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Short segmental duplication: parsimony in growth of microbial genomes

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Short Segmental Duplication: Parsimony in Growth of Microbial Genomes

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Abstract

We compare the distributions of occurrence frequencies of oligonucleotides two to ten bases long (2 to 10-mers) in microbial complete genomes with corresponding distributions obtained from random sequences and find that the genomic distributions are uniformly many times wider in a universal manner, that is, the same for all microbial complete genomes. The difference increases with decreasing word length, with the genomic spectral width about 40 times wider for 2-mers. We show that the observed genomic properties are characteristic of sequences generated in a simple growth model, where a very short initial random sequence (less than 1 kb) grows mainly by maximally stochastic duplication of short segments (of about 25 b). We discuss a number of issues related to the findings and the model, including the proposition that life began in an RNA world before the birth of proteins.

Key words: Complete microbial genomes - Oligonucleotide frequency - Statistical analysis - Genome growth model - Short segmental duplication - Evolution - RNA world

Introduction

There is a long history of textual analysis of DNA sequences and, with the success of the Human Genome Project, such activities have intensified with time. This paper concerns a type of analysis that, as far as the authors are aware, has not been reported in the literature before. It is about the anomalous spectral *widths* of the distributions of occurrence frequencies of short oligonucleotides in complete microbial genomes. For very short oligonucleotides these widths are astonishingly large compared to what are expected of random sequences. Detailed study of such widths of all complete microbial genomes reveals a universality concerning them, which in turn leads to a genome growth model that has many interesting implications.

It is a general rule of statistics that the larger the system the more sharply defined its average properties. When very large numbers of apples are randomly dropped into barrels, the distribution of apples in the barrels is governed by the Poisson distribution. If 1,024 apples were dropped into sixty-four barrels, there is a 5% chance that one of the barrels would have less than 8 or more than 24 apples. If 1 million apples were dropped into the barrels the chances that the number of apples received by any barrel falling outside the range of 14,600 to 16,600 would be exceedingly small, and there is a less than one in 10^{980} (10^{830} , respectively) chance that one barrel would get as few (many) as 8,000 (24,000) apples.

Microbial genomes are seemingly random systems when viewed as texts of the four bases represented by A, C, G and T. To count the number of times each of the sixty-four trinucleotides, or 3-mers, occur in a genome-as-text is similar to counting the number of apples after they have been dropped into barrels. The genome of the bacterium *Treponema pallidum*, the causative agent of syphilis, is about 1M base pairs long and has almost even base composition [1]. In an astonishing departure from what is expected of a system of its size, the genome has six 3-mers (CGC, GCG, AAA, TTT, GCA, TGC) occurring more than 24,000 times per 1 Mb and two (CTA, TAG) less than 8,000 times. Scrambling the genome sequence thoroughly restores it to a random sequence obeying Poisson distribution and the large-system rule.

T. pallidum is not exceptional in disobeying the large-system rule. For the twenty-five complete microbial “Class A” genomes whose combine probability p for AT or CG content is 0.46 to 0.55, the observed standard deviation (std) of the distribution of the frequency of occurrence of 3-mers

Table 1: For given k 's, standard deviation of k -distributions from $p \approx 0.5$ sequences: for the genome *T. pallidum*; averaged over 25 Class A genomes; for a $p = 0.5$ random sequence; for a $p = 0.5$ model sequence (see text). All stds are normalized to correspond to a sequence with $p = 0.5$ (see Methods).

k	<i>T. pallidum</i>	Class A genomes	Random	Model
2	8227	10610±2107	250	8207
3	3977	4379±707	125	3415
4	1384	1490±232	62.5	1202
5	434	468±72.5	31.2	402
6	129	141±22.3	15.6	134
7	37.5	41.6±7.0	7.8	45.3
8	11.0	12.3±2.3	3.9	15.9
9	3.4	3.76±0.85	1.9	5.9
10	1.3	1.29±0.34	1.0	2.3

per 1 Mb (hereafter called 3-distribution) is $4,080 \pm 630$ around the mean of 15,625. This is about 32 times the std of a Poisson distribution of the same mean that a random sequence would yield.

