

IMPLICATIONS OF THE GENETIC INFORMATION SYSTEM

Dr. Sven Östring



An abstract digital background featuring a dark blue and green color palette. The image is filled with glowing binary code (0s and 1s) arranged in horizontal lines on the left and in a curved, perspective-driven path on the right. Overlaid on the binary are complex, translucent geometric patterns, including a large, multi-faceted star-like shape in the center and various intersecting lines and planes that create a sense of depth and digital architecture. The overall effect is a high-tech, futuristic aesthetic.



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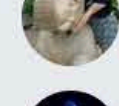
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The background features a light blue gradient with a complex network of thin, light blue lines connecting various points. Scattered throughout are numbers in different colors (blue, green, red, grey), some of which are larger and more prominent than others, creating a digital or data-themed aesthetic.

“

After Watson and Crick, we know that genes themselves, within their minute internal structure, are long strings of pure digital information. What is more, they are truly digital, in the full and strong sense of computers and compact disks, not in the weak sense of the nervous system. The genetic code is not a binary code as in computers, nor an eight-level code as in some telephone systems, but a quaternary code, with four symbols. The machine code of the genes is uncannily computerlike.

-Richard Dawkins

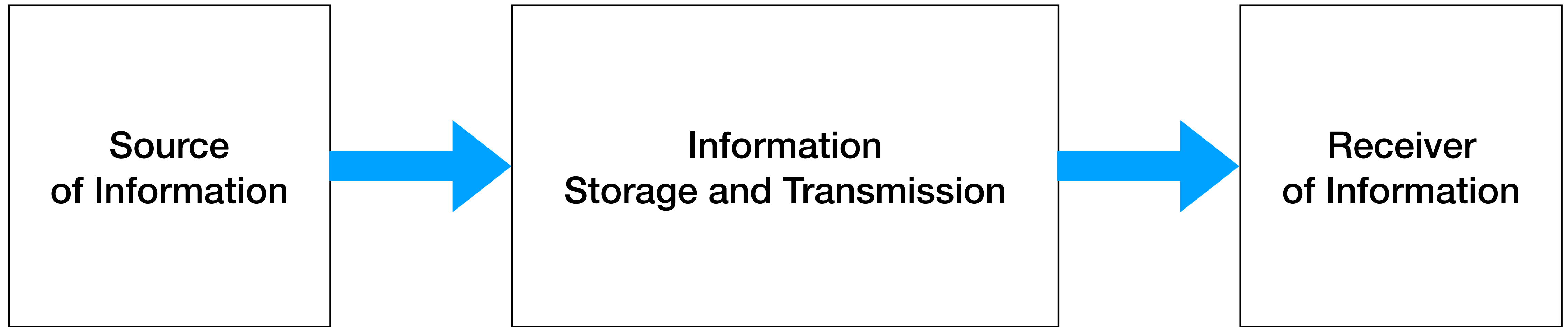
The background is a light blue gradient with a complex network of thin, light blue lines connecting various points. These points are represented by small numbers (0-9) in different colors (blue, green, red, grey). On the left side, there is a vertical column of numbers that appears to be a binary sequence (0s and 1s) or a specific data stream, rendered in a lighter blue color. The overall aesthetic is technological and digital.

“

DNA is like a computer program, but far, far more advanced than any software we've ever created.

-Bill Gates

An Information System





$$C = B \log_2 \left(1 + \frac{S}{N} \right)$$

$$H(X) = - \sum_x p(x) \log p(x)$$

$$C(X|Y) = \max (H(X) - H(X|Y))$$

Reprinted with corrections from *The Bell System Technical Journal*,
Vol. 27, pp. 379–423, 623–656, July, October, 1948.

