Abstract

A new family of compound Poisson distribution functions from statistical linguistic is used to study the n-tuples and nucleotide composition features of DNA sequences. The relative frequency distribution of the 6-tuples and 7-tuples occurrence studies suggest that most of the DNA sequences follow the general shape of the compound Poisson distribution. It is also noted that the $\chi^2$-square test indicated that some of the sequences follow this distribution with a reasonable level of goodness of fit. The compositional segmentation study fits quite well using this new family of distribution functions. Furthermore, the absolute values of the relative frequency come out naturally from the linguistic model without ambiguity. It is suggesting that DNA sequences are not random sequences and they could possibly have subsequence structures.

Keywords: DNA segmentation, Statistical linguistic, Compound Poisson distribution, Jensen-Shannon divergence measure

PACS numbers: 87.10.+e, 87.14.Gg

1 Introduction

In recent years, the subject of bioinformatics has emerged as an active research subject in biology and other fields such as physics. Researchers are beginning to search for DNA words [1,2] and build up dictionaries for genomes
In doing so, people are more willing to regard information stored in DNA sequences as a natural language from nature. A lot of these activities are indeed to employ statistical methods to study DNA sequences. In an early attempt, researchers [4] used the Zipf’s law [5] to study the statistical features that are embedded in DNA sequences. Other researchers [8] subsequently used different distributions to fit the rank of the word distributions in DNA sequences and obtained better fit than the original Zipf plot. The Zipf’s law was first proposed in 1932 when George Zipf made an empirical observation on some statistical regularities of human writings which has become the most prominent statement of statistical linguistic. In his original work, Zipf found that if the number of different words in a given text were arranged in the order of their frequency of usage, there would be an approximate mathematical relation between the frequency of occurrence of each word and its rank in the list of all the words used in the text that were ordered by decreasing frequency. He later pointed out that similar relations also hold in other contexts [6, 7].

Let us associate a particular word by an index \( r \) equal to its rank, and by \( f(r) \) the normalized frequency of occurrence of that word, i.e., the number of times it appears in the text divided by the total number of words \( N \). Zipf’s law states that there is an approximate relation between \( f(r) \) and \( r \)

\[
f(r) = \frac{A}{r^\alpha},
\]

where \( \alpha (>1) \) and \( A \) are constants. The above mathematical relation was used [4] to study the statistical features of DNA sequences where similar scaling behavior was found. It was however noted that for sequences composed of primarily coding regions, the data were well fitted by a logarithmic function [8]. And just like in the case of linguistic, the Zipf’s law could only account for a limited zone of the rank variable.

In the early days of quantitative linguistics, researchers, notably Yule [10] had suggested that the mathematical relation (1) proposed by Zipf was unsatisfactory. He conjectured that the correct distribution for word frequencies would be a compound Poisson model. However, there is no fitting of any mathematical distribution law to the extensive data in his book. Good [11] later proposed to overcome Yule’s objection by introducing a convergence factor into the Riemann distribution which gives

\[
f(r) = Ar^{-\alpha} \theta^r,
\]

where \( r \geq 1, 0 < \theta < 1, \alpha > 0 \) and \( A \) is the normalization constant in terms
of $\theta$ and $\alpha$. Neither Good nor any other authors have fitted (2) to any real
data except for $\theta$ very close to one. One should also note that the primary
reason to introduce $\theta$ was to achieve convergence and secondary to improve
the fit. In [10], Good also proposed a distribution function to fit two sets
of data but were rather poor for large values of $r$. Researchers in the field
have also introduced other distribution functions to fit word frequencies.
However, as pointed out by Herdan [11], the word frequency distribution
functions are characterized by the properties of both combinability and di-
visibility without altering the essential mathematical characteristics of the
distribution function. The only distribution functions have these two prop-
erties are of the compound Poisson type. With this as the starting point,
Sichel [12] introduced a new family of compound Poisson distribution func-
tions to fit word frequencies. He [13] also used this family of distribution
functions to fit sentence-length, which was first considered by Yule [10]. The
fit in both cases were encouraging.

A natural question to ask is whether the quantitative studies made in
linguistics can be carried out in a similar fashion in DNA sequences. In
particular, we would like to know if the compound Poisson distribution
functions introduced in the study of quantitative linguistics are universal, in
the sense that they can be used to study human designed languages such as
the languages we use everyday as well as the language used by nature—the
information stored in DNA sequences. We will answer the above question by
carrying out quantitative studies in DNA sequences using these compound
Poisson distribution functions. In section II, we give a brief review of the
family of compound Poisson distribution function used in this paper, which
was first introduced by Sichel. In section III, we use this family of Poisson
distribution functions to study the statistical features of the word frequencies
in DNA sequences. Section IV is a statistical study of the sentence-length
in DNA sequences. Section V is the discussion and summary.

