Correlation property of length sequences based on global structure of complete genome

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Abstract—This paper considers three kinds of length sequences of the complete genome. Detrended fluctuation analysis, spectral analysis, and the mean distance spanned within time L are used to discuss the correlation property of these sequences. The values of the exponents from these methods of these three kinds of length sequences of bacteria indicate that the long-range correlations exist in most of these sequences. The correlation have a rich variety of behaviours including the presence of anti-correlations. Further more, using the exponent γ, it is found that these correlations are all linear (γ = 1.0 ± 0.03). It is also found that these sequences exhibit 1/f noise in some interval of frequency (f > 1). The length of this interval of frequency depends on the length of the sequence. The shape of the periodogram in f > 1 exhibits some periodicity. The period seems to depend on the length and the complexity of the length sequence.

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Key words: Coding/noncoding segments, length sequence, complete genome, detrended fluctuation analysis, 1/f noise.

I. INTRODUCTION

Recently, there has been considerable interest in the finding of long-range correlation (LRC) in DNA sequences [1–16]. Li et al [16] found that the spectral density of a DNA sequence containing mostly introns shows 1/f⁰ behaviour, which indicates the presence of LRC. The correlation properties of coding and noncoding DNA sequences were first studied by Peng et al [2] in their fractal landscape or DNA walk model. The DNA walk defined in [2] is that the walker steps “up” if a pyrimidine (C or T) occurs at position i along the DNA chain, while the walker steps “down” if a purine (A or G) occurs at position i. Peng et al [2] discovered that there exists LRC in noncoding DNA sequences while the coding sequences correspond to a regular random walk. By doing a more detailed analysis, Chatzidimitriou, Dreismann and Larhammar [3] concluded that both coding and noncoding sequences exhibit LRC. A subsequent work by Prabhu and Claverie [4] also substantially corroborates these results. If one considers more details by distinguishing C from T in pyrimidine, and A from G in purine (such as two or three-dimensional DNA walk model [5] and maps given in [6]), then the presence of base correlation has been found even in coding sequences. In view of the controversy about the presence of correlation in all DNA or only in noncoding DNA, Buldyrev et al [7] showed the LRC appears mainly in noncoding DNA using all the DNA sequences available. Alternatively, Voss [8], based on equal-symbol correlation, showed a power law behaviour for the sequences studied regardless of the percent of intron contents. Investigations based on different models seem to suggest different results, as they all look into only a certain aspect of the entire DNA sequence. It is therefore important to investigate the degree of correlations in a model-independent way.

Since the first complete genome of the free-living bacterium Mycoplasma genitalium was sequenced in 1995 [9], an ever-growing number of complete genomes has been deposited in public databases. The availability of complete genomes induces the possibility to ask some global questions on these sequences. The avoided and under-represented strings in some bacterial complete genomes have been discussed in [10–12]. A time series model of CDS in complete genome has also been proposed in [13]. Maria de Sousa Vieira [13] have done the low-frequency analysis of complete DNA of 13 microbial genomes and shown that its fractal behaviour not always prevails through the entire chain, the autocorrelation function have a rich variety of behaviours including the presence of anti-correlations.

For the importance of the numbers, sizes and ordering of genes along the chromosome, one can refer to Part 5 of the famous book of Lewin (Ref. [23]). Hence one may ignore the composition of the four kinds of bases in coding and noncoding segments and only considers the rough structure of the complete genome or long DNA sequences. Provata and Almirantis [24] proposed a fractal Cantor pattern of DNA. They map coding segments to filled regions and noncoding segments to empty regions of random Cantor set and then calculate the fractal dimension of the random fractal set. They found that the coding/noncoding partition in DNA sequences of lower organisms is homogeneous-like, while in the higher eukaryotes the partition is fractal. This result seems too rough
to distinguish bacteria because the fractal dimensions of bacteria they gave out are all the same. The classification and evolution relationship of bacteria is one of the most important problem in DNA research. Yu and Anh [24] proposed a time series model based on the global structure of the complete genome and considered three kinds of length sequences. After calculating the correlation dimensions and Hurst exponents, it was found that one can get more information from this model than that of fractal Cantor pattern. Some results on the classification and evolution relationship of bacteria were found in [25]. Naturally it is desirable to know if there exists LRC in these length sequences. The quantification of these correlations could give an insight of the role of the ordering of genes on the chromosome, which is far to be irrelevant for gene function. We attempt to answer this question in this paper.

