, n\}$.
G11	A word group collection corresponding to Genesis 1:1 ($= \mathcal{J}_{\text{all}}$, with $n = 7$).
GC	A word group collection corresponding to the genetic code ($n = 14$ linearly independent word groups).
JC	A word group collection corresponding to Jesus Christ ($= \mathcal{J}_{\text{all}}$, with $n = 2$).
$S_{\mathcal{J}}$	Divisibility count, i.e. the number of the word groups in $\mathcal{J}$ whose total numerical values are divisible by m.
$s_{\mathcal{J}}$	Observed value of $S_{\mathcal{J}}$.
$p_{\mathcal{J}}$	The p-value of $\mathcal{J}$, i.e. the probability that the divisibility count $S_{\mathcal{J}}$ by chance (H_0) is at least as large as the observed value $s_{\mathcal{J}}$.
$t_{\mathcal{J}}$	The t-statistic of $\mathcal{J}$, i.e. the number of standard deviations the observed divisibility count $s_{\mathcal{J}}$ is from the mean, under the null hypothesis of chance (H_0).
S_n	Short-hand notation for the divisibility count $S_{\mathcal{J}_{all}}$ of all word groups among n words, when at most one copy of each word is allowed in the word groups.
T_n	Number of word groups in $\mathcal{J}$ whose total numerical values are divisible by m, among those that are formed by the Q_n words (out of n) that have a numerical value not divisible by m.
v	Observed specificity of the combined divisibility pattern of all three word group collections G11, GC, and JC.
p_{comb}	Combined p-value for the word group collections G11, GC, and JC.
$p_{\text{comb}}^{\text{adj}}$	Combined p-value for the word group collections G11, GC, and JC, adjusted for multiple testing.

Shcherbak and Makukov (2013), the first 20 of these words correspond to amino acids, each of which is assigned a nucleon number for its side chain, whereas the last word is the standard block (SB), with a numerical value that corresponds to its nucleon number.

A word group I is a set of words. Assume first that I contains at most one copy of each word, so that I is represented by a subset of $\{1, \ldots, n\}$. The total numerical value

$$Y_I = \sum_{i \in I} Y_i \tag{A.1}$$

of word group I is obtained by adding the numerical values Y_i of all its words i. Let $\mathcal{J}$ be a word group collection, that is, a set of subsets I of $\{1, \ldots, n\}$. The number $|\mathcal{J}|$ of word groups in $\mathcal{J}$ ranges between 1 (one single word group) and $2^n - 1$ (all possible word groups; $\mathcal{J} = \mathcal{J}_{\text{all}}$). If all word groups of $\mathcal{J}$ contain at most one copy of each word, then $\mathcal{J}$ is represented by a binary matrix $\boldsymbol{A} = \boldsymbol{A}_{\mathcal{J}} = (a_{ji})$ of dimension $|\mathcal{J}| \times n$, where a_{ji} equals 1 or 0 depending on whether word i is present in word group j or not. In particular, if I_j is word group number j of $\mathcal{J}$, it is possible to rewrite (A.1) (with $I = I_j$) as

$$Y_{I_j} = \sum_{i=1}^{n} a_{ji} Y_i. \tag{A.2}$$

G11 and JC are word group collections such that each word group contains at most one copy of each word. Whereas G11 contains all $|\mathcal{J}| = |\mathcal{J}_{\text{all}}| = 2^7 - 1$ possible word groups formed by the words of Genesis 1:1, JC contains all $|\mathcal{J}| = |\mathcal{J}_{\text{all}}| = 2^2 - 1 = 3$ word groups formed by the two words "Jesus" and "Christ".

A more general definition of word group collection allows for multiple copies of words within word groups, corresponding to a non-binary matrix $\boldsymbol{A}_{\mathcal{J}}$, where a_{ji} refers to the number of copies of word i in word group j. GC is of this kind, with 13 word groups defined from the 13 divisibility patterns of 37 described in Figure 9 of Section 7.

Tables 3-5 contain some summary statistics for the word group collections G11, JC, and GC. Notice in particular that G11, JC, GC have 0, 0, 10 word groups with multiple occurrences of words, respectively. The last three columns of these tables display, for each word group $I \in \mathcal{J}$, its numerical value Y_I, the value

$$X_I = Y_I \bmod m, \tag{A.3}$$

and a binary divisibility indicator K_I that equals 1 if Y_I is divisible by m, and 0 otherwise. Evidently, K_I equals 1 if and only if $X_I = 0$.

Our object of study is the divisibility count $S_{\mathcal{J}}$. This is the number of word groups in $\mathcal{J}$ whose numerical values are divisible by m. It follows that the divisibility count

$$S_{\mathcal{J}} = \sum_{I \in \mathcal{J}} K_I \tag{A.4}$$

is the sum of the divisibility indicators for all word groups within $\mathcal{J}$. In order to analyze $S_{\mathcal{J}}$ we need to express the observed divisibility pattern of $\mathcal{J}$ in a convenient way. We will make use of the matrix $\boldsymbol{A}$ and phrase the divisibility pattern of $\mathcal{J}$ as a system of linear

Table 2: Illustration of three WGCs $\mathcal{J} = \{I_1, \ldots, I_{|\mathcal{J}|}\}$; G11 from Section 6, GC from Section 7 and JC from Section 8. For G11 and JC each word group is represented by a subset of $\{1, \ldots, n\}$, whereas all word groups of GC are represented by the corresponding rows of $\boldsymbol{A}$, counting the number of occurrences of each word (only the first three and last two word count numbers are shown). The words of each WGC are listed in the same order as the columns of Tables 3-5. In addition, the 13 word groups P1, ..., P13 of GC are listed in the same order as in Figure 9, with SB = Standard block (also word nr. 21), ANSC = All non-stop codons, and NC = Non-redundant codons of the contracted code. For P3, P4, P5, P6, P11, and P12 each WG corresponds to the blue or green subpatterns of Figures 6 and 7.

Word group	Words, with labels and numbers				Word groups in $\mathcal{J}$		
collection $\mathcal{J}$	n	i	Word	Y_i	$\lvert\mathcal{J}\rvert$	j	I_j
Genesis 1:1	7	1	In the beginning	913	127	1	$\{1\}$
(G11)		2	created	203		2	$\{2\}$
		3	God	86		3	$\{1, 2\}$
		4	$*$	401		4	$\{3\}$
		5	the heaven	395		5	$\{1, 3\}$
		6	and	407		...	
		7	the earth	296		127	$\{1, 2, 3, 4, 5, 6, 7\}$
Genetic code	21	1	Ala	15	13	1	P1 = SB = $\{0, 0, 0, \ldots, 0, 1\}$
(GC)		2	Arg	100		2	P2 = ANSC = $\{4, 6, 2, \ldots, 4, 0\}$
		3	Asn	58		3	P3 = blue = $\{2, 4, 2, \ldots, 2, 0\}$
		4	Asp	59		4	P4 = green =$\{1, 1, 0, \ldots, 1, 0\}$
		5	Cys	47		5	P5 = green = $\{1, 1, 2, \ldots, 1, 0\}$
		6	Glu	73		6	P6 = green = $\{2, 0, 0, \ldots, 0, 0\}$
		7	Gln	72		7	P7 = $\{0, 0, 2, \ldots, 0, 0\}$
		8	Gly	1		8	P8 = $\{0, 2, 0, \ldots, 0, 0\}$
		9	His	81		9	P9 = $\{1, 1, 0, \ldots, 0, 0\}$
		...				10	P10 = NC = $\{1, 2, 1, \ldots, 1, 0\}$
		19	Tyr	107		11	P11 = green = $\{1, 1, 0, \ldots, 1, 0\}$
		20	Val	43		12	P12 = green = $\{0, 1, 0, \ldots, 0, 0\}$
		21	SB	74		13	P13 = $\{1, 1, 1, \ldots, 1, 0\}$
Jesus Christ	2	1	Jesus	888	3	1	$\{1\}$
(JC)		2	Christ	1480		2	$\{2\}$
						3	$\{1, 2\}$

