Mechanism of Evolution Shared by Gene and Language

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We propose a general mechanism for evolution to explain the diversity of gene and language. To quantify their common features and reveal the hidden structures, several statistical properties and patterns are examined based on a new method called the rank-rank analysis. We find that the classical correspondence, “domain plays the role of word in gene language”, is not rigorous, and propose to replace domain by protein. In addition, we devise a new evolution unit, syllgram, to include the characteristics of spoken and written language. Based on the correspondence between (protein, domain) and (word, syllgram), we discover that both gene and language shared a common scaling structure and features of self-organization. Like the Rosetta stone, this work may help decipher the secret behind non-coding DNA and unknown languages.

Diversity is fundamental to survival, which means continue to live or exist in space-time. Because there are countless kinds of environment that require different functionalities, diversity is crucial to survive. This development from homogeneity to diversity is ingrained in evolution. It is not just a concept in biology, but can be generalized to many other fields. From the perspective of physics, the word “existence” can be interpreted as something that is measurable. Equation of motion is dictated by the Lagrangian. Once the latter is changed, the state of system has to evolve.

Among the topics of evolution, we are particularly interested in genes and natural languages. The fact that 20 kinds of codon, composed by three nucleotides in the set \{A, T, C, G\}, encode genome sequence is similar to the human written text constituted by dozens of letters that form the alphabet. In the other word, they are arranged with discrete and unblendable units[1]. Therefore, it is intuitive to make an analogy between gene and language. When choosing the “space-time” of organism as nature and that of human as society, their inheritance of survival can be recorded in gene and language, respectively. This is an important feature of evolution: inheritable.

The correspondence between gene and language may be the Rosetta Stone to decipher the language of gene[2–4]. Scientists have applied linguistic formalisms to this goal, such as (a) finding out the Chomsky hierarchy and formal language of RNA may help us understand the formation of secondary structure[3], (b) using Zipf’s and Shannon’s approach to quantify the linguistic features of non-coding DNA sequences[5], and (c) exploring information hidden in genome with the aid of natural language processing (NLP)[6, 7]. On the other hand, linguists have also (a) investigated the relationship between language and the natural selection[8], (b) discussed the language faculty in the broad and narrow sense from the viewpoint of biolinguistics[1, 9–11], (c) discovered that languages also exhibit the signature of both gradual[8] and punctuational evolution[12], etc.

In eyes of these similarities, it is tempting to ask whether it is possible to quantify these features and establish a mechanism of evolution shared by gene and language. To achieve this, we need to determine their correspondence[2, 4]. In the following, we will focus on languages that exhibit the spoken form, and then try to generalize to other forms, such as written and gestural. The first correspondence is the fact that both gene and language are formed by a set of finite “elements” whose number, i.e., cardinality, is about two orders of magnitude. The reason why we care about its magnitude is that it will greatly affect the possible combinations of elements. Gene is encoded by 20 kinds of codon, while in language the total phonemic inventory varies from as few as 11 to 141[13]. For languages that have endured the test of time and are learned and spoken internationally, i.e., world languages, such as English and Chinese, the size of their phonemic inventories are indeed two orders of magnitude.

We should be careful that the nucleotides do not correspond to alphabets for two reasons: (1) Alphabet is not the elementary set for all written systems, it is solely for phonogram. Thus the generality of alphabets in language is not like that of nucleotides in gene. (2) Most languages have spoken form, but many of them do not have written form. Therefore, when deciding the basic elements of languages, we should consider the properties of spoken form. To extend this concept to writing systems, we can use phonetic transcriptions to find out their phonemic inventories. Note that grapheme is not a valid unit to establish the correspondence due to the large difference in its order of magnitude. For example, there are more than 40000 kinds of character[14] in Chinese, while their pronunciation can be composed of Zhuyin[15], whose cardinality is only 37.

Although the cardinality of “elementary set”, whose order is only two, obviously limits its functionalities of survival, the number of combinations of element is huge. In biology, we know gene can be expressed in
the pronunciation of writing system. Therefore, a syl-
sintroduced phonetic transcriptions as a means to decide
if the language has a corresponding writing system
may be syllable\[25\], which can only be defined in spoken
this subunit. The first candidate that comes to our mind
consider the properties of spoken form in the search for
subunit of word. As was delineated before, we should
between domain and protein, we do not yet know the
spondence on closer scrutiny. Why? Unlike the relation
obey PL, it is in fact not sufficient to suggest their corre-

FIG. 1: The dotted/crossed (red/blue) curves in the log-log
plots of (a, b) show FRD of word/syllable (character) in Chi-
nese novels, Demi-Gods and Semi-Devils and Frog. Similarly,
(c, d) are for word/syllable in English novels, Moby-Dick and
The Hobbit. The fitting function is for the red points.

various proteins, while the latter are composed of do-
 mains which are regarded as the evolutionary unit of proteins\[4, 16, 17\]. To what unit in linguistics will do-
main correspond then? Many researchers believed that it is the “word of gene”\[3, 18, 19\] by examining its
frequency-rank distribution (FRD) that is a good fit to
Zipf’s law\[20–22\] $f(x) \propto 1/x^z$, where $z \approx 1$. In general, $f(x)$ is called power law (PL) where $z$ is arbitrary.
However, doman should not be considered as “word” rigor-
ously, based on the following procedures in statistics\[23\]
and semantic complexity\[4\]: (1) Zipf-Mandelbrot law\[24\] $f(x, a) \propto 1/(x + a)^z$ will be a better fit than PL, accord-
ing to the Akaike information criterion\[23\] (AIC) which
provides a means for model selection. When comparing
several statistical models, the one with a lower AIC im-
plies a lower information loss. Our tests for domain are
listed in Tab. III. (2) We discover that PL will be more
suitable for protein than for domain, which is clear from
Fig. 1. (3) If domain plays the role of word, then protein
must be the sentence or merely a string of words\[18, 19\]. Unlike a sentence is rarely repeated in linguistics, a pro-
tein in protein sequence translated from DNA usually
must be the sentence or merely a string of words\[18, 19\].