Viewing from the level of structure, the complete genome of an organism is made up of coding and non-coding segments. Here the length of a coding/noncoding segment means the number of its bases. Based on the lengths of coding/noncoding segments in the complete genome, we can get three kinds of integer sequences by the following ways.

i) First we order all lengths of coding and noncoding segments according to the order of coding and noncoding segments in the complete genome, then replace the lengths of noncoding segments by their negative numbers. This allows to distinguish lengths of coding and noncoding segments. This integer sequence is named whole length sequence.

ii) We order all lengths of coding segments according to the order of coding segments in the complete genome. We name this integer sequence coding length sequence.

iii) We order all lengths of noncoding segments according to the order of noncoding segments in the complete genome. This integer sequence is named noncoding length sequence.

We can now view these three kinds of integer sequences as time series. In the following, we will investigate the correlation property through Detrended Fluctuation Analysis (DFA) and spectral analysis.

II. DETRENDED FLUCTUATION ANALYSIS AND SPECTRAL ANALYSIS

We denote a time series as $X(t), t = 1, \cdots, N$. First the time series is integrated as $y(k) = \sum_{t=1}^{k} [X(t) - \overline{X}]$, where $\overline{X}$ is the average over the whole time period. Next, the integrated time series is divided into boxes of equal length, $n$. In each box of length $n$, a least-squares line is fit to the data, representing the trend in that box. The $y$ coordinate of the straight line segments is denoted by $y_n(k)$. We then detrend the integrated time series, $y(k)$, by subtracting the local trend, $y_n(k)$, in each box. The root-mean-square fluctuation of this integrated and detrended time series is calculated as

$$F(n) = \sqrt{\frac{1}{N} \sum_{k=1}^{N} [y(k) - y_n(k)]^2}$$ (1)

Typically, $F(n)$ will increase with box size $n$. A linear relationship on a double log graph indicates the presence of scaling

$$F(n) \propto n^\alpha.$$ (2)

Under such conditions, the fluctuations can be characterised by the scaling exponent $\alpha$, the slope of the line relating $\ln F(n)$ to $\ln n$. For uncorrelated data, the integrated value, $y(k)$ corresponds to a random walk, and therefore, $\alpha = 0.5$. An value of $0.5 < \alpha < 1.0$ indicates the presence of LRC so that a large interval is more likely to be followed by a large interval and vice versa. In contrast, $0 < \alpha < 0.5$ indicates a different type of power-law correlations such that large and small values of time series are more likely to alternate. For examples, we give the DFA of the coding length sequence of A. aeolicus in FIG. 1.

Now we analyse the time series using the quantity $M(L)$, the mean distance a walker spanned within time $L$. Dunki and Ambuhl [26] used this quantity to discuss the scaling property in temporal patterns of schizophrenia. Denote

$$W(j) := \sum_{i=1}^{j} [X(t) - \overline{X}],$$ (3)

from which we get the walks

$$M(L) := < |W(j) - W(j + L)| >_j,$$ (4)

where $< >_j$ denotes the average over $j$, and $j = 1, \cdots, N - L$. The time shift $L$ typically varies from $1, \cdots, N/2$. From a physics viewpoint, $M(L)$ might be thought of as the variance evolution of a random walker’s total displacement mapped from the time series $X(t)$. $M(L)$ may be assessed for LRC [28] (e.g. $M(L) \propto L^{\alpha'}$, $\alpha' = 1/2$ corresponding to the random case). We give some examples to estimate the scale parameter $\alpha'$ in FIG. 1.