Diophantine equations. More specifically, let $\boldsymbol{Y} = (Y_1, \ldots, Y_n)^T$ and $\boldsymbol{Y}_{\mathcal{J}} = (Y_I;\, I \in \mathcal{J})^T$ refer to the column vectors of numerical values, of all words and of all word groups in $\mathcal{J}$ respectively, with T a symbol for matrix transposition. Then we have that

$$\boldsymbol{Y}_{\mathcal{J}} = \boldsymbol{A}\boldsymbol{Y}. \tag{A.5}$$

In order to analyze the divisibility count in (A.4), it is helpful the express (A.5) modulo m. To this end, if $I = \{i\}$ consists of one single word we let $X_i = X_I$ be the remainder (A.3) when the numerical value Y_i of this word is divided by m. Let $\boldsymbol{X} = (X_1, \ldots, X_n)^T$ and $\boldsymbol{X}_{\mathcal{J}} = (X_I;\, I \in \mathcal{J})^T$ be the column vectors of numerical values modulo m, for all words and all word groups in $\mathcal{J}$ respectively. Then

$$\boldsymbol{X}_{\mathcal{J}} = \boldsymbol{A}\boldsymbol{X} \bmod m, \tag{A.6}$$

if the modulo m operation is taken componentwise for all word groups in $\mathcal{J}$. In particular, if I_j is the j:th word group of $\mathcal{J}$, it follows from (A.6) that

$$X_{I_j} = (\boldsymbol{A}\boldsymbol{X})_{I_j} \bmod m = \sum_{i=1}^{n} a_{ji} X_i \bmod m. \tag{A.7}$$

Although all $X_i \in \{0, 1, \ldots, m-1\}$ in (A.7), the modulo m operation in this equation (and in (A.6)) is still necessary, since it may nevertheless happen that the sum in (A.7) does not belong to $\{0, 1, \ldots, m-1\}$. It follows from (A.4) and (A.6) that the divisbility count $S_{\mathcal{J}}$ is a function of $\boldsymbol{X}_{\mathcal{J}}$ only. Because of the modulo operation in (A.6) we may therefore without loss of generality assume that

$$a_{ji} \in \{0, 1, \ldots, m-1\} \text{ for all } j \in \mathcal{J}, i = 1, \ldots, n. \tag{A.8}$$

A.2 Statistical model

A.2.1 *p*-values

Our objective is to find out, for each word group collection $\mathcal{J}$, whether the observed value $s_{\mathcal{J}}$ of the divisibility count $S_{\mathcal{J}}$, is larger than we would expect if the numerical values of all word groups are formed by chance. This is a statistical hypothesis testing problem, where the null hypothesis (H_0), that the numerical values of all word groups are completely random, is tested against the alternative hypothesis (H_1) that word groups have numerical values divisible by m, more often than we would expect by chance. In mathematical terms our goal is to compute a p-value

$$p_{\mathcal{J}} = P(S_{\mathcal{J}} \geq s_{\mathcal{J}} | H_0), \tag{A.9}$$

that is, to find the probability that a randomly formed divisibility count is at least as large as the observed value $s_{\mathcal{J}}$. In order to specify the null hypothesis more rigorously, recall that X_i is the remainder when dividing the numerical value Y_i of the word with label i, by m. The null hypothesis is defined in terms these remainders; that they are

Table 3: Word group statistics for $\mathcal{J} = \text{G11} = \{I_1, I_2, \ldots, I_{127}\}$. All word groups are listed in lexicographical order, reading digits from left to right. Word group I_j corresponds to all 1 entries of row j of the 127×7 binary matrix $\boldsymbol{A} = (a_{ji})$. For each word group I_j, its numerical value Y_{I_j} is shown as well as its modulo $m(= 37)$ value X_{I_j}. The variable K_{I_j} equals 1 (0) if Y_{I_j} is (is not) divisible by m, and the total word count $s_{\mathcal{J}}$ of the bottom row is the sum of all K_{I_j}.

j	Word label i							Y_{I_j}	X_{I_j}	K_{I_j}
	1	2	3	4	5	6	7			
1	1	0	0	0	0	0	0	913	25	0
2	0	1	0	0	0	0	0	203	18	0
3	1	1	0	0	0	0	0	1116	6	0
4	0	0	1	0	0	0	0	86	12	0
5	1	0	1	0	0	0	0	999	0	1
6	0	1	1	0	0	0	0	289	30	0
7	1	1	1	0	0	0	0	1202	18	0
8	0	0	0	1	0	0	0	401	31	0
9	1	0	0	1	0	0	0	1314	19	0
10	0	1	0	1	0	0	0	604	12	0
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
126	0	1	1	1	1	1	1	1788	12	0
127	1	1	1	1	1	1	1	2701	0	1
Sum										$s_{\mathcal{J}} = 23$

Table 4: Word group statistics for $\mathcal{J} = \text{JC} = \{I_1, I_2, I_3\}$. Word group I_j corresponds to all 1 entries of row j of the 3×2 binary matrix $\boldsymbol{A} = (a_{ji})$. For each word group I_j, its numerical value Y_{I_j} is shown as well as its modulo $m(= 37)$ value X_{I_j}. The variable K_{I_j} equals 1 (0) if Y_{I_j} is (is not) divisible by m, and the total word count $s_{\mathcal{J}}$ of the bottom row is the sum of all K_{I_j}.

j	i		Y_{I_j}	X_{I_j}	K_{I_j}
	1	2			
1	1	0	888	0	1
2	0	1	1480	0	1
3	1	1	2368	0	1
Sum					$s_{\mathcal{J}} = 3$

Table 5: Representation of word group collection $\mathcal{J} = \mathrm{GC} = \{I_1, I_2, \ldots, I_{13}\}$, with some of its word groups having multiple occurrences of words. The construction is based on $n = 21$ words, labeled $i = 1, \ldots, 20$ for amino acids (ordered as in Figure 5), and $i = 21$ for the standard block (SB). The first 20 word numbers $Y_1, \ldots, Y_{20}$ represent number of nucleons of the side chains of amino acids, whereas Y_{21} is the nucleon number of SB. The 13 word groups are listed in the same order as in Figure 9, where word group I_j corresponds to pattern Pj of that table. Word group I_j is represented by row j of the 13×21 matrix $\boldsymbol{A} = (a_{ji})$, where a_{ji} is the number of occurrences of word i in word group I_j. For each word group I_j, the three rightmost columns of the table display Y_{I_j}, its modulo $m(= 37)$ value X_{I_j}, and K_{I_j}, which equals 1 (0) if Y_{I_j} is (is not) divisible by m. The total word count $s_{\mathcal{J}} = 13$ of the bottom row is the sum of all K_{I_j}.

Word group nr	Word																							
	Ala	Arg	Asn	Asp	Cys	Glu	Gln	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val	SB			
	Word label i																							
j	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	Y_{I_j}	X_{I_j}	K_{I_j}
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	74	0	1
2	4	6	2	2	2	2	2	4	2	3	6	2	1	2	4	6	4	1	2	4	0	3404	0	1
3	2	4	2	0	1	2	1	3	1	2	4	1	0	1	3	2	2	1	1	2	0	1998	0	1
4	1	1	0	0	1	0	0	0	1	1	4	0	0	1	3	2	1	0	1	1	0	999	0	1
5	1	1	2	0	0	0	1	2	0	1	2	0	0	1	1	2	1	1	0	1	0	888	0	1
6	2	0	0	1	1	0	1	0	1	1	1	1	1	1	0	2	0	0	0	0	0	703	0	1
7	0	0	2	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	333	0	1
8	0	2	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	1	0	0	0	333	0	1
9	1	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	333	0	1
10	1	2	1	1	1	1	1	1	1	1	2	1	1	1	1	2	1	1	1	1	0	1443	0	1
11	1	1	0	0	0	0	0	1	0	0	1	0	0	0	1	1	1	0	0	1	0	333	0	1
12	0	1	0	0	1	0	1	0	1	0	2	0	0	1	1	1	0	1	1	0	0	814	0	1
13	1	1	1	1	3	0	0	1	1	4	9	0	1	5	1	6	1	1	3	5	0	2664	0	1
Sum																								$s_{\mathcal{J}} = 13$

formed independently, and that each one of them has a uniform distribution, that is, all values $\{0, 1, \ldots, m-1\}$ of X_i are equally likely. More formally, we write this as

$$
\begin{aligned}
H_0: \quad & X_1, X_2, \ldots, X_n \text{ are independent random variables with a uniform distribu-} \\
& \text{tion on } \{0, 1, \ldots, m-1\}, \text{ i.e. } P(X_i = x) = 1/m, \quad x = 0, 1, \ldots, m-1.
\end{aligned}
\tag{A.10}
$$

Other choices of null hypothesis are discussed in Section A.7.