Having argued that it is not suitable to treat domain
as word, we are yet to establish its corresponding role
in language. Although FRD of protein and word all
obey PL, it is in fact not sufficient to suggest their corre-
spondence on closer scrutiny. Why? Unlike the relation
between domain and protein, we do not yet know the
subunit of word. As was delineated before, we should
consider the properties of spoken form in the search for
this subunit. The first candidate that comes to our mind
may be syllable\[25\], which can only be defined in spoken
form if the language has a corresponding writing system
(ask Prof. Su). What about written form? We have
introduced phonetic transcriptions as a means to decide
the pronunciation of writing system. Therefore, a syl-
lable can be written down as a combination of several
graphemes. We should notice that one syllable may be
expressed by different forms, such as the Chinese char-
acters “敢” (dare) and “趕” (hurry) both of which have
the same pronunciation [gˇ an] but with different meaning
and form when written down. This important property
inspires us to define a new linguistic unit, syllgram, that
can share the properties of writing and speaking. A syl-
gram is defined as the unit in written form represents
the corresponding syllable from a word (ask Prof. Su).
What is the major advantage to introduce this new unit?
Many written texts have been digitalised by character
encodings, e.g. unicode and UTF-8, that make the sta-
tistical analysis much more convenient. But when dealing
with speaking data, different people have distinct shapes
of sound pulses. The adopted techniques and standards
vary with different labs. As a result, introducing syllgram
helps cut down the cost.

Whether the relation between protein and domain is
similar with that between word and syllgram? How to
demonstrate the fact that protein/word is composed of
domain/syllgram? In the next section, we will introduce
a new tool, rank-rank analysis, to quantify this relation.

Rank-Rank Analysis and Scaling Structure

Having known that (1) the FRD of syllgram in Fig.
1 is similar to that of domain, i.e., Zipf-Mandelbrot dis-
tribution and (2) both protein and word follow PL, how
do we combine these two facts to gain additional insight
into the correspondence between gene and language?
By coincidence, we discover the key lies in construct-
ing the rank-rank distribution\[26\] (RRD). For gene, let
$(x, y) = (\text{rank of protein, rank of domain})$; while for
language, $(x, y) = (\text{rank of word, rank of syllgram})$, where
the ranks depend on FRD. Figure 2 exhibits the RRD in
(a) genome of human, (b, c) Chinese and English novels,
while (d, e) exemplify the process of plotting RRD. How
we performed the segmentation in gene-language\[27\] and
natural language is an important technical detail: (a)
InterPro\[7\] is used to classify protein and domain from
Ensembl\[28\], (b) CKIP word segmentation system\[29\] is
employed for Chinese texts where the syllgram is equal
to character, and (c) syllabify\[30\] is implemented to syl-
labify words from English texts. We emphasize that clas-
sifying (unit, sub-unit) relation is a prerequisite to doing
rank-rank analysis.

By comparing the RRD plots in Fig. 2 for human
gene and novels in Chinese and English, it is hard to
miss the interesting layer structure that emerges in these
seemingly irrelevant samples. By analyzing the envelopes
that comprise this structure, labelled as $f_n$, where $n$
denotes the $n$-th curve, we discover that they obey a scaling
relation:

$$r_f \equiv f_{n+1}(x)/f_n(x)$$ (1)

is a constant of $n$ and $x$, which is verified\[27\] in Fig. 7.
After inspecting over ten different animals, thirty Chinese corpora, and thirty English corpora[31], we conjecture that this scaling structure (SS) is general to genes and languages. The imminent question then is what causes this universal phenomenon. We were puzzled for a long time[27] why SS is robust against shuffling words and altering texts with different styles of writing, and why it seems to be shared by different languages. After countless trials and errors, we found the key is to include the hidden properties shared by gene and language. To avoid duplication we shall focus on the former. If a syllgram only appears in one word, it will be represented by just one point. In contrast, if it appears in multiple words, several points will share the same rank $y$. This implies that $$\rho_y(\vec{r}) = \sum_{\vec{r} \in D_y(\vec{R})} \lambda(\vec{r}) \rho_x(\vec{r})$$ (2)

for data point $\vec{R} = (R_x, R_y)$ where $D_y(\vec{R}) = \{\vec{r} = (r_x, r_y) \mid r_y = R_y\}$ indicates the words composed of the syllgram with rank $R_y$, and $\lambda(\vec{r})$ denotes how many times the syllgram $r_y$ appears in word $r_x$, e.g., $\lambda((AA, A)) = 2$. This equation can be shorthanded as $\rho_y = \sum \lambda \rho_x$ and lead to an inequality $\rho_x \leq \rho_y$.

Let’s now focus on $f_1$ which is unique because there is no fog in its neighborhood. We notice that the points on $f_1$ are all in the blocks $\{1, 1\}, \{2, 2\}, ..., $ which imply $\rho_x = \rho_y$ and enforce that the syllgram in block $\{m, m\}$ contains only one point. This explains the lack of fog in the right region of $f_1$. Should there be any point in the block $\{m, \ell\}$ where $m > \ell$, it would imply $\rho_x > \rho_y$ which contradicts $\rho_x \leq \rho_y$. This argument therefore rules out fog in the left region of $f_1$. What are those (protein, domain) and (word, syllgram) that locate at $f_1$? They usually refer to special domains/syllgrams that appear in equally special proteins/words. For instance[31], (a) HHH domain 9 (IPR041692) just exists in SPUT6H protein (ENSGALT00000000200) for chicken genome (GRCg6a), (b) fio only shows up in Ba-ruf-fio in Harry Potter 1, and (c) 胺 (amine) is unique in 三聚氰胺 (Melamine) in蛙 (Frog).

The second feature is actually from the stipulation of plotting RRD: when two words or syllgrams share the same frequency, the one that appears earlier in the text will get a smaller rank. That means the data points must stack from the left bottom corner of each block. If there is a new syllgram added in the same block, which simultaneously implies a new word, it will be placed in the upper panels (c, d).

FIG. 2: Panels (a, b) are the RRD plot for Frog and Moby-Dick. Their construction is demonstrated schematically in panels (c, d).
right of old points and become a part of \( f_n \). This answers why \( V_m, H_\ell \), and \( f_n \) must cross at one point. Note that no matter whether a syllgram is used in words with the same or another different \( \rho_x \), its points will appear on the right of the earliest or frequent one. Associate this characteristic with the second feature, we conclude that the points in a block will be only located at \( f_n \) or its right. This is what the third feature described.