Nor is the statistics of 3-mers special in genomes. In Table 1, column 3 gives the std of the k -distribution, $k = 2$ to 10, averaged over the twenty-five Class A genomic sequences and column 4 gives the std for a Poisson distribution with mean value $10^6/4^k$. The genomic stds approach those of a random sequence when k increases beyond 10. For k less than 10, the Poisson std increases as 2^{-k} with decreasing k whereas the genomic std increases at a much higher rate, such that already at $k=8$ the genomic std is many times greater than the Poisson std. Because the variance in the genomic std is typically much smaller than the difference between the genomic and Poisson stds, the genomic k -distribution differs from the Poisson distribution in a universal fashion. Hence we shall speak of a universal (Class A) genome.

The base composition of a genome has a conspicuous effect on its k -distributions. The black curve in Figure 1 shows 6-distributions of three representative genomes: (A) *T. pallidum* with $p \approx 0.5$; (B) *Chlamydia muridarum* [2] with $p \approx 0.6$; (C) *Methanococcus jannaschii* [3] with $p \approx 0.7$. For comparison the cyan curves in the figure show 6-distributions of random sequences with $p = 0.5, 0.6$ and 0.7 , respectively. The k -distribution of a random sequence is composed of $k+1$ Poisson distributions with mean frequencies $10^6 2^{-k} p^m (1-p)^{k-m}$, $m=0$ to k , which coalesce into a single Poisson distribution when p is close to 0.5. In contrast, narrow sharp spikes are completely absent in the 6-distributions for the microbial genomes.

Microbial genomes are large systems with small-system statistics

When examined with a length scale that is short enough, microbial genomes have the statistics

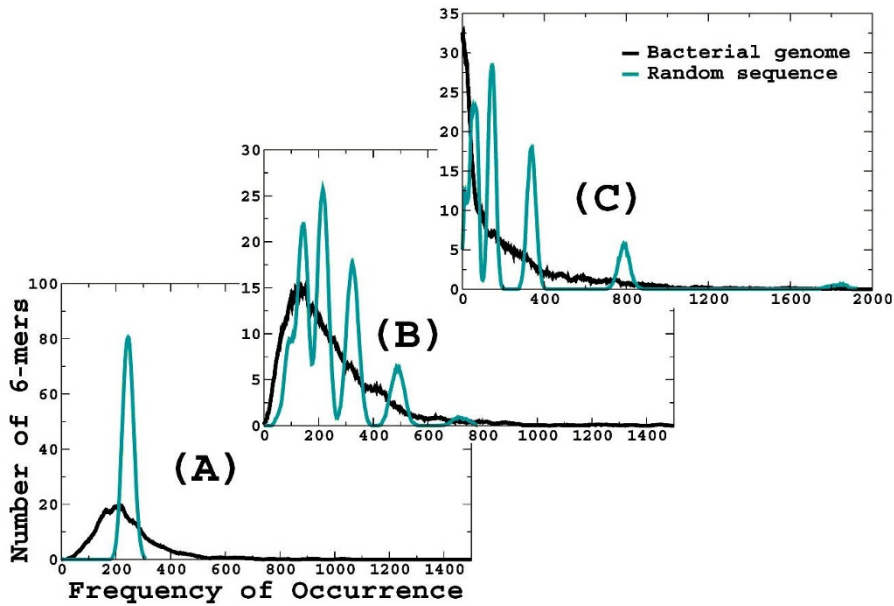


Figure 1: Comparison of 6-distributions of genomes (black) and random sequences (cyan), with abscissa giving the frequency of occurrences of 6-mers and ordinates showing the number of 6-mers having a given frequency: (A) *T. pallidum* genome and a random sequence with $p = 0.5$; (B) *C. muridarum* genome and a random sequence with $p = 0.6$; (C) *M. jannaschii* genome and a random sequence with $p = 0.7$

of multiple replications of random genomes much smaller than itself. To see this, we define the “root-sequence length” L_r of the universal genome as the length of a random sequence that has a k -distribution with a mean to std ratio equal to that of the observed genomic ratio r . This implies that $L_r = 4^k r^2$. Because r has a strong k dependence, so does L_r . Its values for the various k 's are given in column 2 of Table 2. Column 3 gives almost identical results extracted from “Class C”, or $p \approx 0.7$, genomes (see Methods). It is seen that L_r is very short for the smaller k 's - of the order of 1 kb or less for $k \leq 3$ - and grows rapidly with k . When $k=10$ it is about half the length (normalized to 1 Mb) of the real genome.