2 The Mathematical Model

In this section, we give a brief introduction of the mathematical model that
we use throughout this paper. We follow mainly the discussion by Sichel [8].

Let the total vocabulary that an author uses in his writing consist of
$V$ distinct words. For each word in the vocabulary $V$, there is a long-term
probability of occurrence $\pi_1, \pi_2, \ldots, \pi_V$ where $\pi_1(\pi_V)$ refers to the word with
The lowest and highest probability respectively. Theoretically, we have

\[ 0 < \pi_i < 1 ; \quad \sum_i \pi_i = 1 . \tag{3} \]

The probability of a specific word to appear \( r \) times in a total word count of \( N \) tokens is given by,

\[ \phi(r|N) = \binom{N}{r} \int_{0}^{1} \pi^r (1 - \pi)^{N-r} \psi(\pi) d\pi . \tag{4} \]

Since all the \( \pi_i \)'s are small, we may replace the binomial by the Poisson distribution function. We can then write \( \lambda = N \pi \) and Eq.(2) becomes

\[ \phi(r|N) = \frac{1}{r!} \int_{0}^{1} e^{-N \pi} (N \pi)^r \psi(\pi) d\pi = \frac{1}{r!} \int_{0}^{N} e^{-\lambda} \lambda^r f(\lambda) d\lambda . \tag{3} \]

For mathematical convenience, one can substitute \( N \) by infinity in the second integral in Eq.(3) since the latter is negligibly small between \( N \) and infinity.

The choice of the mixing distribution \( \psi(\pi) \), or \( f(\lambda) \), is crucial. A set of distribution functions was first suggested in [7]. Later, Sichel expressed Good’s mixing distribution function as

\[ f(\lambda) = \frac{1}{2} \left( \frac{2(1 - \theta)^{1/2} / \alpha \theta}{K_\gamma(\alpha(1 - \theta)^{1/2})} \right)^\gamma \exp\left\{ -\left( \frac{1}{\theta} - 1 \right) \lambda - \frac{\alpha^2 \theta}{4 \lambda} \right\} , \tag{4} \]

where \( -\infty < \gamma < \infty, 0 < \theta < 1 \) and \( \alpha > 0 \) are constants and \( K_\gamma \) is the modified Bessel function of the second kind of order \( \gamma \). In particular, if \( \gamma = -\frac{1}{2} \), \( f(\lambda) \) will become the so-called inverse Gaussian distribution function, which has applications in many different areas [12]. Substituting Eq.(4) into Eq.(3) and perform a Bessel function integration, one will obtain the corresponding compound Poisson distribution function

\[ \phi(r) = \frac{(1 - \theta)^{1/2} \gamma}{K_\gamma(\alpha (1 - \theta)^{1/2})} \frac{(\alpha \theta / 2)^r}{r!} K_{r+\gamma}(\alpha) , \tag{5} \]

where \( r \geq 0 \). This three parameter family of discrete distribution functions is extremely powerful. A number of known distribution functions such as the Poisson, negative binomial, geometric, Yule, Good and Riemann distribution functions are all special or limiting forms of Eq.(5). If the parameter \( \gamma \) is made negative in Eq.(5), an entirely new set of discrete distribution functions is generated.
In general, the parameter $\alpha$ characterizes the frequency behavior for low values of $r$, whereas $\theta$ influences the tail and $\gamma$ is important for the entire sweep of the distribution function. For the calculation of the individual probabilities in Eq.(5), Sichel derived a very useful formula based on the following Bessel recursion relation

$$K_{\nu+1}(z) = \frac{2\nu}{z}K_{\nu}(z) + K_{\nu-1}(z).$$  \hspace{1cm} (6)

Using this recursion relation, one can easily obtain the following recursion relation for $\phi(r)$

$$\phi(r) = \theta\left(\frac{r + \gamma - 1}{r}\right)\phi(r - 1) + \frac{(\alpha \theta)^2}{4r(r - 1)}\phi(r - 2).$$  \hspace{1cm} (7)

Thus, as one obtains the first two probabilities $\phi(0)$ and $\phi(1)$ from Eq.(5), it is easy to calculate all other probabilities from Eq.(7). It is clear that the word frequency distribution functions start at $r = 1$. A zero truncation of the function in Eq.(5) yields

$$\phi(r) = \left[((1 - \theta)^{1/2})^{-\gamma}K_\gamma(\alpha(1 - \theta)^{1/2}) - K_\gamma(\alpha)]^{-1} \frac{(\alpha \theta / 2)^r}{r!}K_{r+\gamma}(\alpha)\right]^{r \geq 0. \hspace{1cm} (8)}$$

for $r \geq 0$. This is the Sichel model for word frequencies in its most general form.