A Mathematical Theory of Communication

By C. E. SHANNON

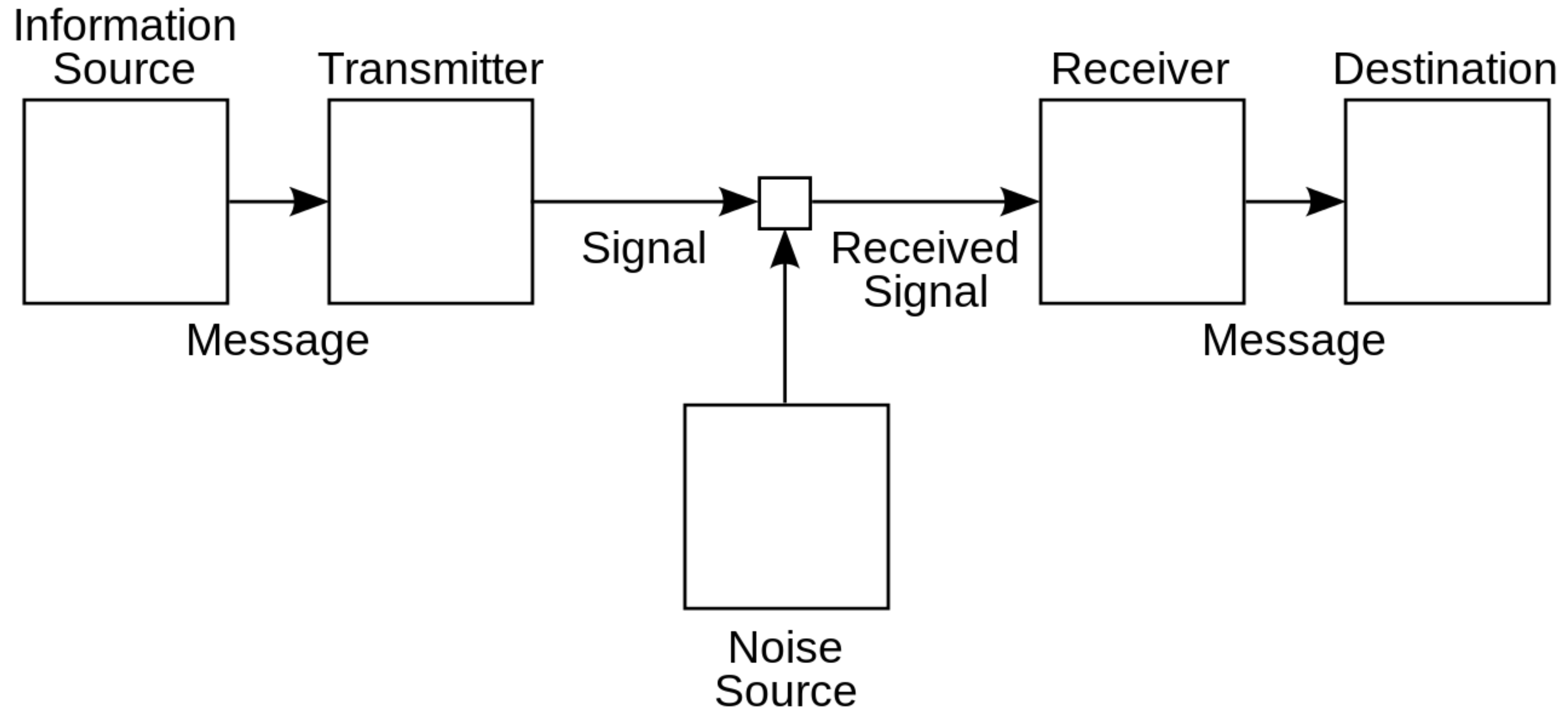
INTRODUCTION

THE recent development of various methods of modulation such as PCM and PPM which exchange bandwidth for signal-to-noise ratio has intensified the interest in a general theory of communication. A basis for such a theory is contained in the important papers of Nyquist¹ and Hartley² on this subject. In the present paper we will extend the theory to include a number of new factors, in particular the effect of noise in the channel, and the savings possible due to the statistical structure of the original message and due to the nature of the final destination of the information.

The fundamental problem of communication is that of reproducing at one point either exactly or approximately a message selected at another point. Frequently the messages have *meaning*; that is they refer to or are correlated according to some system with certain physical or conceptual entities. These semantic aspects of communication are irrelevant to the engineering problem. The significant aspect is that the actual message is one *selected from a set* of possible messages. The system must be designed to operate for each possible selection, not just the one which will actually be chosen since this is unknown at the time of design.