So far, we have explained the source of main features of RRD for gene and language. However, the composition of fog and why \( f_n \) follows scaling relation are still unclear. To answer these questions, the concept of “number partition” will come in handy. The partitions of \( N \) represent all possible combinations for syllgram with \( \rho_y = N \) to distribute over different words. For example, \( N = 3 \) consists of three partitions \((1,1,1), (2,1), \text{and (3)}\). If \( \lambda = 1 \), the partition \((2,1)\) refers to a syllgram with \( \rho_y = 3 \) that appears in two different words with \( \rho_x = 2 \) and 1, respectively.

In fact, Eq. (2) shows the partition of syllgram with rank \( y \). For \( D_y = \{\bar{r}_1, ..., \bar{r}_k\} \) with \( \rho_x(\bar{r}_1) \geq ... \geq \rho_x(\bar{r}_k) \), it implies \( r_{1x} \leq ... \leq r_{kx} \). Based on the second feature, the point \( \bar{r}_i \) will definitely be a part of \( f_n \). According to Fig. 2, it is not hard to discover that \( f_n \) in blocks \( \{m, \ell\} \) will follow the simple relation:

\[
n = \ell - m + 1
\]

that leads to \( n = \rho_y(\bar{R}) - \rho_x(\bar{r}) + 1 \) when \( \ell, m \) are small enough[32]. Other \( \bar{r}_i \) will mostly be in the fog, i.e., join the fog in blocks \( \{\rho_x(\bar{r})\}, \rho_y(\bar{R}) \), or at \( f_n \) by chance. We soon realize that the formation of SS requires a huge number of different partitions, which can be used to fill the scaling lines and fog. Otherwise, the SS will be plagued by many vacancies[31] and become discernable. For instance, if the syllgrams with \( \rho_y = 3 \) only have one kind of partition (3), they will not contribute to the fog in \{1,3\} and \{2,3\} blocks. So if the number of syllgrams that own few kinds of partitions is high, the fog will be diluted.

Based on the partition theory, we discover two hidden properties that can be defined as

\[
\text{Allo}(\bar{R}) \equiv |D_y(\bar{R})|
\]

and

\[
\text{Link}(\bar{R}) \equiv \sum_{\bar{r}_i \in D_x(\bar{R})} \text{Allo}(\bar{r}_i)
\]

for \( \bar{R} = (R_x, R_y) \) where \( |D_y| \) denotes the cardinality of \( D_y \), which is defined in Eq. (2), and \( D_x(\bar{R}) \equiv \{\bar{r} = (r_x, r_y) \mid r_x = R_x\} \) indicates the syllgrams are used in the word with rank \( R_x \). If we project \( \text{Allo}(\bar{R}) \) and \( \text{Link}(\bar{R}) \) to \( y- \) and \( x- \) axis, they will become \( \text{Allo}_y(R_y) \) and \( \text{Link}_x(R_x) \), respectively. The allocation function \( \text{Allo}_y(R_y) \) represents the ability of allocating a syllgram \( R_y \) to other words, while the link function \( \text{Link}_x(R_x) \) indicates how a word \( R_x \) links to other words. For examples, (a) if syllgram A appears in words AB, AC, and KAD, then \( \text{Allo}_y(A) = 3 \); (b) if syllgram H appears only in either H or HH, then \( \text{Allo}_y(H) = 1 \); (c) if syllable T appears in both T and TT, then \( \text{Allo}_y(T) = 2 \); (d) \( \text{Link}_x(ABC) = \text{Allo}_y(A) + \text{Allo}_y(B) + \text{Allo}_y(C) \); and (e) \( \text{Link}_x(AA) = \text{Allo}_y(A) \).

By fitting real data for gene and language in Fig. 8, we observe that they both satisfy two simple empirical relations:

\[
\text{Allo}_y(R_y') = (-\alpha \ln R_y' + \beta)^2
\]

and

\[
\text{Link}_x(R_x') = -\gamma \ln R_x' + \omega
\]

where \( R_y' = (R_x', R_y') \) is the new rank-rank vector depending on \( (\text{Link}_x, \text{Allo}_y) \) instead of \( (\rho_x, \rho_y) \), and \( \alpha, \beta, \gamma, \omega \) are constants[34].

Now, we have introduced several quantitative features shared by gene and language, and used them to build up the preliminary correspondence between the latter. However, there are still some core questions that can not be answered by the partition theory: (a) It is limited to \( \lambda = 1 \) in Eq. (2) to explain the formation of \( f_n \) and fog. (b) What is the mechanism to decide the distributions of set \( D_x \) and \( D_y \)? (c) Both Eq. (2) and partition theory can neither explain the origin of Eqs. (6, 7) and scaling relation in Eq. (1), nor generate them automatically by any given mechanism. In other words, although phenomenologically argued from simple facts, such as words comprise of syllgrams and proteins consist of domains, the partition theory is useful for understanding the formation of SS.

Network for Protein/Word Formation Process

Network is a good tool to describe dynamic process[36–38]. Inspired by Eqs. (2, 4, 5), we realize that \( D_x \) and \( D_y \) can be used to construct a multilayer network[35] \( \mathcal{M} = (G, C) \) where \( G \) is a family of graphs and \( C \) is the set of interlayer connections. \( G \) contains two layers, word \( G_w = (V_w, E_w) \) and syllgram \( G_s = (V_s, E_s) \). As long as two words/syllgrams appear in the same \( D_y/D_x \), there is an edge \( e^w/e^s \) between them. For example, (a) when two words AC and BC share the same syllgram C for layer \( G_w \), we connect them with edge \( e^w = (AC, BC) \); (b) when two syllgram A and C appear in the same word contains A and C for layer \( G_s \), such as AC, they are connected by edge \( e^s = (A, C) \).