### 3 Word frequencies in DNA sequences

In this section, we use the Sichel model to study the word frequencies in DNA sequences. In order to adapt the Sichel model to the quantitative study of DNA sequences, the concept of word must first be defined. In the case of coding regions, the words are the 64 3-tuples which code for the amino acids, AAA, AAT, etc. For noncoding regions, the words are however unknown. Therefore, it is better to consider the word length $n$ as a free parameter and perform analyses for $n$ from say, 3 to 8 as was done in [1]. The number of $n$-tuples will be $4^n$. Thus, for $n = 6$, the number of the 6-tuples will be 4096. To obtain the word frequency for each $n$-tuple, we will start from the first base pair of the DNA sequence that is under study and progressively shift by 1 base with a window of length $n$. For a DNA sequence containing $L$ base pairs, the total number of words will be $L - n + 1$. 
To avoid any bias in DNA sequence selection, we performed analysis of 13 sequences of eukaryotes mammals (GenBank accession codes are HSMMH-CAPG, HUMGHCSA, HUMHBB, HUMHDABCD, HUMHPRTB, HUMMMDBC, HUNNEUROF, HUMRETBLAS, HUMTACDVO, HUMVIT-DBP, MMBGCXD, MUSTCRA, RATICYG), 3 sequences of invertebrate (CEC07A9, CELTWIMUSC, DROABDB), the yeast chromosome III sequence (SCCHRIII), 10 sequences of eukaryotic viruses (ASFV55KB, HE1CG, HEIHCMVGC, HEVVTXX, HS1ULR, HSECOMGEN, HSGEND, IH1CG, VACCV, VVCGAA), 7 sequences of bacteria (BSGENR, ECO110K, ECOHU47, ECOUW82, ECOUW85, ECOUW87, ECOUW89), and 2 sequences of phage (LAMCG, MLCGA).

In Sichel’s model, \( \phi(r) \) is the fraction of the total number of words with a frequency \( r \) of appearance in the article under study. For example, \( \phi(1) \) is the fraction of words among the total number of words used that appear once in the article. To implement our analysis using the Sichel model, we first record the total number \( (N) \) of words \( (n\text{-tuples}) \) among the total number of possible words that are used in the DNA sequence under study. For each frequency of appearance, we record the total number \( (N(r)) \) of words \( (n\text{-tuples}) \) that have such a frequency \( r \) of appearance in that DNA sequence. We divide that number by \( N \) and call it \( \phi(r) \) and then plot \( \phi(r) \) against \( r \). \( \chi^2 \) test is used to obtain the best fit of the data against \( \phi(r) \) in Eq.(5).

Table I is the result of the \( \chi^2 \) test of the DNA sequences chosen from different groups of species using the Sichel model. For each of the DNA sequences, we give the result for the 6-tuples and 7-tuples. We give the best values for \( \gamma, \alpha \) and \( \theta \) in each case, which is determined by minimizing the \( \chi^2 \) value,

\[
\chi^2 = \sum_i \frac{(N_i - n_i)^2}{n_i}
\]

where \( N_i \)'s are the observed values and \( n_i \)'s are the theoretical values. It is interesting to note that in the case of the 7-tuples, most of the DNA sequences can be fit using an inverse Gaussian distribution (i.e. \( \gamma = -\frac{1}{2} \)). Fig.1 is an illustration of the \( \chi^2 \) test of some of the DNA sequences chosen from Table I. We choose one sequence from each group of DNA sequences that we studied. In most cases, \( \phi(r) \) can be fit reasonably well.
4 Sentence Length in DNA sequences