Dunki et al [27] proposed the following scale which seems to perform better than the scale $\alpha'$. The definition

$$W'(j) := \sum_{i=1}^{j} |X(t) - \overline{X}|,$$ (5)

leads to

$$M'(L) := < |W'(j) - W'(j + L)| >_j.$$ (6)

Analyses of test time series showed that [27] are more robust against distortion or discretization of the corresponding amplitudes $X(t)$ than (4). From the $\ln(L)$ v.s. $\ln(M'(L))$ plane, we find the relation
\[ M'(L) \propto L^\gamma. \]  \hfill (7)

The exponent \( \gamma \) measures only the presence of non-linear correlations and remains equal to unity for all sequences with only linear correlations. We carried out this kind of analysis on coding length sequences of \( A.\ aeriformis, B. burgdorferi \) and \( T. maritima. \) The results are reported in the left figure of FIG. 3.

We also consider the discrete Fourier transform of the time series \( X(t), t = 1, \cdots, N \) defined by

\[ \hat{X}(f) = N^{-\frac{1}{2}} \sum_{t=0}^{N-1} X(t+1)e^{-2\pi\text{i}ft}, \]  \hfill (8)

then

\[ S(f) = |\hat{X}(f)|^2 \]  \hfill (9)

is the power spectrum of \( X(t). \) In recent studies, it has been found that many natural phenomena lead to the power spectrum of the form \( 1/f^\beta. \) This kind of dependence was named \( 1/f \) noise, in contrast to white noise \( S(f) = \text{const} \), i.e. \( \beta = 0. \) Let the frequency \( f \) take \( k \) values \( f_k = k/N, k = 1, \cdots, N. \) From the \( \ln(\text{f}) \) v.s. \( \ln(S(f)) \) graph, the existence of \( 1/f^\beta \) doesn’t seem apparent. For example, we give the figure of the coding length sequence of \( A.\ aeriformis \) on the right of FIG. 3.

When we use the least squares line to fit data, we need to consider the errors. If the data are \( \{(x_i, y_i)\}_{i=1}^n \), we can define the coefficient of linear correlation as

\[ r = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2 \sum_{i=1}^n (y_i - \bar{y})^2}}, \]  \hfill (10)

where \( \bar{x} \) and \( \bar{y} \) are the average of the values \( \{x_i\}_{i=1}^n \) and \( \{y_i\}_{i=1}^n \) respectively. If \( r = \pm 1 \), then the points lie exactly on a straight line; that is, there is a perfect linear relationship between \( x \) and \( y. \) If \( r = 0 \), there is no linear relationship. The quantity \( r \) measures the strength of linear relationships between \( x \) and \( y. \) The values of \( r \) in figures of obtaining exponents \( \alpha, \alpha' \) and \( \beta \) are 0.987685, 0.9949939 and 3.7918E-03 respectively. Hence we can see the informations given by exponents \( \alpha \) and \( \alpha' \) are more convincing than that given by exponent \( \beta. \)

### III. DATA AND RESULTS.

More than 21 bacterial complete genomes are now available in public databases. There are five Archaeabacteria: \( Archaeoglobus fulgidus \) (aful), \( Pyrococcus abyssi \) (pabyssi), \( Methanococcus jannaschii \) (mjan), \( Aeropyrum pernix \) (aero) and \( Methanobacterium thermoautotrophicum \) (mth); four Gram-positive Eubacteria: \( Mycobacterium tuberculosis \) (mtub), \( Mycoplasma pneumoniae \) (mpneu), \( Mycoplasma genitalium \) (mgenn), and \( Bacillus subtilis \) (bsub). The others are Gram-negative Eubacteria. These consist of two Hyperthermophilic bacteria: \( Aquifex aeolicus \) (aer) and \( Thermotoga maritima \) (tmr); six Proteobacteria: \( Rhizobium sp.\) NGR234 (pNGR234), \( Escherichia coli \) (ecoli), \( Haemophilus influenzae \) (hinf), \( Helicobacter pylori \) J99 (hpj99), \( Helicobacter pylori \) 26695 (hpjy) and \( Rickettsia prowazekii \) (rpxz); two Chlamydia: \( Chlamydia trachomatis \) (atra) and \( Chlamydia pneumoniae \) (cpeu), and two Spirochaete: \( Borrelia burgdorferi \) (bbur) and \( Treponema pallidum \) (tpal).