If the number of messages in the set is finite then this number or any monotonic function of this number can be regarded as a measure of the information produced when one message is chosen from the set, all

Shannon's Communication System



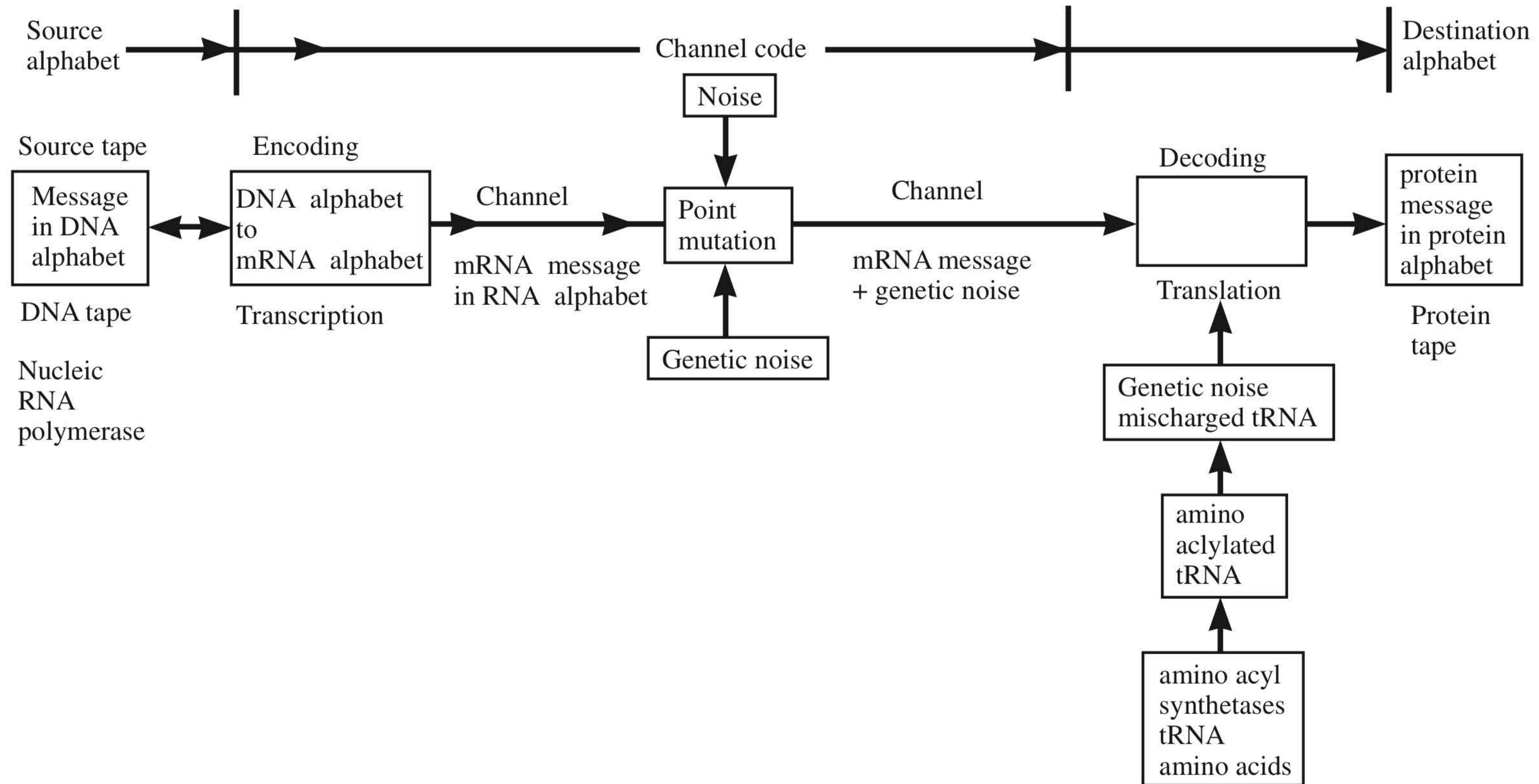


Information theory, evolution, and the origin of life

HUBERT P. YOCKEY

 **CAMBRIDGE**
UNIVERSITY PRESS

Yockey's DNA Communication System



The Genetic Alphabet



Four Nucleotide Letters: A, C, G, T

Why are there 4 letters in the
genetic alphabet?



PERSPECTIVES

OPINION

Why are there four letters in the genetic alphabet?

Eörs Szathmáry

We list, without thinking, the four base types that make up DNA as adenine, guanine, cytosine and thymine. But why are there four? This question is now all the more relevant as organic chemists have synthesized new base pairs that can be

creating alternative genetic alphabets and, at the same time, explaining why we have the four-letter alphabet.

Prompted by Benner's work, further investigation into our genetic alphabet has come mainly from synthesizing new base pairs; these

new ones. Alternatives to the phosphodiester backbone are not the subject of this article and have been addressed elsewhere (see REF. 5 for discussion).