There are three topological properties that characterize the network: degree distribution \( P(k_\alpha) \), clustering coefficients[39] \( C_\alpha \), and the shortest path length \( L_\alpha \), where \( \alpha = w \) for protein/word and \( s \) for domain/syllgram. The degree distribution \( P(k_\alpha) \) denotes the number of vertices exhibiting \( k_\alpha \) edges. One of our results is shown in Fig. 3. A lot of isolated vertices constitute single-domain proteins. We have checked that the features in Fig. 3 are shared by other organisms and
texts[31]. The scale-free behavior we discovered for $G_s$ not only agrees with previous research on genes[38], but also exists in languages[31]. This proves that the use of domains/syllgrams to synthesize proteins/words is crucial to self-organization[40].

With the aid of rank-rank analysis and network, we have found many quantitative features shared by gene and language: (a) frequency-rank distribution of protein/word follows Zipf’s law, (b) rank-rank distribution obeys the scaling structure, (c) allocation and link function can be simply expressed as Eqs. (6, 7), (d) network of domain/syllgram is scale-free, and (e) clustering coefficient for the network of protein/word is high. These facts suggest there exists a strong correspondence between gene and language, as described in Tab. 1.

The next step is to build a mechanism that has the above features. Proteins provide the functionalities of survival in nature for an organism, while signals provides the communication functionalities of survival in society for an organism, i.e., faculty of language in broad sense[1]. Let us talk about language first. A key difference that human can develop language is because the nonhuman repertoires of signals are generally small[41]. The richness of phonetic inventory allows humanity create words. But how humanity constructs words and make it different from the communication unit of other animals? The components of word should reflect certain logical connections among the contents that a word refers to. If two contents are similar, words that looks alike may be used to describe them. It means similar or identical syllgrams would be used to form words describing strongly connected contents. Moreover, different syllgrams in the same word have distinct roles. Since the temporal order is critical in vocal communication, i.e. constrained by phonotactics, syllgrams at different sites within a word have distinct functions. Therefore, in a word, human may use different logical connections for the first syllgram, second syllgram, etc., as shown in Fig. 4. The logical connection between the objects may be different for the first syllgram and second syllgram. We model these connections with weighted networks which the contents are the nodes and the link represent the logical connection between different contents. Link with higher weight means higher connection between the two contents it connects.

Let $C(k)$ be the connection of contents on the $k^{th}$ syllgram. For example, when we create a new word to refer to certain content, we should choose the first syllgram according to $C(1)$, second syllgram according to $C(2)$, respectively. For new contents, like a new object or phenomenon, it’s possible for new syllgrams to be created and used to form word for that content. Therefore, we define an effective connection $z$ for new syllgram to be created. The probability of creating a new syllgram to be the $k^{th}$ syllgram of a word assigned to $j^{th}$ content is:

$$P(k)_{\text{new},j} = \frac{z}{z + \sum_i C_{ij}^{(k)}}.$$ (8)

For most of the time we should be able to recombine existing syllgrams to form new word for a new content. The $k^{th}$ syllgram of an existing word should have some probability to become the $k^{th}$ syllgram of the new word. Probability for syllgrams in word assigned to the $i^{th}$ content to become syllgrams in word assigned to the $j^{th}$ content is:
TABLE I: Hierarchy for gene-language correspondence is supported by qualitative or quantitative features. Since phoneme only exists in spoken form, to find out the elements in written form we should use phonetic transcriptions to obtain its pronunciation.

| Hierarchy | Organism | Human | Features |
|-----------|----------|-------|----------|
| Space-time| nature   | society | survival in space-time |
| Inheritance| gene     | language | arranged hierarchically |
| Elements  | codon    | phoneme | cardinality is two orders of magnitude |
| Sub-unit  | domain   | syllgram | $\rho$, Eqs. (1, 2, 6), $P(k_s)$, and $C_s$ |
| Unit      | protein  | word    | $\rho$, Eqs. (1, 2, 7), $P(k_w)$, and $C_w$ |

\[
P^{(k)}_{i,j} = \frac{C_{ij}^{(k)}}{z + \sum_i C_{ij}^{(k)}}
\]

where $P^{(k)}_{\text{new},j} + P^{(k)}_{i,j} = 1$. If the word assigned to $i^{th}$ content does not have $k^{th}$ syllgram, then $P^{(k)} = 0$. Note that in general, the order of syllgram in a word may not be equal to $k$ directly. Like the second syllgram in “rolling” and the third syllgram in “juggling” should have the same function, i.e., same $k$, despite the difference in their order.

Since two contents may be so similar that we use identical word to describe them, an old word that already exist may be assigned to a content that haven’t been assigned a word yet. The probability to assign $i^{th}$ content’s word to $i^{th}$ content is:

\[
P_{ij}^w = \frac{C_{ij}}{\sum_i C_{ij}}
\]

where $C_{ij} = \sum_k C_{ij}^{(k)}$.

In our model, we will keep adding new content and link it to existing contents with $C^{(k)}$. We assume they are random with weight $0 < C_{ij}^{(k)} < 1$ distributed universally in probability. The first content was assigned with a bi-syllgram word which the first and second syllgram are distinct. Next and following contents were then assigned an old word and new word randomly with probability distribution $P_{ij}^w$ and $P_{ij}^{(k)}$. For the new word, we first decide the number of syllgrams in it with some probability set manually. Each syllgram in it will then be chose by $P_{ij}^{(k)}$.

We assume the order of syllgram in a word is equal to $k$. And then use principle of least effort\cite{41} to determine whether we use the old word or the new word. The old word to a content would be assigned if it causes smaller increment of effort $\Omega$ than the new word. On the other hand, if assigning the old word to a content will increase the effort $\Omega$ more than the new word, we will assign the new word to that content instead of the old word. After a word was assigned to the new content, we will refresh the words of the existing content. All existing content will have a probability $P$ to be refresh. When we refresh the word of a content, we assign an old word and a new word to it. Then, we use principle of least effort\cite{41} to determine whether we use the original word, old word or new word. We refresh the words like this every time we add a new content. We increase the amount of contents until there are $N$ contents. The block diagram of our model was shown in Fig. 5. Note that we assume there’s no synonyms in our model. The result of our model was shown in Fig. 6 to exhibit the features of RRD.

FIG. 5: Flow chart of our model. When we refresh the words, each content will have probability $P$ to be refreshed.