To study the sentence length of DNA sequences, one needs to define what a sentence is. In linguistics, it is easy to identify what a sentence is. In the case of DNA sequences, what exactly a sentence should be is unknown. One can, for example, identify the word clusters in [3] as DNA sentences. In our study here, we proceed with the following strategy. We divide a DNA sequence into segments in such a way as to maximize the compositional divergence between the resulting DNA domains until a stopping criterion is reached. We then identify each segment as a sentence in the DNA sequence. In our analysis, we use the segmentation method which employs the Jensen-Shannon divergence measure [15] to study the bacterial DNA sequence, Eco110K, as an example. We should remind our reader that one can use any other segmentation methods to study the sentence length in DNA sequences. The number of segments ($N(r)$) of length ($r$) is then recorded. We again divide $N(r)$ by the total number of segments to obtain the relative frequency distribution of segments for $r$ and plot it against $r$, which is shown in Fig. 2 [13]. In Fig. 2, we present the results for $d_r = 0.55, 0.60$ and $0.65$ which correspond to significance level about 76%, 79% and 81% respectively. All of the chosen $d_r$s follow an inverse Gaussian distribution. Table II is the result of the $\chi^2$ test of the Eco110K DNA sequences using the Sichel model.

5 Summary and Discussion

In the above, we have introduced a family of compound Poisson distribution functions to the statistical study of DNA sequences. We have used the compound Poisson distribution functions to fit both the $n$-tuple and segment distributions of the DNA sequences. In both cases, we have obtained reasonable fits, both the shape and the normalization. More interestingly, the relative frequency distribution of $n$-tuples and the compositional segmentation study follow the inverse Gaussian distribution among different types of species and the normalization of $\phi(r)$ of both the word frequencies and compositional segmentation comes out naturally from the linguistic model without ambiguity.

In the early linguistics feature studies [4] of DNA sequences, people have plotted the relative occurrence of DNA words against rank and found power law behaviors. It was later shown that [6] the Zipf distribution indeed fits
very poorly in many cases and the Yule (eq.(2)) distribution can give a much better fit. However, as we have mentioned earlier, the Yule distribution was suggested primarily for the reason of convergence and most of the fits are made when $\theta$ approaches one. This is also true in the case of [6] though the fits are better than that of [4]. On the other hand, the distribution suggested by Sichel has a much rigorous base. It is based on the fact that only compound Poisson distribution functions have the properties that characterize the word frequency distribution function in linguistics and has its rigorous derivation. This model incorporates the characteristic features of linguistics and thus a fit using Sichel’s model should be of more theoretical interest. We have indeed shown that one can obtain reasonably good fits using this model.

As mentioned in the above section, one would want to study the compositional segmentation by using segmentation methods other than the one we used here. One of such methods is suggested in [17]. In [17], new different stopping criteria for segmenting DNA sequences are introduced. The size of the segments are plotted against the rank and the result indicates that the Zipf plot is different for different segmentation methods. It would be interesting to see how the Sichel model can fit for different segmentation methods. This would then establish the validity of using the Sichel model in the linguistic study of DNA sequences. It would be inappropriate to conclude that our results imply that DNA sequences have any resemblance to a natural language. However, it does suggest that DNA sequences are not random sequences and they could possibly have subsequence structures [19].

6 Acknowledgment

The work of K.L. Ng is support by the ROC NSC grant NSC 91-2626-E275-001, and the Academia Sinica short term visiting program.
References

[†] Correspondence author: albert@mail.ltc.edu.tw, address after August 1, 2003, Department of Bioinformatics, Taichung Healthcare and Management University No. 500, Lioufeng Road, Wufeng Shiang, Taichung, Taiwan 413, R.O.C.

[*] Electronic address: spli@phys.sinica.edu.tw

[1] M. Ortuno et.al., Europhys. Lett. 57, 759 (2002).
[2] P. Chaudhuri and S. Das, J. Biosci. 27, 1 (2002).
[3] H.J. Bussemaker et.al., PNAS, 97(18), 10096 (2000).
[4] R.N. Mantegna et.al., Phys. Rev. Lett. 73, 3169 (1994).
[5] G.K. Zipf, Selected Studies of the Principle of Relative Frequency in Language, (Harvard University Press, Cambridge, Massachusetts, 1932).
[6] G.K. Zipf, Human Behavior and the Principle of least Effort, (Addison-Wesley, 1949).
[7] G.K. Zipf, The Psycho-Biology of language, An introduction to Dynamic Philology, (MIT Press, Cambridge, Massachusetts, 1965).
[8] M.Yu. Borodovsky and S.M. Gusein-Zade, J. Biomolecular Structure and Dynamics 6, 1001 (1989).
[9] G.U. Yule, A Statistical Study of Vocabulary, (Cambridge University Press, Cambridge, England, 1944).
[10] I.J. Good, Biometrika 40, 237 (1953).
[11] G. Herdan, Applied Statistics, 10, 65 (1961).
[12] H.S. Sichel, J. American Statistical Association 70, 542 (1975).
[13] H.S. Sichel, J.R. Statist. Soc. A, 137, 25 (1974).
[14] G.U. Yule, Biometrika 30, 363 (1939).
[15] J. Lin, IEEE Trans. Info. Theor. 37, 145, (1991). P. Bernaola-Galvan, R. Roman-Roldan and J.L. Oliver, Phys. Rev. E 53, 5181 (1996). I. Grosse et al., Phys. Rev. E 65, 041905 (2002).