Lessons from our genetic alphabet

Studies of the present genetic alphabet and of the contemporary DNA replication machinery highlight certain constraints that any alternative/extended genetic alphabet is expected to be subject to. These should guide us when attempting to synthesize new base pairs; conversely, the successful addition of new base pairs to the alphabet can sharpen our understanding of these constraints. There are four main constraints on the successful incorporation of a new base pair^{6–8}: chemical

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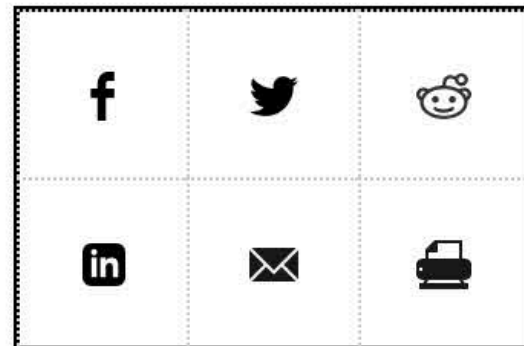
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4 New DNA Letters Double Life's Alphabet

Synthetic DNA seems to behave like the natural variety, suggesting a broader swathe of chemicals could support life than the four that evolved on Earth

By Matthew Warren, Nature magazine on February 22, 2019



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"Alien" DNA Makes Proteins in Living Cells for The First Time

November 30, 2017 — Ewen Callaway

THE SCIENCES

First Life with "Alien" DNA Created in Lab

May 7, 2014 — Ewen Callaway and Nature magazine

BIOLOGY

Mirror-Image Enzyme Copies Looking-Glass DNA

May 17, 2016 — Mark Peplow and Nature magazine



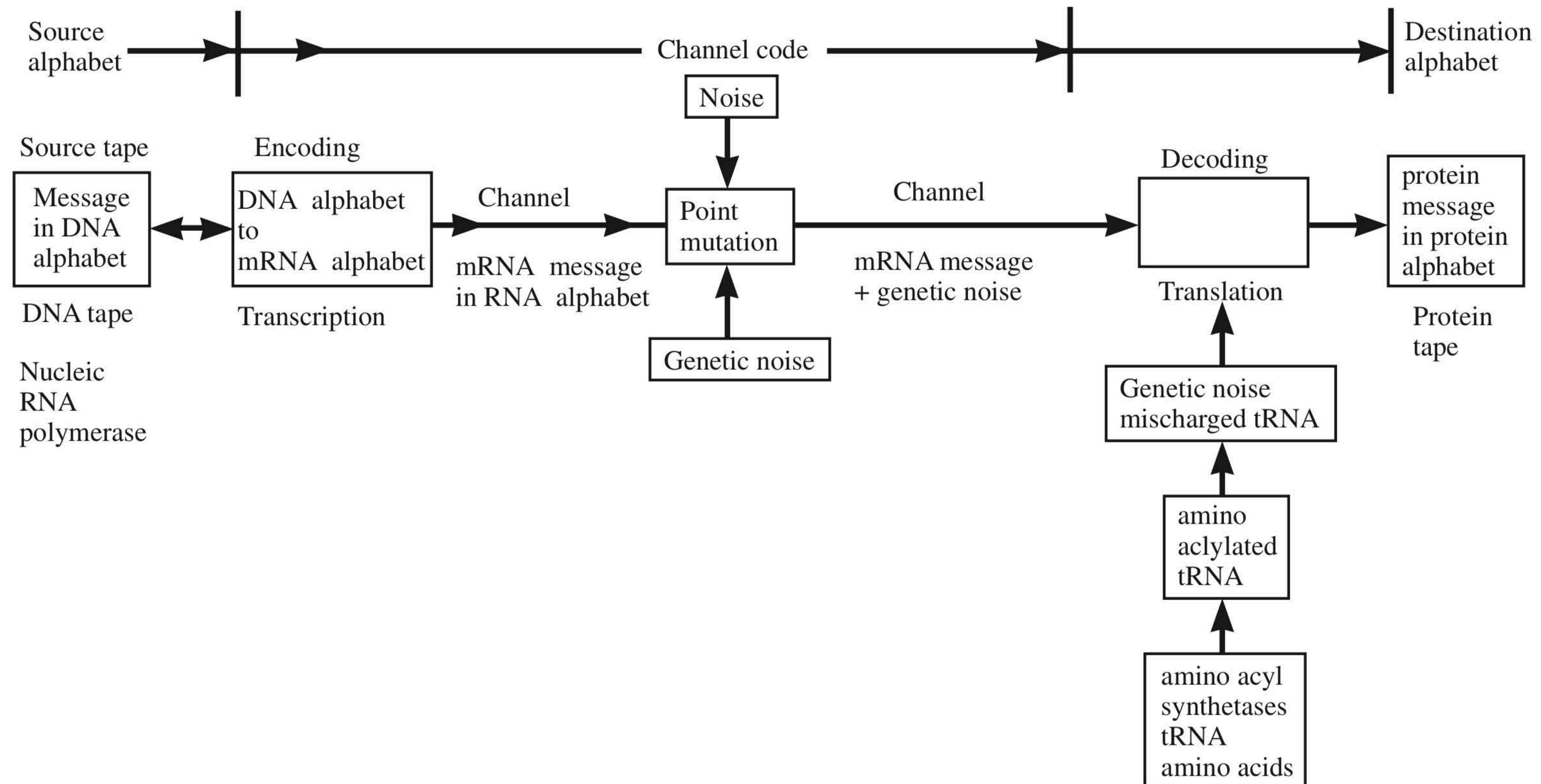
Old Letters: A, C, G, T
New Letters: S, B, P, Z