A.2.2 Mean and variance of the word divisibility count

Before finding ways of approximating the p-value (A.9), we will first compare the observed divisibility count $s_{\mathcal{J}}$ with the expected value and standard deviation of a randomly formed divisibility count. In order to simplify formulas it is convenient to introduce the probability $\pi = 1/m$. It follows from (A.6)-(A.7) that the divisibility indicators K_I satisfy

$$
\begin{aligned}
P(X_I = 0|H_0) = E(K_I|H_0) &= \pi, \\
\mathrm{Var}(K_I|H_0) &= \pi(1-\pi), \\
\mathrm{Cov}(K_I, K_J|H_0) &= 0, \quad I \neq J,
\end{aligned}
\tag{A.11}
$$

where $E(\cdot)$, $\mathrm{Var}(\cdot)$, and $\mathrm{Cov}(\cdot)$ refer to expected values, variance, and covariance of random variable(s). In particular, if (A.11) is inserted into the definition of the divisibility count $S_{\mathcal{J}}$ in (A.4), we find that

$$
\begin{aligned}
E(S_{\mathcal{J}}|H_0) &= \textstyle\sum_{I \in \mathcal{J}} E(K_I|H_0) = |\mathcal{J}|\pi, \\
\mathrm{Var}(S_{\mathcal{J}}|H_0) &= \textstyle\sum_{I \in \mathcal{J}} \mathrm{Var}(K_I|H_0) = |\mathcal{J}|\pi(1-\pi).
\end{aligned}
\tag{A.12}
$$

The ratio

$$
t_{\mathcal{J}} = \frac{s_{\mathcal{J}} - E(S_{\mathcal{J}}|H_0)}{\sqrt{\mathrm{Var}(S_{\mathcal{J}}|H_0)}} = \frac{s_{\mathcal{J}} - |\mathcal{J}|\pi}{\sqrt{|\mathcal{J}|\pi(1-\pi)}}
\tag{A.13}
$$

quantifies how many standard deviations away from the mean the observed word group divisibility count $s_{\mathcal{J}}$ is. Table 6 displays the values of $t_{\mathcal{J}}$ for the three word group collections of Table 2. Since all these WGCs have large t-values, this indicates that the corresponding p-values are small as well. Notice that $t_{\mathcal{J}}$ is standardized, so that $E(t_{\mathcal{J}}|H_0) = 0$ and $\mathrm{Var}(t_{\mathcal{J}}|H_0) = 1$ when $s_{\mathcal{J}}$ is randomly drawn from H_0.

Table 6: Values of the t-statistic (A.13) for the three word group collections of Table 2 when $m = 37$. The rightmost column displays the rank $r_{\mathcal{J}}$ of the matrix $\boldsymbol{A}_{\mathcal{J}}$, for each word group collection.

$\mathcal{J}$	$\lvert\mathcal{J}\rvert$	$s_{\mathcal{J}}$	$E(S_{\mathcal{J}}\lvert H_0)$	$\mathrm{Var}(S_{\mathcal{J}}\lvert H_0)^{1/2}$	$t_{\mathcal{J}}$	$r_{\mathcal{J}}$
G11	127	23	3.432	1.828	10.707	7
GC	13	13	0.351	0.585	21.633	13
JC	3	3	0.081	0.281	10.392	2

A.3 Finding p-values for word group collections with independent word groups (as for GC)

Although $t_{\mathcal{J}}$ in (A.13) gives some information about how likely it is to observe $s_{\mathcal{J}}$ by chance, this information is not sufficient to compute the p-value in (A.9). In order to evaluate the p-value we need to find or approximate the distribution of the divisibility count $S_{\mathcal{J}}$ under the null hypothesis H_0 of chance. This is the topic of Sections A.3-A.4. In Section A.3 we will first develop some theory that makes it possible to compute the p-value of the word group collection GC, where all word group counts are independent. It is more difficult to find the p-values for the other two WGCs G11 and JC, the topic of Section A.4. The reason is that these two WGCs contain so many word groups that the divisbility indicators K_I in (A.4) are no longer independent. For instance, if two words are divisible by 37, then the word group formed by these two words is divisible by 37 as well.

As a preparation for finding the p-value (A.9), we introduce for any word group collection $\mathcal{J}$ the rank $r_{\mathcal{J}} = \text{rank}(\boldsymbol{A}_{\mathcal{J}})$ of the matrix $\boldsymbol{A}_{\mathcal{J}}$, that is, the number of linearly independent rows of this matrix. We have that

$$1 \le r_{\mathcal{J}} \le \min(|\mathcal{J}|, n). \tag{A.14}$$

From the rightmost column of Table 6 we notice that word group collection GC has linearly independent rows, i.e.

$$r_{\mathcal{J}} = |\mathcal{J}|. \tag{A.15}$$

Whenever (A.15) holds and m is a prime number, it follows that the word group numbers of $\mathcal{J}$ satisfy

$$\{X_{I_j}\}_{j=1}^{|\mathcal{J}|} \text{ are independent under } H_0 \text{ with uniform distributions } P(X_{I_j} = x) = \pi, \tag{A.16}$$

for $x = 0, 1, \ldots, m-1$. We will motivate (A.16) below, but first explain how it can be used to evaluate the p-value of a WGC $\mathcal{J}$ that satisfies (A.15). Four our purposes, the important implication of (A.16) is that the divisibility indicators

$$\{K_{I_j}\}_{j=1}^{|\mathcal{J}|} \text{are } \textit{independent} \text{ random variables under } H_0 \text{ with } E(K_{I_j}) = \pi, \tag{A.17}$$

that is, $P(K_{I_j} = 1) = \pi$ and $P(K_{I_j} = 0) = 1 - \pi$. (Notice that this is a stronger assertion than (A.11), which only requires that K_{I_j} are *uncorrelated* random variables under H_0, with expected value π.) Recall from (A.4) that $S_{\mathcal{J}}$ is the sum of the divisibility indicators K_{I_j}. From this and (A.17) it follows that

$$S_{\mathcal{J}} | H_0 \sim \text{Bin}(|\mathcal{J}|, \pi)$$

has a binomial distribution with parameters $|\mathcal{J}|$ and π under the null hypothesis whenever (A.15) holds and m is a prime number. The corresponding p-value (A.9) is the tail probability

$$p_{\mathcal{J}} = \sum_{s=s_{\mathcal{J}}}^{|\mathcal{J}|} \binom{|\mathcal{J}|}{s} (1-\pi)^s \pi^s \tag{A.18}$$

of this binomial distribution at the observed divisibility count $s_{\mathcal{J}}$. Applying formula (A.18), with $m = 37$, to the WGC $\mathcal{J} = \mathrm{GC}$ ($s_{\mathcal{J}} = |\mathcal{J}| = 13$) we find that

$$p_{\mathrm{GC}} = \pi^{13} = \left(\frac{1}{37}\right)^{13} = 4.1056 \cdot 10^{-21}. \tag{A.19}$$

For other values of m, not all word groups of GC will be divisible by m ($s_{\mathcal{J}} < |\mathcal{J}|$). It follows that p_{GC} will involve more terms in (A.18) when $m \neq 37$ and hence be a lot larger than the value for $m = 37$ in (A.19). Unfortunately, formula (A.18) severely underestimates the p-value for WGCs $\mathcal{J} = \mathrm{JC}$ and $\mathcal{J} = \mathrm{G11}$. The reason is that (A.15) fails, and therefore JC and G11 contain too many word groups for $\{K_I;\, I \in \mathcal{J}\}$ to be independent.