[16] V. Seshadri, The inverse Gaussian distribution : statistical theory and applications, (New York : Springer Verlag, 1999).

[17] K.L. Ng, M.C. Chung, and S.P. Li, (to appear in Physica A, 2003, Proceedings for StatPhys-Taiwan 2002).

[18] W. Li, Phys. Rev. Lett. 86, 5815 (2001).

[19] W. Li, Complexity 3, 33 (1977).
Table 1. Summary of the frequency distributions for 6-tuples and 7-tuples

| Species     | GenBankcode | 6-tuples | 7-tuples |
|-------------|-------------|----------|----------|
|             | $\chi^2$    | $\gamma$ | $\alpha$ | $\theta$ | $\gamma$ | $\alpha$ | $\theta$ |
| Mammal      |             |          |          |          |          |          |          |
| HSMHCAPG    | 1.7         | 0.4      | 0.91     | -0.5     | 3.2      | 0.91     |
| HUMGHCSA    | 0.48        | 1.3      | 0.3      | 0.93     | -0.5     | 3.5      | 0.91     |
| HUMHBB      | 1.1         | 0.4      | 0.95     | -0.5     | 3.9      | 0.91     |
| HUMHDABCD   | 1.3         | 2.2      | 0.91     | -0.5     | 2.5      | 0.91     |
| HUMHPRTB    | 1.3         | 0.4      | 0.91     | -0.5     | 2.8      | 0.91     |
| HUMMMDDBC   | 0.5         | 3.9      | 0.95     | -0.5     | 2.4      | 0.93     |
| HUMNEUROF   | 0.9         | 0.6      | 0.97     | 0.3      | 2.3      | 0.91     |
| HUMRETBLAS  | 1.1         | 0.1      | 0.93     | 0.5      | 2.2      | 0.93     |
| HUMTCRADCY | 0.9         | 1.3      | 0.97     | 0.3      | 2.5      | 0.91     |
| HUMVITDBP   | 1.1         | 0.4      | 0.93     | -0.5     | 3.1      | 0.91     |
| MMBGCXD     | 1.1         | 0.4      | 0.93     | -0.5     | 3.3      | 0.91     |
| MUSTCRA     | 1.3         | 0.4      | 0.95     | -0.5     | 4.4      | 0.91     |
| RATCRYG     | 1.3         | 0.4      | 0.91     | -0.5     | 2.7      | 0.91     |
| Invertebrate| CEC07A9     | 0.5      | 4.5      | 0.93     | -0.5     | 2.5      | 0.91     |
| CELTWIMUSC  | 0.62        | 0.5      | 3.9      | 0.93     | -0.7     | 2.5      | 0.91     |
| DROAABDB    | 1.5         | 4.5      | 0.91     | -0.5     | 3.4      | 0.91     |
| Yeast ChrIII| SCCHRIII    | 2.3      | 2.1      | 0.97     | 0.5      | 4.5      | 0.95     |
| Virus       | ASVF55KB    | 0.5      | 4.5      | 0.91     | -0.7     | 2.5      | 0.91     |
| HE1CG       | 0.5         | 4.5      | 0.97     | -0.5     | 3.2      | 0.97     |
| HEHCMVCG    | 2.9         | 2.5      | 0.95     | 0.5      | 4.5      | 0.93     |
| HEVZVXX     | 3.1         | 2.5      | 0.91     | -0.5     | 4.5      | 0.93     |
| HS1ULR      | 0.5         | 3.8      | 0.97     | -0.5     | 3.1      | 0.95     |
| HSECOMGEN   | 2.5         | 4.5      | 0.93     | 0.5      | 4.0      | 0.91     |
| HSGEND      | 0.9         | 0.3      | 0.97     | 0.7      | 0.1      | 0.91     |
| HICG        | 2.5         | 0.1      | 0.93     | -0.5     | 4.5      | 0.95     |
| VACCG       | 1.3         | 1.0      | 0.97     | -0.5     | 4.2      | 0.97     |
| VVCAG       | 1.3         | 0.4      | 0.97     | 1.3      | 0.8      | 0.97     |
| Bacteria    | BSGENR      | 0.18     | 1.5      | 4.5      | 0.93     | -0.5     | 4.1      | 0.91     |
| ECO110K     | 0.24        | 2.7      | 0.2      | 0.91     | -0.5     | 4.5      | 0.91     |
| ECOHU47     | 0.26        | 1.5      | 4.5      | 0.91     | -0.5     | 3.6      | 0.91     |
| ECOUW82     | 2.5         | 2.8      | 0.93     | 0.5      | 3.2      | 0.91     |
| ECOUW85     | 2.1         | 2.5      | 0.91     | -0.5     | 4.1      | 0.91     |
| ECOUW87     | 2.3         | 2.5      | 0.91     | 0.5      | 4.4      | 0.91     |
| ECOUW89     | 3.1         | 0.4      | 0.93     | 0.5      | 4.5      | 0.91     |
Table 1. Summary of the frequency distributions for 6-tuples and 7-tuples