IMPLICATIONS OF THE GENETIC ALPHABET

- **Not Restricted by Physical Necessity:** The four-letter alphabet “A, C, G, T” is not restricted by physical necessity—larger alphabets like the eight-letter alphabet “A, C, G, T, S, B, P, Z” are also possible.
- **Optimal Size:** Mathematical studies have shown that the four-letter alphabet “A, C, G, T” is optimal.
- **No Evidence of Evolution:** We have no evidence that other genetic alphabets existed in nature, and there is no feasible pathway for a genetic alphabet to evolve.
- **Intelligent Design Choice:** The four-letter alphabet points clearly to Intelligent Design choice.



The DNA Communication System



Standard genetic code

1st base	2nd base								3rd base
	U		C		A		G		
U	UUU	(Phe/F) Phenylalanine	UCU	(Ser/S) Serine	UAU	(Tyr/Y) Tyrosine	UGU	(Cys/C) Cysteine	U
	UUC		UCC		UAC		UGC		C
	UUA		UCA		UAA	Stop (Ochre) ^[B]	UGA	Stop (Opal) ^[B]	A
	UUG ^[A]		UCG		UAG	Stop (Amber) ^[B]	UGG	(Trp/W) Tryptophan	G
C	CUU	(Leu/L) Leucine	CCU	(Pro/P) Proline	CAU	(His/H) Histidine	CGU	(Arg/R) Arginine	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	(Gln/Q) Glutamine	CGA		A
	CUG ^[A]		CCG		CAG		CGG		G
A	AUU	(Ile/I) Isoleucine	ACU	(Thr/T) Threonine	AAU	(Asn/N) Asparagine	AGU	(Ser/S) Serine	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	(Lys/K) Lysine	AGA	(Arg/R) Arginine	A
	AUG ^[A]	(Met/M) Methionine	ACG		AAG		AGG		G
G	GUU	(Val/V) Valine	GCU	(Ala/A) Alanine	GAU	(Asp/D) Aspartic acid	GGU	(Gly/G) Glycine	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	(Glu/E) Glutamic acid	GGA		A
	GUG		GCG		GAG		GGG		G

Where did the genetic code
come from?



Critical Review

Origin and Evolution of the Genetic Code: The Universal Enigma

Eugene V. Koonin and Artem S. Novozhilov

*National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health,
Bethesda, MD, USA*

Summary

The genetic code is nearly universal, and the arrangement of the codons in the standard codon table is highly nonrandom. The three main concepts on the origin and evolution of the code are the stereochemical theory, according to which codon assignments are dictated by physicochemical affinity between amino acids and the cognate codons (anticodons); the coevolution theory, which posits that the code structure coevolved with amino acid biosynthesis pathways; and the error minimization theory under which selection to minimize the adverse effect of point mutations and translation errors was the principal factor

INTRODUCTION

Shortly after the genetic code of *Escherichia coli* was deciphered (1), it was recognized that this particular mapping of 64 codons to 20 amino acids and two punctuation marks (start and stop signals) is shared, with relatively minor modifications, by all known life forms on earth (2, 3). Even a perfunctory inspection of the standard genetic code table (Fig. 1) shows that the arrangement of amino acid assignments is manifestly nonrandom (5–8). Generally, related codons (*i.e.*, the codons that differ by only one nucleotide) tend to code for either the same or two related amino acids, *i.e.*, amino acids that are

The background is a light blue gradient with a complex network of thin, dark blue lines connecting various points. These points are represented by small numbers (0-9) in different colors (blue, green, red, grey). The network is denser on the left side, where it forms a vertical column of numbers, and becomes more sparse towards the right.