Let us now return to (A.16) and prove this claim. The details are a bit involved, and a reader who prefers to skip the proof of (A.16) may proceed to Section A.4. In view of (A.6), (A.16) is equivalent to

$$P(\boldsymbol{AX} = \boldsymbol{x} \bmod m | H_0) = \pi^{|\mathcal{J}|}, \tag{A.20}$$

for any vector $\boldsymbol{x} = (x_1, \ldots, x_{|\mathcal{J}|})^T$ of integers. It is therefore sufficient to prove (A.20), whenever (A.15) holds and m is a prime number. The proof of (A.20) is based on the fact that since m is a prime number, the set of elements $\{0, 1, \ldots, m-1\}$ forms a field under the two operations multiplication and addition modulo m. It is therefore possible to find an invertible matrix $\boldsymbol{C}$ of dimension $|\mathcal{J}| \times |\mathcal{J}|$, whose entries are natural numbers, such that

$$\boldsymbol{CA} = \boldsymbol{B} \bmod m, \tag{A.21}$$

where the equality is modulo m for all $|\mathcal{J}|n$ matrix elements on both sides of (A.21), and the entries b_{ji} of the $|\mathcal{J}| \times n$ upper triangular matrix $\boldsymbol{B}$ satisfy

$$b_{ji} = \begin{cases} 0, & 1 \leq i < i_j, \\ 1, & i = i_j \end{cases}$$

for some increasing sequence $1 \leq i_1 < i_2 < \ldots < i_{|\mathcal{J}|} \leq n$ of $|\mathcal{J}|$ word indeces. Multiplying both sides of the equality sign of (A.20) by $\boldsymbol{C}$, it follows that (A.20) is equivalent to

$$P(\boldsymbol{BX} = \boldsymbol{z} \bmod m | H_0) = \pi^{|\mathcal{J}|}, \tag{A.22}$$

with $\boldsymbol{z} = \boldsymbol{Cx} = (z_1, \ldots, z_{|\mathcal{J}|})^T$. In order to prove (A.22), we rewrite its left hand side as an integral

$$\begin{aligned} & P(\boldsymbol{BX} = \boldsymbol{z} \bmod m | H_0) \\ & \quad = E\left[P\left(X_{i_1} = -z_1 - \textstyle\sum_{i=i_1+1}^n b_{1i}X_i \bmod m | X_{i_1+1}, \ldots, X_n, H_0\right)\right. \\ & \qquad \cdot P\left(X_{i_2} = -z_2 - \textstyle\sum_{i=i_2+1}^n b_{1i}X_i \bmod m | X_{i_2+1}, \ldots, X_n, H_0\right) \\ & \qquad \vdots \\ & \qquad \left.\cdot P\left(X_{i_{|\mathcal{J}|}} = -z_{i_{|\mathcal{J}|}} - \textstyle\sum_{i=i_{|\mathcal{J}|}+1}^n b_{|\mathcal{J}|i}X_i \bmod m | X_{i_{|\mathcal{J}|}+1}, \ldots, X_n, H_0\right)\right] \end{aligned} \tag{A.23}$$

that involves $|\mathcal{J}|$ nested conditional probabilities, and an outer expectation that is taken with respect to $X_{i_1+1}, \ldots, X_n$. Recall from (A.10) that $\{X_i\}_{i=1}^n$ are independent random variables under H_0, with a uniform distribution on $0, 1, \ldots, m-1$. From this it follows that all conditional probabilities in (A.23) equal π regardless of the values of the random variables to the right of the vertical bars that they are conditioned on. Consequently, since (A.23) is the expected value of the product of $|\mathcal{J}|$ such conditional expectations, it simplifies to $\pi^{|\mathcal{J}|}$, and (A.22) is verified.

A.4 Finding p-values for word group collection when word groups are not independent (as for JC and G11)

In this subsection we will first in Section A.4.1 find an upper bound of the p-value of the divisbility count of any word group collection. This is of independent interest, but it will also be used in Section A.6, in connection with multiple testing. In Section A.4.2 we obtain an exact formula for the divisibility count when $\mathcal{J} = \mathcal{J}_{\text{all}}$ contains all $|\mathcal{J}| = 2^n - 1$ word groups, with the restriction that multiple occurrences of words are not allowed. Then in Sections A.4.3 and A.4.4, this formula is applied to the p-values of $\mathcal{J} = \text{JC}$ and $\mathcal{J} = \text{G11}$ respectively.

A.4.1 A general formula for p-values of word group collections

In order to derive the general upper upper bound of the p-value, we rewrite (A.9) as

$$\begin{array}{rcl} p_{\mathcal{J}} & = & P\left(\cup_{I_1,\ldots,I_s}\{K_{I_1} = \ldots = K_{I_s} = 1\}|H_0\right) \\ & \leq & \sum_{I_1,\ldots,I_s} P(K_{I_1} = \ldots = K_{I_s} = 1|H_0) \\ & = & \sum_{I_1,\ldots,I_s} E(K_{I_1} \cdot \ldots \cdot K_{I_s}|H_0) \\ & = & \sum_{\mathcal{I}} E(K_{\mathcal{I}}|H_0), \end{array} \tag{A.24}$$

where $s = s_{\mathcal{J}}$ and the sum is taken over all $\binom{|\mathcal{J}|}{s}$ word group collections $\mathcal{I} = \{I_1, \ldots, I_s\}$ with s word groups that belong to $\mathcal{J}$. In the first step of (A.24) we used the fact that the event $\{S_{\mathcal{J}} \geq s\}$ is equivalent to the union of the events $\{K_{I_1} = \ldots = K_{I_s} = 1\}$ for all such word group collections.

The upper bound of the p-value in (A.24) is typically too crude if $\mathcal{J} = \mathcal{J}_{\text{all}}$ consists of all $2^n - 1$ word groups without multiple occurrences of words (as for $\mathcal{J} = \text{G11}$). However, (A.24) is accurate when $\mathcal{J}$ is small enough so that $|\mathcal{J}|$ only slightly exceeds $r_{\mathcal{J}}$ (cf. (A.15)).

Recall from Section A.1 that $\mathcal{J}$ is represented by a $|\mathcal{J}| \times n$ matrix $\boldsymbol{A}_{\mathcal{J}}$, whose entries are natural numbers. Analogously, any WGC $\mathcal{I} \subset \mathcal{J}$ is equivalent to a submatrix $\boldsymbol{A}_{\mathcal{I}}$ of $\boldsymbol{A}_{\mathcal{J}}$ of dimension $|\mathcal{I}| \times n$, obtained by extracting all rows in $\mathcal{I}$ from $\boldsymbol{A}_{\mathcal{J}}$. The requirement $K_{\mathcal{I}} = 1$ in (A.24), for each WGC $\mathcal{I}$ with s word groups, corresponds to having

$$\boldsymbol{A}_{\mathcal{I}}\boldsymbol{X} = \boldsymbol{0} \text{ modulo } m.$$

If m is a prime number, the expected value of $K_{\mathcal{I}}$ is

$$E(K_{\mathcal{I}}|H_0) = \pi^{r_{\mathcal{I}}} \tag{A.25}$$

under the null hypothesis, where $r_{\mathcal{I}} = \text{rank}(\boldsymbol{A}_{\mathcal{I}})$ is the number of independent restrictions that the rows of $\boldsymbol{A}_{\mathcal{I}}$ impose. Formula (A.25) is shown in the same way as (A.20) when $\boldsymbol{x} = \boldsymbol{0}$ (which corresponds to the special case $\mathcal{I} = \mathcal{J}$ and $r_{\mathcal{J}} = |\mathcal{J}|$). Inserting (A.25) into (A.24), it follows that

$$p_{\mathcal{J}} \le \sum_{r=1}^{s} N_{nsr} \pi^r, \tag{A.26}$$

where N_{nsr} is the number of WGCs $\mathcal{I}$ in (A.24) that have s word groups (constructed from n words) that belong to $\mathcal{J}$, and additionally satisfy $r_{\mathcal{I}} = r$.