FIG. 6: The result of our model with $N = 10000$, $\lambda = 0.495$, $P = 0.0005$ and $z = 1000$. The probability of creating a 1-syllgram, 2-syllgram, 3-syllgram, 4-syllgram and 5-syllgram word are 0.15, 0.40, 0.25, 0.15 and 0.05 respectively.

Conclusions and Open Questions

In this paper, we propose a mechanism of evolution shared by gene and language. Based on both qualita-
tive and quantitative analysis, the gene-language correspondence can be established as described in Tab.I. In genomes, we have argued and proved “regarding protein as sentence and domain as word” are quantitatively incorrect based on their $\rho_{x,y}$. To find generalized properties shared by spoken and written language, we introduce syllgram as a new unit, and show its statistical features and role on evolution of language.

Our research provides three tools to investigate the topic of evolution, and elaborate diversity. The first tool is a framework to describe what is crucial to survive in space-time. By selecting correct space-time, the correspondence between gene and language may be generalized to other fields, such as music. The second tool is rank-rank analysis, which can be used reveal the hidden-information behind evolutionary units and their subunits. Once the researchers do not segment the right unit, the scaling structure of RRD plot will be ruined as shown in Fig. 9. This phenomenon is potential to be applied on developing a segmentation algorithm of evolutionary unit for non-coding DNA and unknown languages. The third tool is our partition-network theory. It provide an understanding for self-organization in gene and language. Their evolution is based on the principle of least effort and preferential attachment. The principle of least effort decides whether we need to develop a new functionality or just utilize the old one for survival. The preferential attachment, according to connection between functionalities, decides how we construct a function for survival. This theory can be used to predict the appearance of new protein and new word once the researchers find out $C^{(k)}$.

Although has explained several quantitative features of evolution, our work still leaves some open questions: (A) although we know how to produce scaling structure, we do not know why it should be and what is its precisely mathematical format. (B) the determination of $C^{(k)}$ is obviously based on the interaction among individuals and environment, which is very complicated. Our result merely imply that a random $C^{(k)}$ is somehow reasonable, but the actual form of it is still unknown. (C) our theory can only produce $\rho_x$ with exponent $\approx 1$, however that for gene is in the range of $0.5 \sim 0.8$. A more general mechanism of the principle of least effort is important and necessary to complete this flaw.

Author contributions.

T.M.H. and L.M.W. prepared the manuscript. L.M.W., H.Y.L., and T.M.H. proposed the theoretical models. L.M.W. designed the statistical indicies and technical details. S.J.W. and M.X.T. designed the basic function of program. S.T.T. collected and tested corpora. D.W.W. suggested the addition of $V_n$ and $H_n$ lines. Y.C.S. provided the knowledge of linguistics. C.S.N provided the knowledge of genome analysis.

Competing interests

The authors declare no competing interests.

Additional information

Supplementary Materials

The corpora analyzed in this work are listed in https://github.com/godofhoe/Reference-of-scaling

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Note that the last point at $f_l$, whose $(\text{Link}_x, \text{Allo}_y) = (1, 1)$, can be approximated as $R_0 \approx (V_1, H_1)$. When $R'$ is transformed to $R''$, $R_0 \approx R'_0$. From the definition of Eqs. (6, 7), we can deduce that $\beta/\alpha \approx \ln H_1$ and $\omega/\gamma \approx \ln V_1$ by taking $y' = H_1$ and $x' = V_1$. $V_1$ and $H_1$ represent not only the block boundaries, but also the size of inventories for word and syllgram in the text.

For rigorous expression of network theory, please refer to METHOD section. The formalism we use is based on Boccaletti, S. et al. The structure and dynamics of multilayer networks. *Physics Reports* **544**, 1 (2014).

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METHODS

A. Prior work and data type

The Python program used to investigate this research can be found in Ref. [1]. The following method can be used to analyze 1-D data. For those who want to study the RRD structure in high-dimensional data, they should map their data into 1-D. For example in Fig. 10, to find out the statistical structure of music, we can use waveform of recording file instead of sheet music that contains high-dimensional details such as pitch, note value, and polyphony.

Before RRD analysis, choose a corpus and segment it with your algorithm. In this work, we use syllabify[2] to syllabify English words and several algorithms[3–5] to segment Chinese sentences into words. After segmentation, rank word and syllable by counting their frequency and Rule 1. Group this information into dataframe as Fig. 11.

B. Maximum likelihood estimate of FRD

We use standard error optimization to fit Link/Col, but switch to maximum likelihood estimation to fit FRD for statistical reasons[6]. The discrete Zipf’s distribution is[7] \( P_k = Ck^{-\alpha} \) where \( k \) is the rank of word in frequency table and \( P_k \) is the probability of the word at rank \( k \). The normalized condition of probability gives:

\[
1 = \sum_{k=1}^{n} P_k = C \sum_{k=1}^{n} \frac{1}{k^\alpha} = C(\zeta(\alpha, 1) - \zeta(\alpha, n + 1))
\]

which implies \( C = 1/H(1, n, \alpha) \) where \( H(m, n, \alpha) \equiv \sum_{m}^{n} \frac{1}{k^\alpha} = \zeta(\alpha, m) - \zeta(\alpha, n + 1) \) and \( \zeta(\alpha, m) \) is Hurwitz zeta function.

Given a raw data \( X = [x_1, x_2, x_3, ..., x_N] \) where \( x_i \) is the word of utterance, the likelihood is[6]:

\[
L = \prod_{i=1}^{N} P(x_i|\alpha) = \prod_{i=1}^{k} P(y_{i1}|\alpha)^{\rho(y_{i1})} = \prod_{i=1}^{k} \left[ \frac{y_{i1}^{\alpha}}{H(y_{i1}, y_{k}, \alpha)} \right]^\rho(y_{i1})
\]

where \( Y = [y_{11}, y_{21}, ..., y_{k1}] \) is a rank set of non-repeat \( X \) with frequency \( \rho(y_{i1}) \). For instance, \( X = \{\text{apple, is, terrible, apple}\} \) then \( Y = \{\text{rank(apple), rank(is), rank(terrible)}\} = \{1, 2, 3\} \) with frequency \( \{N(\text{apple}), N(\text{is}), N(\text{terrible})\} = \{2, 1, 1\} \).