Another way of understanding the meaning of L_r is the following. If for some k the root-sequence length of a genome of length L is L_r , then the k -distribution of the genome will be the same as that of a sequence obtained by replicating L/L_r times a random sequence of length L_r (so that that sequence and the genome have the same length). From Table 2 we see that, say, the 2-distribution of a (typical) genome of length 1 Mb has about the same width as that of a 2000-fold concatenate of a 500 b long random sequence, and the 6-distribution of the genome that of a 77-fold concatenate of a 13 kb long random sequence. All of this suggests that, depending on the length scale k with which it is examined, a microbial genome has the statistical characteristics of a replicate of a much shorter random sequence when $k < 10$.

Compared to a random sequence, a typical genome has very large numbers of both overrepresented and underrepresented oligonucleotides. For instance, the genome of *E. coli* [4] has 500 and 510 6-mers whose frequencies of occurrence are greater than 400 and less than 100 per 1 Mb, respectively, while a 1 Mb random sequence has none in either category. On the other hand, a 1 Mb sequence obtained by replicating 77 times a 13 kb (L_r for $k=6$) random sequence would have overrepresented and underrepresented 6-mers as numerous as those in *E. coli*. There are many known examples of individual oligonucleotide that exhibit extreme relative abundance. For 2-mers this was noted to be common and has genome-wide consistency [6]; 4- and 6-palindromes are almost always underrepresented in bacteriophages and are systematically underrepresented in bacteria where 4-cutting and/or 6-cutting restriction enzymes are common [5]; an 8-mer that appears as Chi sites, hotspots of homologous recombination, is highly overrepresented in *E. coli* [7]; in the human pathogens *Haemophilus influenzae* [8, 9] and *Neisseria* [10] there are 9- and 10-mers functioning as uptake signal sequences that are vastly overrepresented. The causes for these extreme cases are generally not known but generally such individual cases do not decisively determine the statistical properties of a genome.

What caused a genome to have k -distributions so much wider than those of a random sequence? Natural selection suggests itself as a prime explanatory candidate. For instance, the 64 frequencies of codons, 3-mers used by the genome to code proteins in genes, exhibit very wide distributions. Yet the occurrence frequency of codons is not a deciding factor of the 3-distribution of a genome. This is because: (a) The 3-distribution is read with a sliding window that moves one base at a time, while codons must be read by a sliding window that moves three bases at a time. (b) In a single

Table 2: Universal statistical lengths of microbial genomes. Genomes in Class A have $p \approx 0.5$ and those in Class C have $p \approx 0.7$.

k	L_r (kb)	
	Class A genomes	Class C genomes
2	0.65 ± 0.35	0.53 ± 0.30
3	1.0 ± 0.3	1.1 ± 0.6
4	1.9 ± 0.5	2.1 ± 1.1
5	4.7 ± 1.3	5.2 ± 2.5
6	13 ± 4	14 ± 6
7	37 ± 12	36 ± 17
8	110 ± 40	93 ± 44
9	300 ± 130	230 ± 110
10	640 ± 300	600 ± 240

strand of a microbial genome, typically about 80 to 85% of the sequence is coded, and the coded portion is about equally divided among positively and negatively oriented genes; this means that only about one in every seven 3-mers read by a sliding window over the whole genome is a codon. (c) This one-seventh contribution from codons is further reduced by the fact that the deviation from randomness in the 3-distribution caused by positively oriented genes is often mostly canceled by that caused by negatively oriented genes. This canceling effect is seen most clearly in the case of base composition in genomes: In most genomes, say, the A and T contents in coding regions may be quite different, but contributions to the difference from coding regions in the two opposite orientations usually cancel such that overall the A and T contents for the whole genome are always almost equal.

If unequal codon usage is not the dominating cause for the large width of 3-distribution, then it also cannot be the cause of the large widths of other k -distributions.

Model for early genome growth

The mechanism generating the large width of genomic k -distributions must still be part of natural selection - everything about evolution is, but it probably is not single mutation. We believe the age of the universe is not long enough for the combined actions of single mutation and natural selection to generate genomes with widths of k -distributions as wide as those reported here. Here we propose a biologically plausible model for the growth and evolution of a universal genome that can generate the observed statistical characteristics of genomic sequences. The model is very simple and consists of two phases. In the first phase the genome initially grows by unspecified means to a random sequence whose size is much smaller than the final size of the genome. In the second phase the genome grows by random segmental duplications possibly modulated by random single mutations. In this work a snapshot is taken of the model sequence shortly after it reaches a length of 1 Mb. The key aspect of the model is growth by segmental duplication, the most straightforward and biologically viable way for the universal genome to become what it appears to be - a large system that exhibits small-system statistical characteristics.