We calculate scales \( \alpha, \alpha', \beta \) of low frequencies \( (f < 1) \) and \( \gamma \) of three kinds of length sequences of the above 21 bacteria. The estimated results are given in Table I (where we denote by \( \alpha_{\text{whole}}, \alpha_{\text{cod}} \) and \( \alpha_{\text{noncod}} \) the scales of DFA of the whole, coding and noncoding length sequences, from top to bottom, in the increasing order of the value of \( \alpha_{\text{whole}} \)). Table II (where we denote by \( \alpha'_{\text{whole}}, \alpha'_{\text{cod}} \) and \( \alpha'_{\text{noncod}} \) the scales of \( M(L) \) of the whole, coding and noncoding length sequences, from top to bottom, in the increasing order of the value of \( \alpha'_{\text{whole}} \)).

From the right figure of FIG. 3 it is seen that \( S(f) \) does not display clear power-law \( 1/f \) dependence on the frequencies when \( f < 1. \) Although the meaning of region \( f > 1 \) of the power spectrum is not clear, whether \( S(f) \) displays perfect power-law \( 1/f \) in this region is important. When one considers the electrical characteristics of polysilicon emitter bipolar transistors, for high frequency analog applications the transistor \( 1/f \) noise is also an important parameter since it can degrade the spectral purity of the circuit. There is also some evidence that \( 1/f \) noise spectral density in the low and in the high current region have a different physical origin (the reader can refer Ref. \( \text{[33]} \) and reference therein). We want to know if there is another region of frequencies in which \( S(f) \) displays perfect power-law \( 1/f \) dependence on the frequencies. We carried out the spectral analysis for \( f > 1, \) and found that \( S(f) \) displays almost a perfect power-law \( 1/f \) dependence on the frequencies in some interval:

\[ S(f) \propto \frac{1}{f^\beta}. \]  \hfill (11)

We give the results for coding length sequences of \( M.\ genitalium, A.\ fulgidus, A.\ aeolicus \) and \( E.\ coli \) (their lengths are 303, 1538, 891 and 3034 respectively) in FIG. \( \text{[4]} \) where we take \( k \) values \( f_k = 3k \) \((k = 1, \cdots, 1000)\) of the frequency \( f. \) From FIG. \( \text{[4]} \) it is seen that the length of the interval of frequency in which \( S(f) \) displays almost a perfect power-law \( 1/f \) depends on the length of the length sequence. The shorter sequence corresponds to the larger interval.
From FIG. 4, one can see that the power spectrum exhibit some kind of periodicity. But the period seems to depend on the length of the sequence. We also guess that the period also depends on the complexity of the sequence. To support this conjecture, we got a promoter DNA sequence from the gene bank, then replaced A by -2, C by -1, G by 1 and T by 2 (this map is given in [5]); so we obtained a sequence on alphabet \{-2, -1, 1, 2\}. Then a subsequence was obtained with the length the same as the coding length sequences of A. aeolicus, A. fulgidus and M. genitalium (their lengths are 891, 1538 and 303 respectively). A comparison is given in FIG. 5 but the results are not clear-cut.

IV. DISCUSSION AND CONCLUSIONS

Although the existence of the archaebacterial urkingdom has been accepted by many biologists, the classification of bacteria is still a matter of controversy \[24\]. The evolutionary relationship of the three primary kingdoms (i.e. archaebacteria, eubacteria and eukaryote) is another crucial problem that remains unresolved \[25\].

From Table III we can roughly divide bacteria into two classes, one class with \(\alpha_{\text{whole}}\) less than 0.5, and the other with \(\alpha_{\text{whole}}\) greater than 0.5. All Archaebacteria belong to the same class except Pyrococcus abyssi. All Proteobacteria belong to the same class except E. coli; in particular, the closest Proteobacteria Helicobacter pylori 26695 and Helicobacter pylori J99 group with each other. In the class with \(\alpha_{\text{whole}} < 0.5\), we have \(\alpha_{\text{cod}} < \alpha_{\text{noncod}}\) except H. pylori J99 and M. genitalium; but in the other class we have \(\alpha_{\text{cod}} > \alpha_{\text{noncod}}\).