“

Despite extensive and, in many cases, elaborate attempts to model code optimization, ingenious theorizing along the lines of the coevolution theory, and considerable experimentation, very little definitive progress, has been made.

-Eugene Koonin & Artem Novozhilov



“

if what we see operating in cells is not *like* a code, but genuinely *is* a code—then we should seek its explanation in the only cause “true and sufficient” to such effects: intelligence.

-Stephen Myer & Paul Nelson



Two proofreading steps amplify the accuracy of genetic code translation

Ka-Weng leong^a, Ülkü Uzun^{a,1}, Maria Selmer^a, and Måns Ehrenberg^{a,2}

^aDepartment of Cell and Molecular Biology, Uppsala University, Uppsala 75124, Sweden

Edited by Ada Yonath, Weizmann Institute of Science, Rehovot, Israel, and approved October 12, 2016 (received for review July 4, 2016)

Aminoacyl-tRNAs (aa-tRNAs) are selected by the messenger RNA programmed ribosome in ternary complex with elongation factor Tu (EF-Tu) and GTP and then, again, in a proofreading step after GTP hydrolysis on EF-Tu. We use tRNA mutants with different affinities for EF-Tu to demonstrate that proofreading of aa-tRNAs occurs in two consecutive steps. First, aa-tRNAs in ternary complex with EF-Tu·GDP are selected in a step where the accuracy increases linearly with increasing aa-tRNA affinity to EF-Tu. Then, following dissociation of EF-Tu·GDP from the ribosome, the accuracy is further increased in a second and apparently EF-Tu-independent step. Our findings identify the molecular basis of proofreading in bacteria, highlight the pivotal role of EF-Tu for fast and accurate protein synthesis, and illustrate the importance of multistep substrate selection in intracellular processing of genetic information.

ribosome | error correction | fidelity | EF-Tu | ternary complex

We have found that the bacterial ribosome uses two proof-

kinetic efficiency to substrate-selective, enzyme-catalyzed reactions than single-step proofreading (5, 14, 15), it has been taken for granted that there is but a single proofreading step in tRNA selection by the translating ribosome (16). Here, we present data showing that the proofreading factor (F), by which the accuracy (A) is amplified from its initial selection value (I) by aa-tRNA in ternary complex with EF-Tu and GTP, increases linearly with increasing association equilibrium constant, K_A , for aa-tRNA binding to EF-Tu. We suggest the cause of this linear increase to be the activity of a first proofreading step, in which aa-tRNA is discarded in complex with EF-Tu and GDP whereas the forward reaction is release of EF-Tu·GDP. In the limit of zero affinity between aa-tRNA and EF-Tu, where the first proofreading step is expected to be completely turned off, we observe a remaining accuracy amplification by proofreading. This amplification, we suggest, comes from the activity of a second proofreading step, involving aa-tRNA only (Fig. 1). We use the present results to discuss the molecular basis for proofreading of aminoacyl-tRNAs, which, until now, has remained obscure (17). We suggest that multistep proofreading in genetic

Proof-reading tRNA

“

We have found that the bacterial ribosome uses two proof-reading steps following initial selection of transfer RNAs (tRNAs) to maintain high accuracy of translation of the genetic code.