Growth by whole-genome duplication [11, 12, 13] coupled with mutation is ruled out because such a mode of growth yields genomes whose k -distributions have the incorrect k -dependence - their L_r vary with k too weakly. Indeed we found it comparatively easy to generate a sequence that could faithfully reproduce the genomic k -distribution for any given k , say $k = k'$, but not simultaneously

Table 3: Name, GenBank code, length and base composition of microbial complete genomes analyzed in the paper; p_{AT} is the combined probability of A and T in the genome, and p is the greater of p_{AT} and $1 - p_{AT}$. Top-half entries are the 25 Class A genomes with $0.46 \geq p \geq 0.55$ and the bottom-half are the 28 Class C genomes with $0.66 \geq p \geq 0.75$.

Code	Name	length (M bp)	p_{AT}	p
NC_000853	<i>Thermotoga maritima</i>	1.86	0.54	0.54
NC_000868	<i>Pyrococcus abyssi</i> 1.76		0.55	0.55
NC_000911	<i>Synechococcus</i> sp. PCC 6803	3.57	0.52	0.52
NC_000913	<i>Escherichia coli</i> K12	4.64	0.49	0.51
NC_000916	<i>Methanobacterium thermoautotrophicum</i>	1.75	0.50	0.50
NC_000917	<i>Archaeoglobus fulgidus</i>	2.18	0.51	0.51
NC_000919	<i>Treponema pallidum</i>	1.14	0.47	0.53
NC_002488	<i>Xylella fastidiosa</i> 9a5c	2.67	0.47	0.53
NC_002505	<i>Vibrio cholerae</i> chromosome 1	2.96	0.52	0.52
NC_002506	<i>Vibrio cholerae</i> chromosome 2	1.07	0.53	0.53
NC_002578	<i>Thermoplasma acidophilum</i>	1.56	0.54	0.54
NC_002655	<i>Escherichia coli</i> O157:H7 EDL933	5.52	0.50	0.50
NC_002695	<i>Escherichia coli</i> O157:H7	5.49	0.49	0.51
NC_003112	<i>Neisseria meningitidis</i> serogroup B strain MC58	2.27	0.48	0.52
NC_003116	<i>Neisseria meningitidis</i> serogroup A strain Z2491	2.18	0.48	0.52
NC_003143	<i>Yersinia pestis</i> strain CO92	4.65	0.52	0.52
NC_003197	<i>Salmonella typhimurium</i> LT2 LT2	4.86	0.48	0.52
NC_003198	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhi</i>	4.80	0.48	0.52
NC_003364	<i>Pyrobaculum aerophilum</i>	2.22	0.49	0.51
NC_003450	<i>Corynebacterium glutamicum</i> ATCC 13032	3.31	0.46	0.54
NC_004088	<i>Yersinia pestis</i> KIM	4.60	0.52	0.52
NC_004113	<i>Thermosynechococcus elongatus</i> BP-1	2.59	0.46	0.54
NC_004337	<i>Shigella flexneri</i> 2a str. 301	4.60	0.49	0.51
NC_004347	<i>Shewanella oneidensis</i> MR-1	4.96	0.54	0.54
NC_004431	<i>Escherichia coli</i> CFT073	5.23	0.50	0.50
NC_000908	<i>Mycoplasma genitalium</i>	0.580	0.68	0.68
NC_000909	<i>Methanococcus jannaschii</i>	1.66	0.69	0.69
NC_000962	<i>Mycobacterium tuberculosis</i>	4.41	0.34	0.66
NC_000963	<i>Rickettsia prowazekii</i> strain Madrid E	1.11	0.71	0.71
NC_001263	<i>Deinococcus radiopugans</i> R1 chromosome 1	2.64	0.33	0.67
NC_001264	<i>Deinococcus radiopugans</i> R1 chromosome 2	0.412	0.33	0.67
NC_001318	<i>Borrelia burgdorferi</i>	0.910	0.71	0.71
NC_002162	<i>Ureaplasma urealyticum</i>	0.751	0.75	0.75
NC_002163	<i>Campylobacter jejuni</i>	1.64	0.69	0.69
NC_002516	<i>Pseudomonas aeruginosa</i>	6.26	0.33	0.67
NC_002528	<i>Buchnera</i> sp. APS APS	0.640	0.74	0.74
NC_002607	<i>Halobacterium</i> sp. NRC-1	2.01	0.32	0.68
NC_002696	<i>Caulobacter crescentus</i>	4.01	0.33	0.67
NC_002745	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> N315	2.81	0.67	0.67
NC_002755	<i>Mycobacterium tuberculosis</i> CDC1551	4.40	0.34	0.66
NC_002758	<i>Staphylococcus aureus</i> strain Mu50	2.87	0.67	0.67
NC_002771	<i>Mycoplasma pulmonis</i>	0.963	0.73	0.73
NC_003030	<i>Clostridium acetobutylicum</i> ATCC824	3.94	0.69	0.69
NC_003103	<i>Rickettsia conorii</i> Malish 7	1.27	0.68	0.68
NC_003106	<i>Sulfolobus tokodaii</i>	2.69	0.67	0.67
NC_003295	<i>Ralstonia solanacearum</i>	3.71	0.33	0.67
NC_003296	<i>Ralstonia solanacearum</i>	2.09	0.33	0.67
NC_003366	<i>Clostridium perfringens</i>	3.03	0.71	0.71
NC_003454	<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> ATCC 25586	2.17	0.73	0.73
NC_003888	<i>Streptomyces coelicolor</i> A3(2)	8.66	0.28	0.72
NC_003923	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2	2.82	0.67	0.67
NC_004061	<i>Buchnera aphidicola</i> str. Sg	0.641	0.75	0.75
NC_004432	<i>Mycoplasma penetrans</i>	1.35	0.74	0.74