Using the exponent \(\alpha'\), we can also divide bacteria into two class as in Table III. In one class, \(\alpha'_{\text{cod}} < \alpha'_{\text{noncod}}\). In another class, we have \(\alpha'_{\text{cod}} > \alpha'_{\text{noncod}}\) except Treponema pallidum and Borrelia burgdorferi. Two hyperthermophilic bacteria Aquifex aeolicus and Thermotoga maritima group with each other.

From Tables II and III we can see the similar rules as above if we use the exponents \(\alpha_{\text{cod}}\) and \(\alpha'_{\text{cod}}\). This follows the fact that the coding sequences occupy the main part of space of the DNA chain of bacteria. This coincides with the conclusion of Ref. \[25\].

Although from Table III we get \(\gamma = 1.0 \pm 0.03\). Hence we can conclude that the long-range correlations exist in most length sequences are linear.

We find in an interval of frequency \((f > 1)\), \(S(f)\) displays perfect power-law \(1/f\) dependence on the frequencies (see FIG. 4)

\[
S(f) \propto \frac{1}{f^\beta}.
\]

The length of the interval of frequency in which \(S(f)\) displays almost a perfect power-law \(1/f\) depends on the length of the length sequence. The shorter sequence corresponds to the larger interval. The shape of the graph of power spectrum in \(f > 1\) also exhibits some kind of periodicity. The period seems to depend on the length and the complexity of the length sequence.

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TABLE I. $\alpha_{\text{whole}}, \alpha_{\text{cod}}$ and $\alpha_{\text{noncod}}$ of 21 bacteria.

| Bacteria                      | Category                                   | $\alpha_{\text{whole}}$ | $\alpha_{\text{cod}}$ | $\alpha_{\text{noncod}}$ |
|-------------------------------|--------------------------------------------|--------------------------|------------------------|--------------------------|
| Rhizobium sp. NGR234          | Proteobacteria                             | 0.24759                  | 0.11158                | 0.34342                  |
| Mycoplasma genitalium         | Gram-positive Eubacteria                    | 0.37003                  | 0.25374                | 0.18111                  |
| Chlamydia trachomatis         | Chlamydia                                  | 0.42251                  | 0.37043                | 0.49373                  |
| Thermotoga maritima           | Hyperthermophilic bacteria                  | 0.43314                  | 0.47559                | 0.49279                  |
| Mycoplasma pneumoniae         | Gram-positive Eubacteria                    | 0.44094                  | 0.45208                | 0.49922                  |
| Pyrococcus abyssi             | Archaebacteria                              | 0.48568                  | 0.39271                | 0.42884                  |
| Helicobacter pylori J99       | Proteobacteria                              | 0.48770                  | 0.43562                | 0.42089                  |
| Helicobacter pylori 26695     | Proteobacteria                              | 0.49538                  | 0.37608                | 0.41374                  |
| Haemophilus influenzae        | Proteobacteria                              | 0.49771                  | 0.42432                | 0.53013                  |
| Rickettsia prowazekii         | Proteobacteria                              | 0.49950                  | 0.33089                | 0.51923                  |
| Chlamydia pneumoniae          | Chlamydia                                  | 0.53982                  | 0.53615                | 0.38085                  |
| Methanococcus jannaschii      | Archaebacteria                              | 0.54516                  | 0.58380                | 0.34482                  |
| M. tuberculosis               | Gram-positive Eubacteria                    | 0.55621                  | 0.57479                | 0.52949                  |
| Aeropyrum pernix              | Archaebacteria                              | 0.57817                  | 0.63248                | 0.44829                  |
| Bacillus subtilis             | Gram-positive Eubacteria                    | 0.58047                  | 0.59221                | 0.54480                  |
| Borrelia burgdorferi          | Spirochaete                                 | 0.58258                  | 0.53687                | 0.51815                  |
| Archaeoglobus fulgidus        | Archaebacteria                              | 0.59558                  | 0.59025                | 0.46596                  |
| Aquifex aeolicus              | Hyperthermophilic bacteria                  | 0.59558                  | 0.55964                | 0.43141                  |
| Escherichia coli              | Proteobacteria                              | 0.60469                  | 0.62011                | 0.52000                  |
| M. thermoautotrophicum        | Archaebacteria                              | 0.62055                  | 0.64567                | 0.38825                  |
| Treponema pallidum            | Spirochaete                                 | 0.67964                  | 0.70297                | 0.60914                  |