The likelihood \( L \) is the conditional probability of observing \( X \) under given parameter \( \alpha \). We hope to find the \( \alpha \) that makes theoretical values closest to data, i.e., maximize the probability of observing raw data, \( P(x|\alpha) \). Bayes’ law gives[7]:

\[
P(\alpha|x) = P(x|\alpha) \frac{P(\alpha)}{P(x)}
\]

We can not maximize \( P(x|\alpha) \) directly because \( x \) is fixed and \( \alpha \) is unknown, but we can maximize \( P(\alpha|x) \). The following problem is whether these two actions are equivalent. The prior probability \( P(x|\alpha) \) of data is fixed once \( x \) is given. Without any information of \( \alpha \), we have to treat the prior probability \( P(\alpha) \) of parameter \( \alpha \) as uniform. Since \( P(x) \) and \( P(\alpha) \) are fixed, maximizing \( P(x|\alpha) \) and \( P(\alpha|x) \) becomes equivalent according to Bayes’ law. This is required by maximum likelihood estimation[7]. We use the minimize function in scipy[8]: \( \max(\ln L(\alpha)) = \min(-1 \times \ln L(\alpha)) \) implies \( C = 1/H(y_{i1}, y_{k}, \alpha_1) \) when \( \alpha = \alpha_1 \).

Before analyzing RRD, one needs to first determine what the main-unit is. This is made possible by checking if Zipf’s or Zipf-like FRD can be reproduced. For example, FRD of red grids in Fig. 10 precedes the action of segmenting green grids as its sub-unit.

C. An approximated analytic form of scaling curve

To facilitate the identification of points on the scaling lines, knowledge of the analytic form of \( f_n \) will help. Based on the scaling property, we assign \( f_n(x) = a_n f(x) \). According to Fig. 2,

\[
H_n = a_m f(V_{n+1-m})
\]

which is similar to Eq. (3). By comparing Eq. (14) for each horizontal and vertical lines, we prove that

\[
\frac{H_{n+1}}{H_n} = \frac{a_{n+1}}{a_n} \frac{f(V_{n+1})}{f(V_n)} = r
\]

where ratio, \( r \), is a constant of \( n \). The evidence of this nontrivial consequence is shown in Fig. 7. We tend to use \( r f(x) \) rather than \( r H \) because the former covers more data. We discover from the case in Fig. 9 that: \( \{H_n\} \) remains a geometric sequence even without the scaling structure. In other words, the existence of a constant \( r_H \) is likely a mere statistical outcome. By use of Zipf’s law and frequency-index identity (Ref.[32] in the main text),

\[
n \approx N(V_{n+1} + V_a) = a(V_{n+1} + V_a)^{-b}. \]

Since the mid-point of each block \( (x, \bar{y}) = (V_{n+1} + V_a, \frac{H_{n+1} + H_a}{2}) \) roughly falls on the scaling line, it can be shown that

\[
\bar{y} \approx a_1 f(x) \approx H_1(1 + \frac{1}{r})^{a_1 x^{-b}}.
\]

Note that this equation can be used to derive the form of scaling function as

\[
y \approx A r^{N(x)}
\]

where \( N(x) \) is FRD of word. The SS and Eq. (17) quantify the hidden rule of word-composition based on the usage rate of syllgrams. This can be observed from the differential form of Eq. (17), \( dN \propto dy/y \), that reveals the increase of word usage \( (dN) \) is proportional to the difference in popularity among syllgrams \( (dy) \) weighted
by the inverse of their rank \((1/y)\), similar to the rich-get-richer spirit of the preferential attachment (Ref.[37] in the main text) that leads to scale-free behavior. In the next section, we will show the scaling function can be used to recognize scaling patterns; therefore, expand the method of text categorization[9] by pattern recognition.

D. Denoising and pattern reconstruction

In the section of partition theory, we discover that syllable on \(f_1\) are rarely used to compose other words. Being one-element partition, they can be excluded without destroying SS. For example, \(3 = 2 + 1\) (two-element) and \(3 = 1 + 1 + 1\) (three-element) will affect SS, but not \(3 = 3\) (one-element). The procedures of fitting the scaling lines include three steps:

1. locate the points that fall on the scaling lines
2. calculate \(r_f(x)\) in Fig. 7(b, d)
3. find the best fitting curve for each scaling line by standard error optimization

Assigning data points to different blocks in Step 1 is helpful because only blocks \((m, n)\) where \(n - m = k - 1\) are involved for the \(k\)-th scaling line. In order to fit good scaling lines, we deal with points in \((m, n) \sim (m + 5, n + 5)\). As can be seen in Fig. 7, scaling lines are envelopes of convex sets so we only need to look for points whose \(y\) are bigger than that of the diagonal line in each block. The above procedure of eliminating most of the fog is crucial since it allows us to focus on the high-density area, i.e., points on the scaling lines. Now we can use total variation reconstruction[10] (TVR) to locate the scaling lines.

The technique of TVR rebuilds points by minimizing the following function:

\[
\sum_i \left[ P(\hat{x}_i - x_{0i}) + P(\hat{y}_i - y_{0i}) \right] + \lambda \cdot \phi_{tv}(\hat{r})
\]

where \(\hat{r} = (\hat{x}, \hat{y})\) is the reconstructed point, \(r_0 = (x_0, y_0)\) is original point, and \(\lambda\) is the regularization parameter.

The penalty function \(P\) and the regularization function \(\phi_{tv}\) are defined as

\[
P(d) = \begin{cases} 
   |d| & \text{if } d \leq d_0 \\
   d^2 & \text{if } d > d_0
\end{cases}
\]

\[
\phi_{tv}(\hat{r}) = \sum_i [ |\hat{x}_i + 1 - \hat{x}_i| + |\hat{y}_i + 1 - \hat{y}_i|]
\]

where \(d\) is the difference between reconstructed and original data, and the threshold \(d_0\) is set to be 50 in our studies. Better than the method of least square, \(P\) can deal with outliers, while \(\phi_{tv}\) makes reconstructed points more compact. Figure 12(a) shows the reconstructed data via TVR.