Recall that two of the WGCs ($\mathcal{J}$ = GC and $\mathcal{J}$ = JC) of Table 2 have $s = |\mathcal{J}|$. Then there is only one single term $\mathcal{I} = \mathcal{J}$ of (A.24), so that this upper bound of $p_{\mathcal{J}}$ is exact. This corresponds to $N_{nsr_{\mathcal{J}}} = 1$, and $N_{nsr} = 0$ for all $r \neq r_{\mathcal{J}}$ in (A.26), and consequently

$$p_{\mathcal{J}} = \pi^{r_{\mathcal{J}}}. \tag{A.27}$$

In particular, when $r_{\mathcal{J}} = |\mathcal{J}| = s_{\mathcal{J}}$ (as for GC), formula (A.27) agrees with (A.19).

A.4.2 p-values of word group collections with all word groups

It is assumed in this subsection that all word groups have at most one occurrence of each word. We will derive an exact formula for the p-value (A.9) of the word group collection $\mathcal{J} = \mathcal{J}_{\text{all}}$ that consists of all such word groups, i.e. $|\mathcal{J}| = 2^n - 1$. This includes $\mathcal{J}$ = JC and $\mathcal{J}$ = G11 as special cases $n = 2$ and $n = 7$ respectively. For ease of notation we denote the divisibility count by $S_{\mathcal{J}} = S_n$ whenever $\mathcal{J} = \mathcal{J}_{\text{all}}$ consists of all word groups obtained from n words.

Let R_n be the number of words among the n given ones, that have a numerical value Y_i divisible by m. Let also T_n be the number of word groups divisible by m which are formed by the remaining $Q_n = n - R_n$ words. For instance, $T_n = 0$ when $Q_n = 0$, and more generally

$$S_n = 2^{R_n} - 1 + (2^{R_n} - 1)T_n + T_n = 2^{n-Q_n}(T_n + 1) - 1, \tag{A.28}$$

where the first term $2^{R_n} - 1$ is the number of word groups formed by the words whose numerical values are divisible by m, the second term $(2^{R_n} - 1)T_n$ is the number of word groups with numerical values divisible by m that contain at least one word divisible by m and at least one word not divisible by m, and the third term T_n is defined as above. In order to find the null hypothesis distribution of S_n we will condition on the value of Q_n. This enables us to express the p-value in (A.9) as

$$\begin{aligned} p_{\mathcal{J}_{\text{all}}} &= P(S_n \ge s | H_0) \\ &= \textstyle\sum_{q=0}^{n} P(Q_n = q | H_0) P(S_n \ge s | Q_n = q, H_0) \\ &= \textstyle\sum_{q=0}^{n} P(Q_n = q | H_0) P(2^{n-q}(T_n + 1) - 1 \ge s | Q_n = q, H_0) \\ &= \textstyle\sum_{q=0}^{n} P(Q_n = q | H_0) P(T_n \ge \lceil 2^{-(n-q)}(s+1) - 1 \rceil | Q_n = q, H_0), \end{aligned} \tag{A.29}$$

where $\lceil \cdot \rceil$ refers to the smallest integer greater or equal to the number in brackets. We thus need to know the joint distribution of Q_n and T_n under the null hypothesis H_0 in order to simplify (A.29). It follows from (A.10) that Q_n has a binomial distribution

$$Q_n|H_0 \sim \mathrm{Bin}(n, 1-\pi) \Longrightarrow P(Q_n = q|H_0) = \binom{n}{q}\pi^{n-q}(1-\pi)^q \tag{A.30}$$

under the null hypothesis. Since none of the Q_n words have a numerical value divisible by m, if H_0 holds and $Q_n = q$, the joint distribution of these q words corresponds to the adjusted null hypothesis

$$H_0' : \{X_i\}_{i;X_i \neq 0} \text{ independent with } P(X_i = x) = \frac{1}{m-1} =: \pi', \quad x = 1, 2, \ldots, m-1. \tag{A.31}$$

In words, formula (A.31) tells that if H_0 holds, those q words whose numerical values Y_i are not divisible by m, have remainders modulo m that are independent and uniformly distributed on $\{1, \ldots, m-1\}$. From this it follows that the distribution of T_n under the null hypothesis H_0 is the same as the distribution of S_q under the adjusted null hypothesis H_0', when $Q_n = q$. We therefore condition on the valule of $Q_n = q$, make use of (A.30) and rewrite (A.29) as

$$\begin{aligned} p_{\mathcal{J}_{\text{all}}} &= P(S_n \geq s|H_0) \\ &= \textstyle\sum_{q=0}^{n} \binom{n}{q}\pi^{n-q}(1-\pi)^q P\left(S_q \geq \lceil 2^{q-n}(s+1)-1)\rceil |H_0'\right) \\ &= \pi^n + \textstyle\sum_{q=1}^{n} \binom{n}{n-q}\pi^{n-q}(1-\pi)^q P\left(S_q \geq \lceil 2^{q-n}(s+1)-1)\rceil |H_0'\right), \end{aligned} \tag{A.32}$$

a formula also derived by van der Valk (2015) for $n = 7$ and $m = 37$.

A.4.3 *p*-value of JC

In this section we will apply the theory of Section A.4.2 in order to approximate the p-value of JC. To this end we apply formula (A.32) with $n = 2$, $s = 3$, $m = 37$, and $\pi = 1/37$, and find that

$$\begin{aligned} p_{\text{JC}} &= P(S_2 \geq 3|H_0) \\ &= (1/37)^2 \\ &+ 2(1-1/37)(1/37)P(S_1 \geq 1|H_0') \\ &+ (1-1/37)^2 P(S_2 \geq 3|H_0') \\ &= (1/37)^2 \\ &= 7.3046 \cdot 10^{-4}, \end{aligned} \tag{A.33}$$

where in the third step we used that $P(S_1 \geq 1|H_0') = P(S_2 \geq 3|H_0') = 0$. Note that (A.33) agrees with (A.27), since $r_{\text{JC}} = 2$. This is not surprising, since JC satisfies the necessary condition $s = |\mathcal{J}|(= 3)$ for (A.27) to hold.