| Species     | GenBankcode | $P^{2}$ | $\gamma$ | $\alpha$ | $\theta$ | $\gamma$ | $\alpha$ | $\theta$ |
|-------------|-------------|---------|----------|----------|----------|----------|----------|----------|
| Bacteriophage | LAMCG       | 0.5     | 4.5      | 0.91     | -0.7     | 2.5      | 0.91     |
|             | MLCGA       | 1.1     | 0.2      | 0.93     | -0.5     | 2.8      | 0.91     |

Table 2. The frequency distribution for segmentation

| $d_r$ | $\gamma$ | $\alpha$ | $\theta$ |
|-------|----------|----------|----------|
| 0.50  | -0.5     | 4.2      | 0.97     |
| 0.60  | -0.5     | 4.1      | 0.99     |
| 0.65  | -0.5     | 4.5      | 0.99     |
Fig 1a. The $\phi(\tau)$ vs $\tau$ plot for the mammal sequence HUMHDABCD, where $\gamma=1.30$, $\alpha=2.20$ and $\theta=0.91$ and $\gamma=-0.5$, $\alpha=2.50$ and $\theta=0.91$ for 6 -tuples and 7 -tuples word length cases respectively.
Fig 1b. The $\Phi(r)$ vs $r$ plot for the invertebrate sequence CELTWIMUSC, where $\gamma=0.50$, $\alpha=3.90$ and $\theta=0.93$ and $\gamma=-0.7$, $\alpha=2.50$ and $\theta=0.91$ for 6-tuples and 7-tuples word length cases respectively.
Fig 1c. The $\phi(r)$ vs $r$ plot for the yeast chromosome III sequence, where $\gamma=2.30$, $\alpha=2.10$ and $\theta=0.97$ and $\gamma=0.5$, $\alpha=4.50$ and $\theta=0.95$ for 6-tuples and 7-tuples word length cases respectively.
Fig 1d. The $\Phi(r)$ vs $r$ plot for the virus sequence HS1ULR, where $\gamma=0.50$, $\alpha=3.80$ and $\theta=0.97$ and $\gamma=-0.5$, $\alpha=3.10$ and $\theta=0.95$ for 6-tuples and 7-tuples word length cases respectively.
Fig 1e. The $\Phi(r)$ vs $r$ plot for the bacteria sequence BSGENR, where $\gamma = 1.50$, $\alpha = 4.50$ and $\theta = 0.93$ and $\gamma = -0.5$, $\alpha = 4.10$ and $\theta = 0.91$ for 6-tuples and 7-tuples word length cases respectively.
Fig 1f. The \( \Phi(t) \) vs \( t \) plot for the phage sequence MLCGA, where \( \gamma=1.10, \alpha=0.20 \) and \( \theta=0.93 \) and \( \gamma=-0.5, \alpha=2.80 \) and \( \theta=0.91 \) for 6-tuples and 7-tuples word length cases respectively.
Fig. 2(a)

Fig. 2(b)

Fig. 2(c)

Fig. 2. The $\Phi(r)$ vs $r$ plot for the (a) $dr = 0.55$, (b) $dr = 0.60$ and (c) $dr = 0.65$ cases.