If the structure is a non-convex set \(\Gamma = \{(x_i, y_i)\}\), the original method needs some adjustments:

(a) prepare a convex function \(C(x)\) that makes \(\hat{\Gamma} = \{(x_i, y_i + C(x_i))|(x_i, y_i) \in \Gamma\}\) convex
(b) execute Step 1 to reconstruct \(\hat{\Gamma}\) into \(\Omega = \{(a_i, b_i)\}\)
(c) remove \(C\) function of Step (a) to obtain the envelope of non-convex set \(\Gamma = \{(a_i, b_i - C(a_i))|(a_i, b_i) \in \Omega\}\).

In Step 2, the data on each scaling line are further coarse-grained into fifty points \(\{(X_i, Y_i)\}_n\) where \(n\) denotes \(n\)-th line and \(i = 1 \sim 50\). We calculate

\[
(r_f)_n \equiv \left\{ \frac{(Y_i)_{n+1}}{(Y_i)_n} \right\}, \quad r_f \equiv \langle (r_f)_n \rangle + \sigma_f
\]

where \(\sigma_f\) is total standard error from propagation of error of each \((r_f)_n\) and \(\langle \cdot \rangle\) denotes the weighted average:

\[
\langle Q_n \rangle \equiv \frac{\sum_n \rho((r_f)_n) \cdot \bar{Q}_n}{\sum_n \rho((r_f)_n)}
\]

where \(\rho(V)\) is number of \(x|x \in V, x \neq nan\\) and \(\bar{Q}_n\) as average of \(Q_n\). Now we define \(SP\), an index to quantify the goodness of scaling, as

\[
S \equiv 1 - \frac{\sigma_f}{\langle (r_f)_n \rangle}, \quad P \equiv \left\{ \frac{\rho((r_f)_n)}{50} \right\}
\]

These two quantities target respectively the soundness of scaling and the clearness of lines.

Now we can use Eq. (17) with free parameters \(A, (a, b)\) in \(N(x) = ax^{-b}\), and constant \(r_f\) to fit the scaling lines. Step 3 includes the following processes:

(a) fit data whose word rank \(x \geq 0.75V_i\)
(b) select \(f_3, f_1\), and \(f_4\) alternatively to be the base of scaling function
(c) fit each base by standard error optimization and use it to define other scaling lines. For example, if \(f_2\) is the base, then \(f_3 = r_f \cdot f_2\) and \(f_1 = r_f^2 \cdot f_2\).
(d) calculate total standard error of base \(f_n\),

\[
Dev(f_n) \equiv \left[ \sum_{i=2}^{4} \sum_x (y_i(x) - f_i(x))^2 \right]_n
\]

where \(y_i(x)\) represents real data, \(f_i\) is the fitting line, and \([\cdot]_n\) reminds us which \(f_n\) is being used as the base.
(e) The \(f_n\) that enjoys the smallest \(Dev(f_n)\) will consequently be chosen as the best base.
(f) If 0.75 is insufficient to determine the optimization parameters, increase this proportion till \(P_{cut}\) when the optimization succeeds.

Figure 12(b) shows the result of Step 3. To avoid overfitting, the statistical method AIC[23] is employed. It is a direct measurement of information loss and emphasizes the need to strike a balance between model simplicity and goodness of fit. According to AIC, our processes are better than trying to fit \(f_2 \sim f_4\) separately with Eq. (17), i.e., use 9 parameters.

How can we judge the goodness of fitting by the score \(G\)? To be pragmatic, it should be able to judge the effectiveness of a segmentation algorithm by quantifying the smoothness of a curve. In Step 3(a) 0.75 of data are used
for fitting. But when encountering an unsmooth curve or high standard-error structure in Step 3(c), 0.75 will not be enough to pin down the optimization parameters. This is the reason why we need to install Step 3(f). Empirically, we found it convenient to define the goodness of fitting as

\[
G = \begin{cases} 
0.75/P_{\text{cut}} & \text{if } 0.75 \leq P_{\text{cut}} < 1 \\
0.5 & \text{if } P_{\text{cut}} \geq 1 
\end{cases}
\]  

(25)

where \( G = 0.5 \) describes an unsmooth curve whose segmentation algorithm is very bad. \( P_{\text{cut}} > 1 \) means the program can not fit successfully even run out all data. If we had defined \( G = 0.75 \) when \( P_{\text{cut}} = 1 \), the index \( GL^{0.15}/(MV_1) \) would not have performed so well as in Fig. 13.

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TABLE II: Statistical quantities of different corpora. All corpora obey Zipf’s law, except No. 16~19. No. 6 ~ 8 are scientific articles in English. Data for 60 more corpora can be found in Supplementary material.