A.4.4 p-value of G11

In order to find the p-value of G11, we will once again apply formula (A.32), but this time with $n = 7$, $s = 23$, and $m = 37$. This yields

$$\begin{aligned} p_{\text{G11}} &= P(S_7 \geq 23|H_0) \\ &= (1/37)^7 \\ &+ 7(1-1/37)(1/37)^6 \\ &+ 21(1-1/37)^2(1/37)^5 \\ &+ 35(1-1/37)^3(1/37)^4 \cdot P(S_3 \geq 1|H_0') \\ &+ 35(1-1/37)^4(1/37)^3 \cdot P(S_4 \geq 2|H_0') \\ &+ 21(1-1/37)^5(1/37)^2 \cdot P(S_5 \geq 5|H_0') \\ &+ 7(1-1/37)^6(1/37) \cdot P(S_6 \geq 11|H_0') \\ &+ (1-1/37)^7 \cdot P(S_7 \geq 23|H_0'). \end{aligned} \tag{A.34}$$

In order to evaluate p_{G11}, we thus need to compute all terms $P(S_q \geq k|H_0')$ that appear in (A.34). Following van der Valk (2015), it is possible to give exact values of these quantities by letting a computer go through all $(m-1)^q = 36^q$ possible in vectors $\boldsymbol{X}_q = (X_1, \ldots, X_q)^T$ with nonzero elements, which under H_0' have the same probability $1/(m-1)^q = 1/36^q$. van der Valk also noted that in order to find the number of these vectors $\boldsymbol{X}_q$ for which the corresponding divisibility count satisfies $S_q \geq k$, it is possible to first assume $X_1 = 1$, and calculate the number of sequences $(1, X_2, \ldots, X_q)^T$ for which $S_q \geq k$, and then multiply this number by $m - 1 = 36$. Based on this it follows that

$$\begin{aligned} P(S_3 \geq 1|H_0') &= 5040/36^3 = 0.1080, \\ P(S_4 \geq 2|H_0') &= 40140/36^4 = 0.02390, \\ P(S_5 \geq 5|H_0') &= 92340/36^5 = 0.001527, \\ P(S_6 \geq 11|H_0') &= 74880/36^6 = 3.4399 \cdot 10^{-5}, \\ P(S_7 \geq 23|H_0') &= 46368/36^7 = 5.9170 \cdot 10^{-7}, \end{aligned} \tag{A.35}$$

where the first three equations appear in van der Valk (2015), whereas we derived the last two. Inserting (A.35) into (A.34) we find that

$$\begin{aligned} p_{\text{G11}} &= (1/37)^7 \\ &+ 7(1-1/37)(1/37)^6 \\ &+ 21(1-1/37)^2(1/37)^5 \\ &+ 35(1-1/37)^3(1/37)^4 \cdot 0.1080 \\ &+ 35(1-1/37)^4(1/37)^3 \cdot 0.02390 \\ &+ 21(1-1/37)^5(1/37)^2 \cdot 0.001527 \\ &+ 7(1-1/37)^6(1/37)^1 \cdot 3.4399 \cdot 10^{-5} \\ &+ (1-1/37)^7 \cdot 5.9170 \cdot 10^{-7} \\ &= 4.3383 \cdot 10^{-5} \end{aligned} \tag{A.36}$$

is the p-value for word group collection G11.

A.5 Combined p-values

In this section we combine information from the divisibility patterns of the first verse of the Bible (G11), the genetic code (GC), and Jesus Christ (JC). It is reasonable to believe that the first verse of the Bible, the genetic code and Jesus Christ are independent sources of evidence under the null hypothesis H_0 that all three texts are formed by chance. If H_0 is true, then p_{G11}, p_{GC}, and p_{JC} are observations of independent random variables P_{G11}, P_{GC}, and P_{JC}. It is possible to regard these three word group collections as one single *meta analysis* and combine the three p-values into one combined p-value. This can be done in many different ways. We will employ Fisher's method (Fisher, 1925, Mosteller and Fisher, 1948) with a combined p-value[1]

$$p_{\mathrm{comb}} = P(V \geq v | H_0), \tag{A.37}$$

where

$$V = -\log(P_{\mathrm{G11}}) - \log(P_{\mathrm{GC}}) - \log(P_{\mathrm{JC}})$$

is a random variable that combines information from all three word group collections, and

$$\begin{aligned} v &= -\log(p_{\mathrm{G11}}) - \log(p_{\mathrm{GC}}) - \log(p_{\mathrm{JC}}) \\ &= -\log(4.3383 \cdot 10^{-5}) - \log(4.1056 \cdot 10^{-21}) - \log(7.3046 \cdot 10^{-4}) \\ &= 64.2092 \end{aligned} \tag{A.38}$$

is the observed value of V. The last step of (A.38) follows from (A.19), (A.33), and (A.36).

It is possible to interpret v as a measure of how surprised we are to observe the three p-values p_{G11}, p_{GC}, and p_{JC} for the divisibility patterns of Genesis 1:1, the genetic code and the words "Jesus" "Christ". This measure of surprisedness is quantified in units of nats of information, and it is closely related to the so called functional information used to quantify rareness of functional proteins (Szostak, 2003, Hazen et al., 2007).

Thorvaldsen and Hössjer (2020) argue that the smallness of (A.37) is a general way of inferring *fine-tuning* of biological and other systems. Once a null hypothesis of chance and a measure of specificity has been defined, the p-value of the system is the probability that a randomly generated structure has a specificity V at least as large as the observed one v. Here, v is the specificity that the divisibility patterns of Genesis 1:1, the genetic code and "Jesus" "Christ" convey. In this context, the combined p-value (A.37) is the probability that the specificity V of a randomly generated divisibility pattern is at least as large as the observed specificity v.

In order to evaluate the combined p-value (A.37), we will approximate the distribution of V under the null hypothesis H_0. We will assume that P_{G11}, P_{GC}, and P_{JC} have uniform null distributions on the interval $(0, 1)$. This would be true if the three divisibility counts S_{G11}, S_{GC}, and S_{JC} had continuous distributions under H_0. However, since the number of possible values of these divisibility counts is finite, the uniformity assumption is only an approximation. It is still conservative though, since it leads to an estimate of the combined p-value that is too large. Given this assumption, that the three p-values are

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[1] Fisher's method, with c combined tests, is usually stated in terms of a test statistic $2V$ that has a chisquare distribution χ^2_{2c} with $2c$ degrees of freedom under the null hypothesis H_0. However, this is equivalent to V having a gamma distribution with shape parameter c and scale parameter 1 under H_0. We apply Fisher's method with $c = 3$ combined tests.

independent with uniform distributions, V will have a gamma distribution with shape parameter 3 and scale parameter 1. From this and (A.37) it follows that

$$\begin{aligned} p_{\text{comb}} &\le e^{-v}(1+v+v^2/2) \\ &= 2.7668 \cdot 10^{-25}, \end{aligned} \tag{A.39}$$

where the first inequality follows from the uniform distribution approximation of P_{G11}, P_{GC}, and P_{JC}, and the equality of the second step is a consequence of (A.38). In the next section we describe how to adjust (A.39) for multiple testing.

A.6 Adjusting for multiple testing

In the previous section we found that the combined p-value for observing the divisibility patterns of G11, GC, and JC is very low. The question arises whether (A.39) is too small and should be corrected for other possible divisibility patterns. Such a correction would safeguard against *observational bias*, where one first notices a pattern and then tests a hypothesis that only includes this pattern. Instead, one should rather perform multiple comparisons or *multiple tests*, of other potential and similar types of patterns. Several methods of multiple testing have been developed, see for instance Ge et al. (2003) for a review. The Bonferroni correction (Bonferroni, 1936, Miller, 1966) is the simplest and most well known multiple test adjustment. Its purpose is to control the so called familywise error rate by multiplying the observed p-value with the number of tests. We will use Bonferroni type corrections to adjust the individual p-values of G11, GC, and JC, as well as the p-value of the combined test. In this context we introduce

$$\begin{aligned} N_{\text{G11}} &= \text{number of possible and relevant Bible verses in the Old Testament} \\ &\quad \times \text{number of possible Hebrew gematria schemes}, \\ N_{\text{GC}} &= \text{number of biologically relevant and linearly independent word groups} \\ &\quad \text{from the genetic code}, \\ N_{\text{JC}} &= \text{number of namnes of the Lord}, \\ N_m &= \text{number of relevant divisibility numbers } m. \end{aligned}$$

The adjusted individual p-values are defined as

$$\begin{aligned} p_{\text{G11}}^{\text{adj}} &= \min(N_{\text{G11}} p_{\text{G11}}, 1), \\ p_{\text{GC}}^{\text{adj}} &= \min(\tbinom{N_{\text{GC}}}{13} p_{\text{GC}}, 1), \\ p_{\text{JC}}^{\text{adj}} &= \min(N_{\text{JC}} p_{\text{JC}}, 1). \end{aligned} \tag{A.40}$$