those of other k 's. Typically such a sequence had an L_r that has a k -dependence far too weak than required to fit genomic data and, consequently, k -distributions that are too narrow when $k < k'$ and too broad when $k > k'$. Ways to generate several such examples are given in the Methods. Generating a sequence that would emulate a real genome was a much more exacting task.

Results

After extensive experimentation, it was found that sequences having the statistical characteristics sought after could be generated by choosing: (i) the length (L_0) of the initial random sequence to be approximately 1 kb; (ii) the average length (\bar{l}) of the (randomly chosen) duplicated segments to be 25b with a spread (δ_l) of approximately 11b. It is emphasized that every step in the growth procedure is taken stochastically.

The stds of the k -distributions of a $p = 0.5$ model sequence thus generated are given in column five of Table 1. They agree quite well with the observed genomic values in columns 2 and 3 although their k -dependence is still slightly too weak. Histograms of k -distributions of *T. pallidum* (black) and the model sequence (orange), $k=2, 3$ and 4, are compared in Fig. 2. In all three cases, the histogram for a random sequence would be represented by a single narrow tower located at the mean

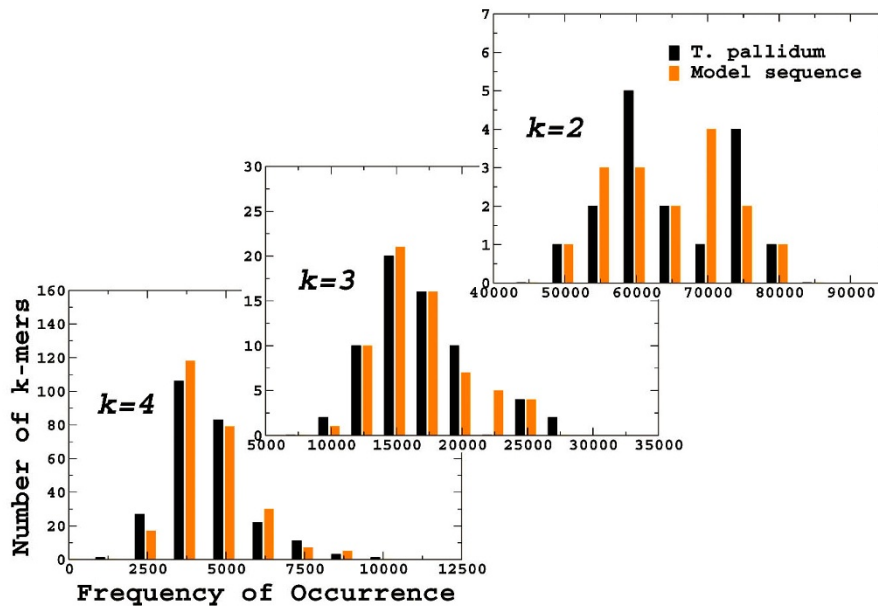


Figure 2: Histograms of k -distributions for genome of *T. pallidum* (black) and a $p = 0.5$ model sequence (orange), $k=2$ to 4, with abscissa indicating intervals of frequency of occurrence of k -mers and ordinates giving the number of k -mers falling within a given interval of frequency of occurrence. In each case the histogram of the k -distributions for a random sequence would be represented by a single tower located at the mean $10^6 4^{-k}$.

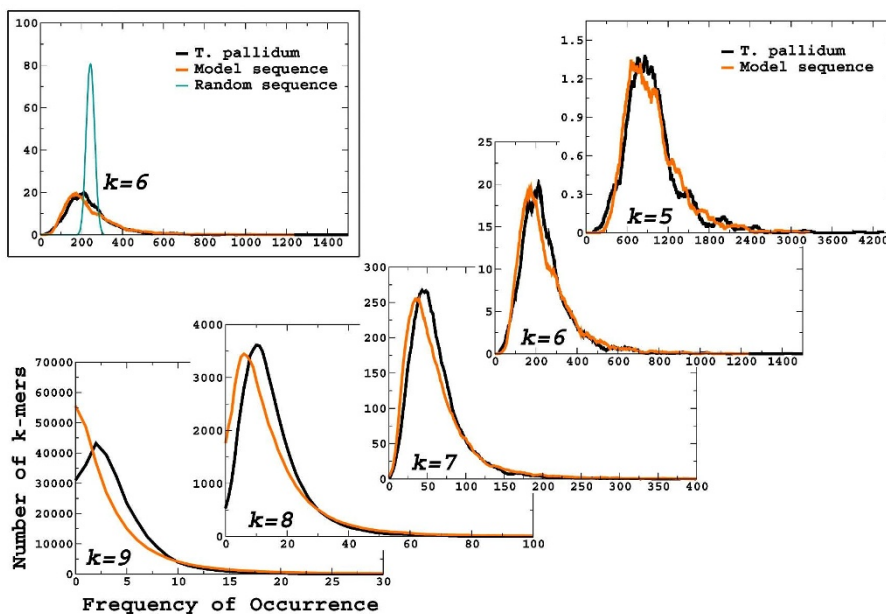