| No. | Sample                          | Zipf \( (a, b) \) | Geometric \( (r_H, \sigma_H, r_f, \sigma_f) \) | Scaling \( (S_P, M, V_1, L) \) | Language   |
|-----|--------------------------------|-------------------|------------------------------------------|--------------------------|-------------|
| 1   | *Moby-Dick*                     | (0.092, 0.99)     | (0.691, 0.033, 0.870, 0.023)             | (0.905, 2402, 20688, 203k) | English     |
| 2   | *The Hobbit*                    | (0.099, 0.99)     | (0.959, 0.035, 0.864, 0.028)             | (0.871, 642, 7690, 94k)   | English     |
| 3   | Xu Zhimo 徐志摩                  | (0.078, 0.86)     | (0.853, 0.047, 0.695, 0.025)             | (0.713, 36, 1235, 3k)     | Chinese     |
| 4   | *Frog*                          | (0.080, 0.95)     | (0.967, 0.018, 0.925, 0.009)             | (0.862, 682, 14380, 110k) | Chinese     |
| 5   | *Demi-Gods and Semi-Devils* 天龍八部 | (0.080, 0.97)     | (0.984, 0.012, 0.955, 0.011)             | (0.88, 1632, 35223, 695k) | Chinese     |
| 6   | LIGO 2016                        | (0.053, 0.81)     | (0.939, 0.057, 0.780, 0.026)             | (0.734, 336, 2830, 7.9k)  | Sci. English|
| 7   | Chopstick                        | (0.072, 0.84)     | (0.904, 0.057, 0.729, 0.025)             | (0.637, 144, 1153, 3.1k)  | Sci. English|
| 8   | Empirical Test of Zipf          | (0.083, 0.86)     | (0.911, 0.050, 0.791, 0.033)             | (0.345, 95, 910, 2.8k)    | Sci. English|
| 9   | Newspaper                        | (0.032, 0.74)     | (0.943, 0.031, 0.857, 0.021)             | (0.869, 150, 4143, 12k)   | Chinese     |
| 10  | Mix (various authors)            | (0.079, 0.96)     | (0.929, 0.008, 0.929, 0.008)             | (0.893, 981, 22716, 174k) | Chinese     |
| 11  | Paper generator[14]              | (0.068, 0.85)     | (0.961, 0.021, 0.934, 0.012)             | (0.138, 344, 2128, 26k)   | Fake English|
| 12  | 1-gram Fake                      | (0.108, 0.95)     | (0.938, 0.040, NAN, NAN)                 | (NAN, 1, 1541, 20k)       | Fake Chinese|
| 13  | 2-gram Fake                      | (0.097, 0.96)     | (0.950, 0.032, 0.873, 0.013)             | (0.719, 105, 4019, 20k)   | Fake Chinese|
| 14  | 3-gram Fake                      | (0.097, 0.96)     | (0.957, 0.027, 0.883, 0.012)             | (0.849, 157, 3931, 20k)   | Fake Chinese|
| 15  | 4-gram Fake                      | (0.097, 0.96)     | (0.962, 0.025, 0.898, 0.013)             | (0.779, 265, 3964, 20k)   | Fake Chinese|
| 16  | 2-gram log-normal               | (0.096, 0.96)     | (0.956, 0.029, 0.982, 0.016)             | (0.756, 181, 4146, 20k)   | Fake Chinese|
| 17  | 2-gram double power law          | (0.333, 1.40)     | (0.967, 0.029, 0.889, 0.021)             | (0.762, 68, 3308, 200k)   | Fake Chinese|
| 18  | 2-gram exponential              | (0.049, 0.69)     | (0.990, 0.008, 0.942, 0.014)             | (0.039, 17, 596, 20k)     | Fake Chinese|
| 19  | 2-gram Gaussian                 | (0.005, 0.42)     | (0.993, 0.004, 0.944, 0.005)             | (0.537, 105, 3561, 20k)   | Fake Chinese|
| 20  | Excerpts from Frog              | (0.051, 0.71)     | (0.809, 0.080, 0.678, 0.026)             | (0.423, 33, 637, 1.2k)    | Chinese     |
| 21  | Excerpts from Moby-Dick          | (0.064, 0.77)     | (0.861, 0.077, 0.712, 0.026)             | (0.318, 58, 653, 1.4k)    | English     |
TABLE III: This table determines that a sound SS, represented by a large $SP$ value, relies on a large size of word bank $V_1$, and can still exist for fake corpora that consist of words composed of random characters or do not follow rules of writing.

|                | corpora, scientific article | fake, No.11 (real words) | fake, No.12~17 (random words) |
|----------------|-----------------------------|--------------------------|-------------------------------|
| real words     | yes                         | yes                      | yes                           |
| grammar        | yes                         | yes                      | no                            |
| $V_1 > 1200$   | yes                         | no                       | yes                           |
| Zipf or Zipf-like | yes                         | yes                      | no                            |
| $SP > 0.75$    | yes                         | no                       | yes                           |
FIG. 7: Left figures show the weighted average scaling relation of $r_H \equiv H_{n+1}/H_n$, while right ones depict $r_f$ with standard error, $\sigma_H$ and $\sigma_f$. Panels (a, b) are for *Moby-Dick*, (c, d) for *Frog*, (e, f) for *Angels-Demons*, (g, h) for *The scholar*. Note that $f_2/f_1$ is excluded when calculating $r_f$. Detail definitions of $r_f$ and SP, a measure of goodness of scaling, are given in METHODS.
FIG. 8: Left figures depict Col-rank plot, while right ones are for Link-rank. Panels (a, b) are for *Harry Potter 3*, (c, d) work by Lung Yingtai, (e, f) *David-Copperfield*, and (g, h) work by Yu Guangzhong. Dashed lines are fitting curves.
FIG. 9: Cases with $SP < 0.75$ due to different reasons: (a, b) $L$ is too small, (c, d, e) FRD is neither Zipf nor Zipf-like, (f) $V_1$ is too small. Their parameters can be found in Tab. II. Note that the computer-generated paper in (e) is created by SCIgen[14] which has succeeded at deceiving the editors of many journals and conference organizers. But our RRD analysis can tell it from real paper.
FIG. 10: Schematic demonstration of segmenting Toccata and Fugue in D minor, BWV 565, written by J. S. Bach. With the aid of waveform, we can display music in 1-D data type and segment it into possible units that have scaling structure. To deal with such 1-D type data without precise definition of main-unit, we need to segment their main-unit before segment their sub-unit. We guess the red grids are main-unit while the green grids are sub-unit. This method provides us with a tool to analyze the statistical property of music. The pictures of violin, cello and double bass are accessed from wikipedia. The waveform is displayed by Sonic Visualiser.
FIG. 11: Dataframe of RRD, word and syllable in Moby-Dick, where SeqOrder is sequence order that follows Rule 1, and $y_n$ is the rank of $n$-th syllable.
FIG. 12: Yellow (grey) points in (a, b) sketch out the scaling lines and are selected by Step 1. (b) The fitting form of scaling lines follows \( f(x) = A \times r_N^N(x) \) where \( N(x) = ax^{-b} \). Step 3 chose \( f_2 \) as the best base, while \( r_f = 0.870 \) that also appeared in Fig. 7(b) is obtained in Step 2. The fitting score is defined in Eq. (25).
FIG. 13: The $A - GL^{0.15}(MV_1)$ plot for corpora segmented by different algorithms[11, 12]. We use CKIP[3], the best Chinese algorithm, as the standard in cases (a, b, c, d), while (e, f) employ the word bank[13] segmented by linguists in Academia Sinica. Initially we were alarmed by the violation of positive correlation in (e, f). But soon it dawned on us that the version of standard bank we used is older than the one by CKIP. This realization reveals that the $A - GL^{0.15}(MV_1)$ plot has the potential to function as an empirical index for the accuracy of algorithm.