TABLE II. $\alpha'_{\text{whole}}, \alpha'_{\text{cod}}$ and $\alpha'_{\text{noncod}}$ of 21 bacteria.

| Bacteria                      | Category                                   | $\alpha'_{\text{whole}}$ | $\alpha'_{\text{cod}}$ | $\alpha'_{\text{noncod}}$ |
|-------------------------------|--------------------------------------------|--------------------------|------------------------|--------------------------|
| Rhizobium sp. NGR234          | Proteobacteria                             | 0.17021                  | 0.11223                | 0.28573                  |
| Chlamydia trachomatis         | Chlamydia                                  | 0.17234                  | 0.23801                | 0.66431                  |
| M. tuberculosis               | Gram-positive Eubacteria                    | 0.20185                  | 0.18451                | 0.43716                  |
| Mycoplasma genitalium         | Gram-positive Eubacteria                    | 0.21632                  | 0.25185                | 0.25971                  |
| Escherichia coli              | Proteobacteria                              | 0.25837                  | 0.24567                | 0.62126                  |
| Pyrococcus abyssi             | Archaebacteria                              | 0.29809                  | 0.18061                | 0.48169                  |
| Bacillus subtilis             | Gram-positive Eubacteria                    | 0.36791                  | 0.46816                | 0.55325                  |
| Mycoplasma pneumoniae         | Gram-positive Eubacteria                    | 0.37148                  | 0.46475                | 0.46829                  |
| Chlamydia pneumoniae          | Chlamydia                                  | 0.37216                  | 0.26039                | 0.50734                  |
| Rickettsia prowazekii         | Proteobacteria                              | 0.41040                  | 0.23109                | 0.50930                  |
| Archaeoglobus fulgidus        | Archaebacteria                              | 0.43149                  | 0.35370                | 0.60835                  |
| Helicobacter pylori 26695     | Proteobacteria                              | 0.44082                  | 0.38500                | 0.39325                  |
| Haemophilus influenzae        | Proteobacteria                              | 0.46121                  | 0.44842                | 0.34842                  |
| Aeropyrum pernix              | Archaebacteria                              | 0.46203                  | 0.45520                | 0.24850                  |
| M. thermoautotrophicum       | Archaebacteria                              | 0.48038                  | 0.48870                | 0.36249                  |
| Thermotoga maritima           | Hyperthermophilic bacteria                  | 0.49453                  | 0.50457                | 0.27005                  |
| Aquifex aeolicus              | Hyperthermophilic bacteria                  | 0.50237                  | 0.50582                | 0.31488                  |
| Helicobacter pylori J99       | Proteobacteria                              | 0.54547                  | 0.50999                | 0.48640                  |
| Treponema pallidum            | Spirochaete                                 | 0.56357                  | 0.56808                | 0.65350                  |
| Borrelia burgdorferi          | Spirochaete                                 | 0.61186                  | 0.58016                | 0.61772                  |
| Methanococcus jannaschii      | Archaebacteria                              | 0.72726                  | 0.73884                | 0.33780                  |
### Table III. $\beta_{\text{whole}}$, $\beta_{\text{cod}}$ and $\beta_{\text{noncod}}$, $\gamma_{\text{whole}}$, $\gamma_{\text{cod}}$ and $\gamma_{\text{noncod}}$ of 21 bacteria.