Figure 3: k -distributions for genome of *T. pallidum* (black) and a $p = 0.5$ model sequence (orange), $k = 5$ to 9. See legend of Fig. 1 for further detail. The cyan curve in the top-left panel is the 6-distribution for a $p = 0.5$ random sequence.

frequency. For $k=2$ and to a lesser extent $k=3$, the histograms for both genomic and model sequences display large fluctuations. The model sequence is not expected to exactly reproduce the counts of the genomic sequence. Indeed, generated stochastically, another model sequence (generated using the same parameters) will yield histograms that differ in detail from those shown in the $k=2$ and 3 panels of Fig. 2 but show patterns of fluctuation still similar to those exhibited by the genomic sequence and have stds very close to those given in column 5 of Table 1. Fig. 3 shows comparisons for $k=5$ to 9. The panel in the top-left corner gives the 6-distributions from *T. pallidum*, a random sequence (cyan) and the model sequence. In every case the model sequence succeeds in broadening out the narrow peaks that come with a random sequence and has k -distributions very similar to those obtained from *T. pallidum*.

The same growth model also can account for the k -distributions of genomes with p significantly different from 0.5. We demonstrate this by comparing the k -distributions for *M. jannaschii* (black), which has $p \approx 0.7$, with those of a $p = 0.7$ model sequence (orange) in Fig. 4 (histograms for $k=2, 3$ and 4) and Fig. 5 (distributions for $k=5$ to 9). The model sequence was generated using exactly the same procedure and parameters that generated the $p = 0.5$ model sequence (see Methods), except that the initial 1 kb random sequence has $p = 0.7$ rather than 0.5. The top-left panel of Fig. 5 shows that a k -distribution from a $p \neq 0.5$ random sequence (cyan), with its $k+1$ narrow peaks, is entirely distinct from a genomic distribution.