The first adjusted p-value of (A.40) is a Bonferroni correction. It corresponds to having N_{G11} hypothetical data sets, one for each combined Bible verse and gematria scheme, with $p_{\text{G11}}^{\text{adj}}$ an upper bound for the probability, under H_0, that at least one of these hypothetical tests would have a p-value at least as small as the one observed for Genesis 1:1 and the *mispar hechraci* numbering scheme. The third adjusted p-value of (A.40) is also a Bonferroni correction, with a similar interpretation in terms of N_{JC} hypothetical data sets and tests, one for each possible name of our Lord. The second adjusted p-value of (A.40) corresponds to enlarging the given data set from 13 to N_{GC} linearly independent word

Table 7: Combined p-values p_{comb} and $p_{\text{comb}}^{\text{adj}}$ for the divisibility patterns of Genesis 1:1 (G11), the genetic code (GC) and Jesus Christ (JC), computed without (A.41) and with (A.43) adjustment for N_m possible values of m respectively, for six different multiple testing scenarios. The non-adjusted p-values ($p_{\text{GC}} = 4.1056 \cdot 10^{-21}$, $p_{\text{JC}} = 7.3046 \cdot 10^{-4}$, $p_{\text{G11}} = 4.3383 \cdot 10^{-5}$), defined in (A.19), (A.33), and (A.36), were used for each word group collection. Scenario 1 does not correct for multiple testing, whereas Scenario 2, with $N_{\text{GC}} = 25$, corresponds to a minimal adjustment for multipel testing (the 25 word groups P1-P13 and N1-N12 of the genetic code, as described in the text). The most conservative scenario (Scenario 6) is illustrated in Figure 1.

Scenario	N_{G11}	N_{GC}	N_{JC}	N_m	p_{comb}	$p_{\text{comb}}^{\text{adj}}$
1	1	13	1	1	$2.7668 \cdot 10^{-25}$	$2.7668 \cdot 10^{-25}$
2	1	25	1	1	$8.3746 \cdot 10^{-19}$	$8.3746 \cdot 10^{-19}$
3	10	30	2	10	$2.9652 \cdot 10^{-16}$	$2.9652 \cdot 10^{-15}$
4	20	35	3	20	$9.2265 \cdot 10^{-15}$	$1.8453 \cdot 10^{-13}$
5	30	40	4	30	$1.3016 \cdot 10^{-13}$	$3.9048 \cdot 10^{-12}$
6	40	45	5	40	$1.1577 \cdot 10^{-12}$	$4.6307 \cdot 10^{-11}$

groups. If this does not enlarge the unadjusted divisibility count ($S_{\text{GC}} = 13$), an upper bound of the adjusted p-value after the first step, is obtained from (A.24) by multiplying p_{G11} with $\binom{N_{\text{GC}}}{13}$.

In the next step Fisher's method is used to combine the p-values in (A.40). This gives

$$p_{\text{comb}} = P(V \geq \tilde{v} | H_0) = e^{-\tilde{v}}(1 + \tilde{v} + \tilde{v}^2/2), \tag{A.41}$$

where

$$\tilde{v} = -\log(p_{\text{G11}}^{\text{adj}}) - \log(p_{\text{GC}}^{\text{adj}}) - \log(p_{\text{JC}}^{\text{adj}}) \tag{A.42}$$

is the observed specificity. Note that equations (A.41)-(A.42), in contrast to (A.37)-(A.38), make use of the adjusted (rather than the unadjusted) individual p-values for computing the specificity. As a final step of the p-value computation a new Bonferroni correction

$$p_{\text{comb}}^{\text{adj}} = \min\left(N_m p_{\text{comb}}, 1\right) \tag{A.43}$$

is applied to the combined p-value in (A.41) in order to control for different choices of divisbility numbers m.

The adjusted combined p-value (A.43) is computed for several multiple testing scenarios in Table 7. It can be seen that $p_{\text{comb}}^{\text{adj}}$ remains very small for all of these scenarios. We argue that Scenario 6, with the highest amount of multiple testing adjustment, is far too conservative. Indeed, there is plenty of *external* information available that makes a value of 5 for N_{JC}, and a value of 40 for N_{G11} and N_m too large (cf. sections 9-10 for a motivation).

We also argue that the value $N_{\mathrm{GC}} = 45$ of Scenario 6 is too large. On one hand, patterns P1-P13 of Figure 9 are word groups with a biological interpretation in terms of predefined criteria. This includes standard blocks and side chains of amino acids, division of nucleotides into purines A/G and pyrimidines T/C, the concept of synonymous codons, and dublicate bases of codons. Interestingly, Gamow and Yčas (1955) suggested P3, with codons having duplicate bases, based on a hypothetical amino acid model before the standard genetic code was cracked. On the other hand, with $N_{\mathrm{GC}} = 45$, it seems challenging to find 32=45-13 additional and linearly independent word groups, with a clear biological interpretation. We have found 12 such additional word groups, and since none of them are divisible by 37 we refer to them as "non-hit" gropus N1-N12. These non-hit groups N1-N12 are generated as alternatives to P1-P13 in the following way:

- P1 has no alternative.
- P2 has one alternative N1, where all amino acids' nucleon numbers are summed (without accounting for multiplicity in terms of number of occurrences of each amino acid in the genetic code).
- P3 has three alternatives N2-N4, corresponding to subsets of codons for which 1, 2 or 3 of the nucleotides are purines (the fourth case of no purines is redundant).
- P4 has no alternative.
- P5 has no alternative.
- P6 has one alternative N5, where P3=grey is divided into codons with three unique letters (green) and three identical letters (grey) respectively. Then N5=green and N5=grey give rise N6 and N7 respectively, based on whether the missing letter or the triplet is a purine or not.
- P7 has one alternative N8, where TTx/xTT is extracted from P4=green (rather than AAx/xAA from P4=grey).
- P8 has one alternative N9, where CCx/xCC is extracted from P4=green (rather than GGx/xGG from P4=grey).
- P9 has one alternative N10, where Txx/Cxx is extracted from P5=green (rather than Axx/Gxx from P5=grey).
- P10 has no alternative.
- P11 has no alternative.
- P12 has no alternative.
- P13 has two alternatives N11-N12, where C is separated from T/A/G and A from T/C/G respectively (the pattern whereby G is separated from T/C/A is redundant).

If these 12 word groups N1-N12 are added to the 13 word groups P1-P13 of GC, the total number of word groups is $N_{\mathrm{GC}} = 25 = 12 + 13$. We acknowledge though that probably some other biologically relevant non-hit groups are missed. Therefore, the value $N_{\mathrm{GC}} = 25$ of Scenario 2 represents the minimal amount of multiple testing adjustment for the genetic code.

The adjustment for multiple testing can be done in many ways. There is always a balance between using external information on one hand, and thereby decreasing the adjusted p-value, and on the other hand correct for various factors that potentially could be varied in order to increase $p_{\mathrm{comb}}^{\mathrm{adj}}$. In our view we used conservative adjustments in Scenarios 5-6. Consequently, we argue that the probability that the divisibility patterns within the first verse of the Bible, the genetic code, and Jesus Christ occurred by chance is well below 10^{-10}, and hence points towards an Intelligent Designer.

A.7 Choice of null hypothesis

In this appendix we analyzed divisibility patterns of numerical values of word groups from the first verse of the Hebrew Bible, amino acid subsets of the genetic code, and the two words Jesus Christ. These word groups are very often divisible by 37, and we found that the probability (the p-value) for this to happen by chance is very small, also with adjustment for multiple testing. Our p-value computations rely on what we mean by the statement that the divisbility patterns of 37 occur by chance, that is, the choice of null hypothesis when testing divisibility patterns from the Bible, the genetic code and the words Jesus Christ. In this section we will discuss the choice of null hypothesis in more detail.