*-Ka-Weng Yeong, Ülkü Uzuna,
Maria Selmera, and
Måns Ehrenberg*



Proof-reading tRNA

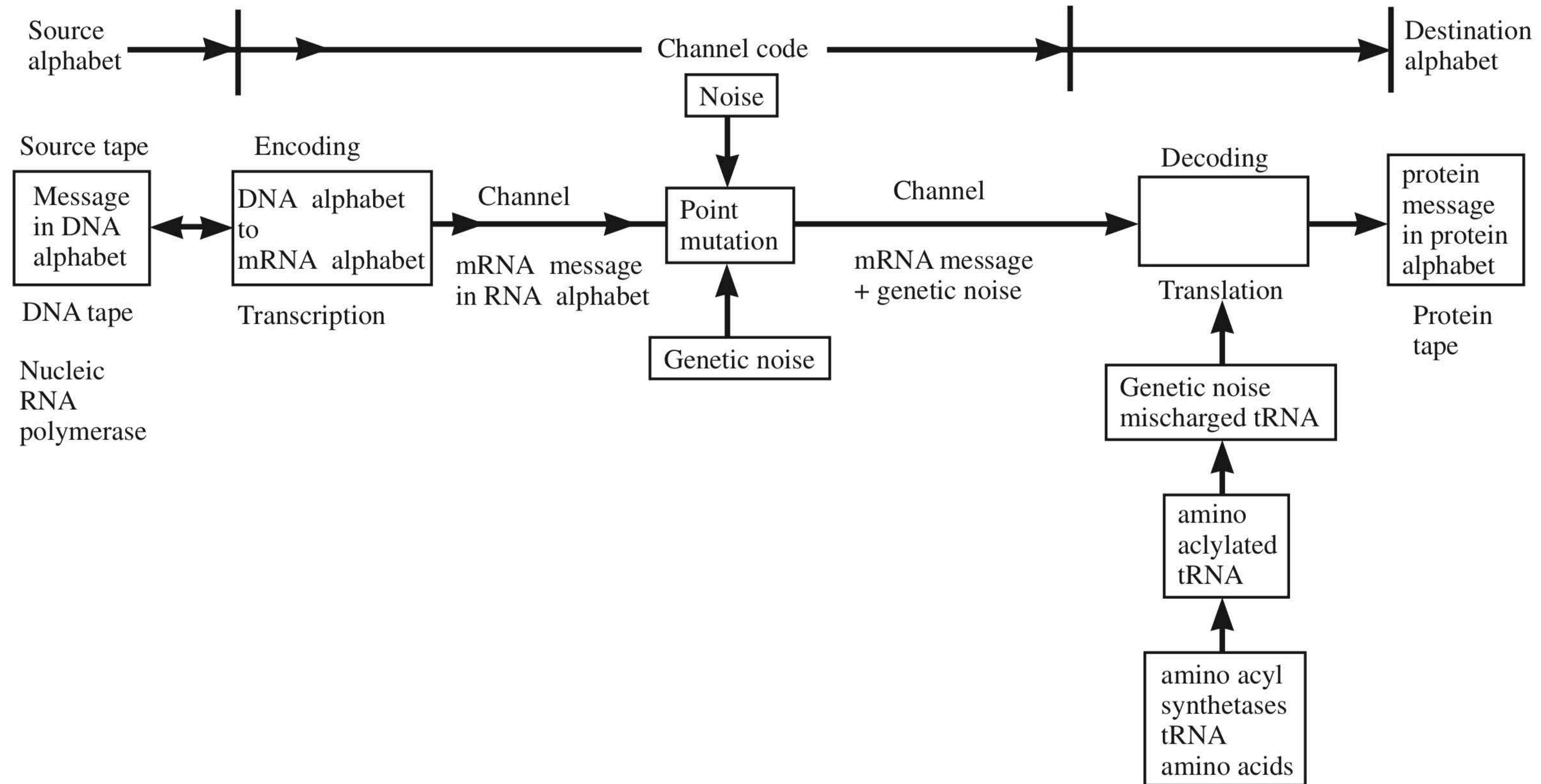
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The existence of two distinct proofreading steps may appear surprising, because the accuracy of initial codon selection by ternary complex normally is remarkably high.

*-Ka-Weng Jeonga, Ülkü Uzuna,
Maria Selmera, and
Måns Ehrenberg*



The DNA Communication System





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Thus, the process of the origin of life is possible but unknowable.

-Hubert Yockey

EVIDENCE FOR THEISTIC EVOLUTION

Is the universal genetic alphabet and the virtually universal genetic code evidence for theistic evolution?

➤ No—because the genetic information system demonstrates evidence of Intelligent Design choice:

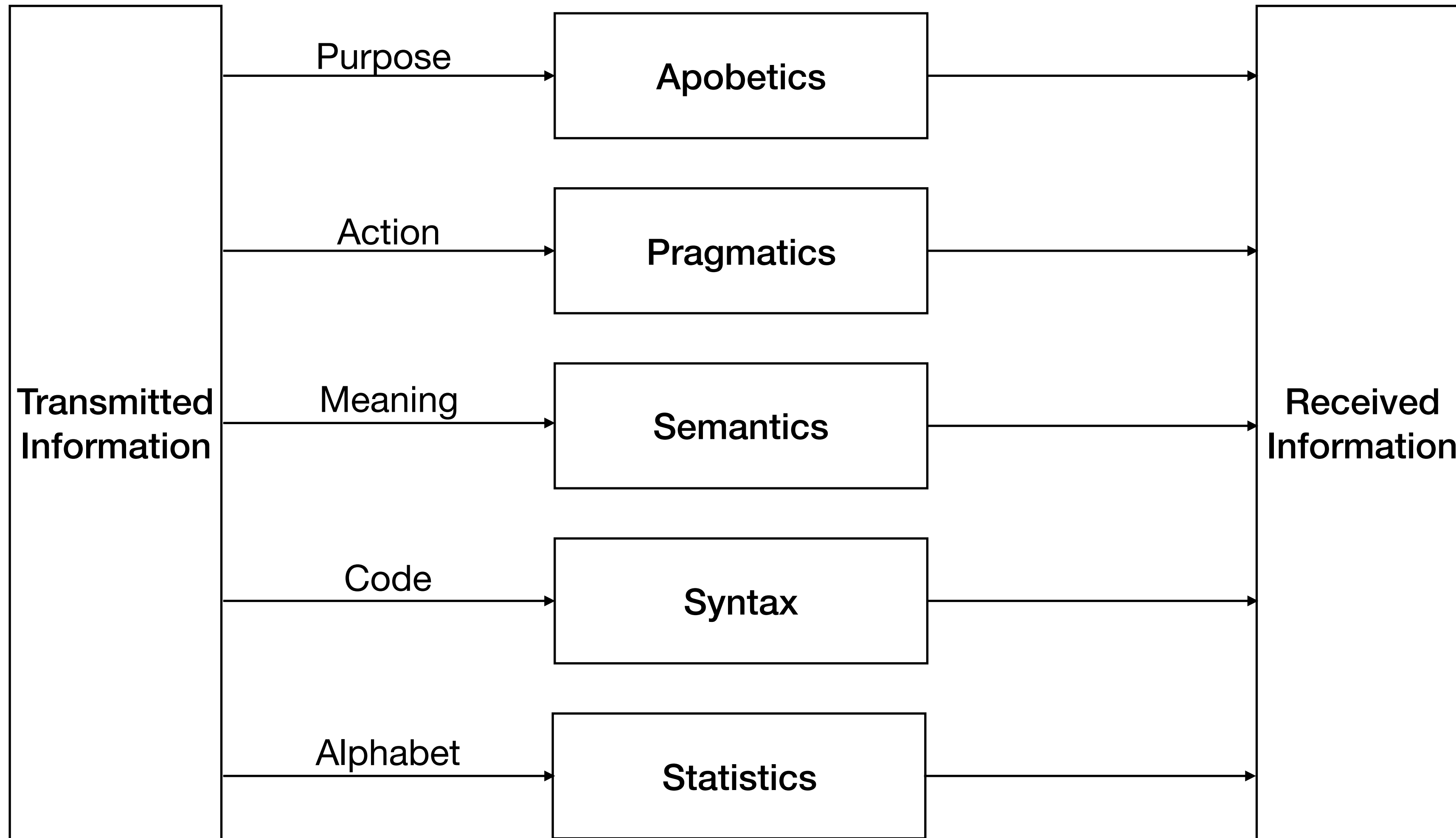
1. Number of nucleotide letters: 4
2. Number of nucleotide letters in codons: 3
3. Number of amino acids: 20
4. Type of amino acids: Left-handed isomers

➤ Therefore, this opens up the genuine possibility for Intelligent Design choice in other areas:

1. Creation of new genetically similar animal kinds *ex nihilo*.
2. Time frame of Creation, for example over six literal days.



Gitt's Information System Model



“

The problem of the origin-of-life is clearly basically equivalent to the problem of the origin of biological information.

-Bernd-Olaf Küppers

Information and the Origin of Life

(Cambridge, MA: MIT Press, 1990), 170-172.





“

The laws of nature can transmit but not generate information.

Invoking chance as an attempt to explain the origin of information fails as well.

Intelligent design provides the best explanation for the information necessary to produce the first living cell.

-Stephen Myer

“The Difference It Doesn’t Make: Why the ‘Front-End Loaded’ Concept of Design Fails to Explain the Origin of Biological Information”

Theistic Evolution: A Scientific, Philosophical, and Theological Critique

(Wheaton, IL: Crossway, 2017), 226,234,235.

Genetic Information System: Evidence of Intelligent Design