| Bacteria               | $\beta_{\text{whole}}$ | $\beta_{\text{cod}}$ | $\beta_{\text{noncod}}$ | $\gamma_{\text{whole}}$ | $\gamma_{\text{cod}}$ | $\gamma_{\text{noncod}}$ |
|------------------------|-------------------------|-----------------------|--------------------------|--------------------------|------------------------|---------------------------|
| M. genitalium          | 0.05880                 | 0.02030               | -0.00708                 | 1.00017                  | 0.99698                | 1.01652                   |
| H. pylori 26695        | 0.05026                 | -0.01412              | 0.01196                  | 0.99902                  | 1.00057                | 0.99538                   |
| M. jannaschii          | 0.04850                 | -0.02640              | -0.12547                 | 0.99727                  | 0.99079                | 0.99767                   |
| C. pneumoniae          | 0.04405                 | 0.01071               | -0.01906                 | 0.99998                  | 1.00099                | 0.99348                   |
| A. aeolicus            | 0.03152                 | 0.00811               | -0.00115                 | 1.00441                  | 0.99816                | 0.99870                   |
| H. pylori J99          | 0.01968                 | 0.04512               | -0.05815                 | 0.99867                  | 0.99926                | 0.99349                   |
| T. maritima            | 0.00737                 | -0.02656              | 0.01965                  | 0.99726                  | 0.99524                | 0.98866                   |
| C. trachomatis         | 0.00256                 | -0.05829              | -0.02549                 | 0.99767                  | 1.00211                | 0.98553                   |
| R. sp. NGR234          | 0.00230                 | 0.04048               | -0.10905                 | 1.00570                  | 0.99612                | 1.01515                   |
| M. thermoauto.         | -0.00217                | -0.11916              | 0.02079                  | 1.00479                  | 1.00171                | 1.00063                   |
| T. pallidum            | -0.00422                | -0.02902              | 0.09510                  | 1.01009                  | 1.01532                | 1.00222                   |
| M. pneumoniae          | -0.01137                | 0.03437               | -0.05573                 | 0.98820                  | 0.98783                | 0.97261                   |
| P. abyssi              | -0.01589                | -0.04242              | 0.00071                  | 0.99888                  | 0.99816                | 0.99293                   |
| E. coli                | -0.01917                | -0.05513              | 0.01772                  | 0.99856                  | 1.00197                | 0.98938                   |
| M. tuberculosis        | -0.02653                | -0.05653              | -0.02698                 | 1.00062                  | 0.99974                | 1.00801                   |
| A. pernix              | -0.03882                | 0.01648               | -0.09395                 | 1.00298                  | 1.00407                | 1.00286                   |
| B. burgdorferi         | -0.04420                | -0.05189              | -0.10710                 | 0.99287                  | 0.99792                | 1.03206                   |
| R. prowazekii          | -0.04884                | -0.12438              | -0.07581                 | 1.00284                  | 0.99043                | 0.99911                   |
| H. influenzae          | -0.05338                | -0.04833              | -0.03441                 | 0.99798                  | 1.00248                | 0.98884                   |
| A. fulgidus            | -0.06372                | -0.08130              | -0.00881                 | 1.00347                  | 1.00610                | 0.98219                   |
| B. subtilis            | -0.06887                | -0.17231              | -0.02380                 | 0.99629                  | 1.00853                | 0.98666                   |
FIG. 1. An example to show how to do detrended fluctuation analysis, \textbf{Left}) To get the sequence $y_n(k)$; \textbf{Right}) To get the exponent $\alpha$ using least-square linear fit.

FIG. 2. \textbf{Left}) To get the exponent $\alpha'$ using least-square linear fit; \textbf{Right}) The analysis of coding length sequences of three bacteria using mean distance a walker spanned within time $L$.

FIG. 3. \textbf{Left}) Estimate the scale $\gamma$. \textbf{Right}) An example of spectral analysis of low frequencies $f < 1$. 
FIG. 4. There exists $1/f$ noise in the interval of $f > 1$.

FIG. 5. Compare the power spectral of length sequences and DNA sequences when $f > 1$. 