A.7.1 Violations of independence and uniformity for null hypothesis (A.10)

The p-values of this article are based on a statistical model (A.10) for the null hypothesis that the numeric values of words are generated by chance. This model asserts that the numerical values of Hebrew and Greek words, and the nucleon numbers of amino acids, are independent between words and amino acids respectively. Moreover, when these numbers are divided by 37, it is assumed that the remainders are uniformly distributed on $0, 1, \ldots, 36$. The advantage of this approach is its analytical tractability and the fact that the same type of null hypothesis is used for all three word group collections.

But equation (A.10) is still a simplification: First, words of languages are not independent, and neither are the nucleon numbers of amino acids, since the same letters/atoms appear in several linguistic words/amino acids.

Second, the numerical values of Hebrew and Greek words, and the nucleon numbers of amino acids, are sums of a finite number of letters (gematria values of Hebrew/Greek letters and nucleon counts of atoms respectively), with pre-specified numbers. The uniformity assumption is therefore not exact, in particular not if we condition on the values of the numbers assigned to letters. It is also well known that nucleon numbers of amino acids are negatively correlated with their redundancy (Hasegawa and Miyata, 1980), so that amino acids with smaller nucleon numbers tend to appear more frequently in the genetic code. This strengthens the conclusion that word numbers modulo 37 are not uniformly distributed on $0, 1, \ldots, 36$. Such departures from uniformity are well known and related to Benford's law with extensions (Berger and Hill, 2020).

A.7.2 Permutation-based null hypotheses

The null hypothesis may be chosen in other ways than (A.10). One possibility is to keep the n word counts $Y_1, \ldots, Y_n$ fixed, and to randomly vary the elements of the matrix $\boldsymbol{A} = \boldsymbol{A}_{\mathcal{J}}$ for the word group collection $\mathcal{J}$. In view of (A.5)-(A.6), although the word counts modulo m in $\boldsymbol{X}$ are fixed, since $\boldsymbol{A}$ is random, it follows that the collection $\boldsymbol{X}_{\mathcal{J}}$ of word group counts modulo m is random as well. Recall from (A.4) that the divisbility count $S_{\mathcal{J}}$ is a function of $\boldsymbol{X}_{\mathcal{J}}$, and therefore $S_{\mathcal{J}}$ is random as well.

In the context of the genetic code, one could for instance keep the redundancy pattern of synonymous codons fixed, so that the 21 sets of synonymous codons (of total size 64) are fixed, but allocate them randomly to 20 amino acids and 1 stop signal. For the genetic code, this corresponds to first adding one word for the stop signal, so that $n = 22$ and $Y_{22} = 0$. Then a 22d column for the stop signal is added to $\boldsymbol{A}_{\mathcal{J}}$, so that $a_{j,22}$ contains the number of stop signals in each word group I_j. Then those 21 of all 22 columns of the 14×22 matrix $\boldsymbol{A}$ that correspond to amino acids or a stop signal are permuted randomly. A similar approach was used by Shcherbak and Makukov (2013, Appendix B). They considered all surjective mappings from 64 codons to 21 amino acids/stop signals that correspond to codes with (1) similar redundancy as the canonical genetic code, (2) a reduced effect of mutations/mistranslations, (3) a small departure from cytoplasmic balance. However, the score S_{GC} they assigned to the genetic code was not a divisibility count. Rather it was based on the number of nucleon count balances, symmetries and equal splits of the code.

A.7.3 Evolutionary null hypotheses

Another possibility is to view the genetic code as the outcome of a chemical evolutionary model (Knight et al, 1999, Koonin and Novozhilov, 2009, 2017). In the appendix of Makukov and Shcherbak (2018), genetic codes were generated randomly from a number of different evolutionary models (corresponding to different null hypotheses), and for each of these the p-value was defined as the fraction of generated codes whose scores S_{GC} were at least as large as the observed score s_{GC} for the canonical genetic code. This score S_{GC} was not a divisibility count, as in (A.4), but rather a quantifier of mirror symmetries and nucleotide inversions. In Table A3 of Makukov and Shcherbak (2018), this resulted in p-values between 10^{-6} and 10^{-5}. It is also possible to define the score function S_{GC} in yet other ways. It is well known that the standard genetic code is very robust towards point mutations of single nucleotides, its redundancy pattern has a biological interpretation (Ronneberg et al., 2000), and it carries a cytoplasmic balance. If these and a number of other pieces of evidence (Wichmann and Ardern, 2019), that reveal the fine-tuning of the genetic code and its high degree of optimization for function, are added to the score

Table 8: Combined p-values $p_{\text{comb}}^{\text{adj}}$ for the divisibility patterns of Genesis 1:1 (G11), the genetic code (GC) and Jesus Christ (JC). These combined p-values are computed from (A.40)-(A.43), making use of unadjusted p-values p_{GC}, p_{JC}, and p_{G11}, and the six multiple testing scenarios of Table 7. The unadjusted p-value p_{GC} of the genetic code varies, with the lowest value $p_{\text{GC}} = 4.1056 \cdot 10^{-21}$ corresponding to (A.19), whereas $p_{\text{GC}} = 10^{-18}$ and $p_{\text{GC}} = 10^{-14}$ represent possible p-values for a chemical evolutionary null hypothesis model. The other two unadjusted p-values $p_{\text{JC}} = 7.3046 \cdot 10^{-4}$ and $p_{\text{G11}} = 4.3383 \cdot 10^{-5}$ are defined in (A.33) and (A.36). The results for Scenario 6 and $p_{\text{GC}} = 10^{-14}$ are reported as blue text in Figure 1.

	p_{GC}				
Scenario	$4.1056 \cdot 10^{-21}$	10^{-18}	10^{-14}	10^{-10}	10^{-6}
1	$2.77 \cdot 10^{-25}$	$5.65 \cdot 10^{-23}$	$4.04 \cdot 10^{-19}$	$2.70 \cdot 10^{-15}$	$1.63 \cdot 10^{-11}$
2	$1.63 \cdot 10^{-18}$	$3.13 \cdot 10^{-16}$	$1.95 \cdot 10^{-12}$	$1.04 \cdot 10^{-8}$	$5.30 \cdot 10^{-6}$
3	$2.97 \cdot 10^{-15}$	$5.52 \cdot 10^{-13}$	$3.18 \cdot 10^{-9}$	$1.48 \cdot 10^{-5}$	$7.42 \cdot 10^{-4}$
4	$1.85 \cdot 10^{-13}$	$3.35 \cdot 10^{-11}$	$1.80 \cdot 10^{-7}$	$7.29 \cdot 10^{-4}$	$3.84 \cdot 10^{-3}$
5	$3.90 \cdot 10^{-12}$	$6.91 \cdot 10^{-10}$	$3.48 \cdot 10^{-6}$	$1.04 \cdot 10^{-2}$	$1.04 \cdot 10^{-2}$
6	$4.63 \cdot 10^{-11}$	$8.01 \cdot 10^{-9}$	$3.78 \cdot 10^{-5}$	$2.14 \cdot 10^{-2}$	$2.14 \cdot 10^{-2}$

function S_{GC}, it is likely that the resulting p-value for an evolutionary null hypothesis gets considerably smaller than in Makukov and Shcherbak (2018).

It is also likely to assume that nucleon numbers' divisibility by 37 has no selective advantage. It is therefore very challenging for an evolutionary process to produce a genetic code for which the numerical values of 13 pre-specified amino acid word groups are divisible by 37. This suggests that the p-value (p_{GC}) of an evolutionary null hypohtesis, based on our divisibility count score function S_{GC}, is well beyond 10^{-10}, and not too far away from the value $4.11 \cdot 10^{-21}$ obtained with the null hypothesis in (A.10). In Table 8 we illustrate adjusted and combined p-values for GC, G11, and JC, assuming that the genetic code is generated by an evolutionary process with different values of p_{GC}. It can be seen that $p_{\text{comb}}^{\text{adj}}$ remains small for all realistic values of p_{GC} and all six multiple testing scenarios of Table 7.