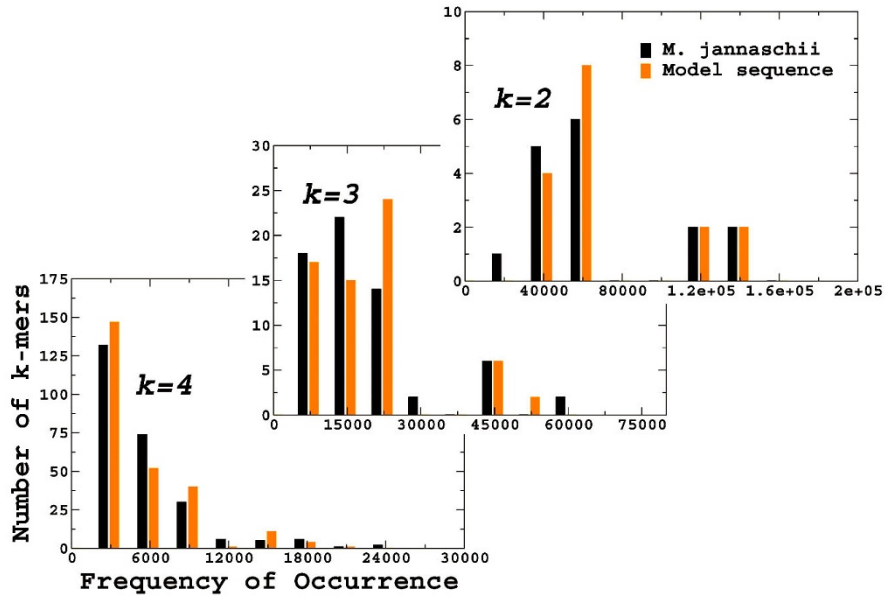


Figure 4: Histograms of k -distributions for genome of *M. jannaschii* (black) and a $p = 0.7$ model sequence (orange), $k=2$ to 4. See legend of Fig. 2 for further detail. The histograms for a random sequence would be given by $k + 1$ narrow towers.

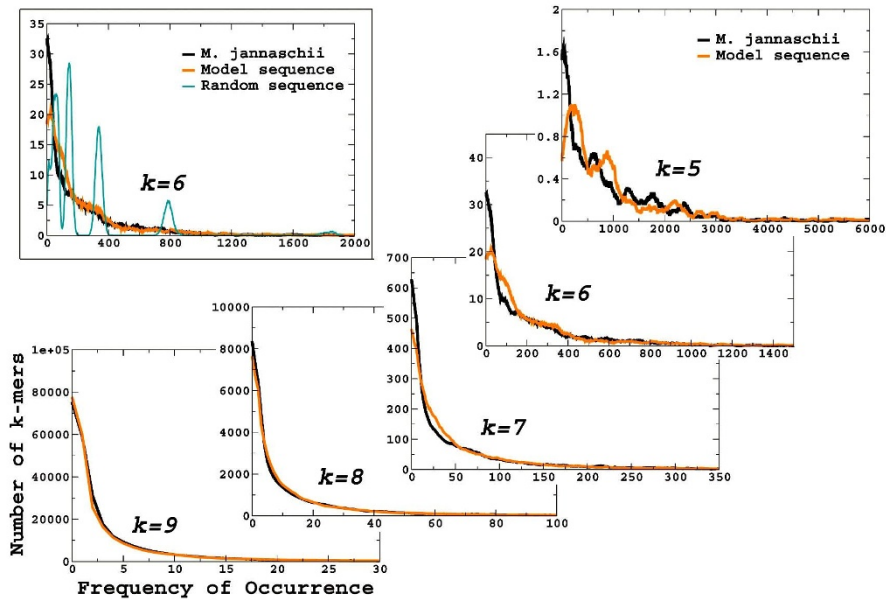


Figure 5: k -distributions for genome of *M. jannaschii* (black) and a $p = 0.7$ model sequence (orange), $k=5$ to 9. See legend of Fig. 1 for further detail. The cyan curve in the top-left panel is the 6-distribution for a $p = 0.7$ random sequence.

Because the L_r 's depend only on k but not on the length and base composition of the genomes (Table 2), they are universal - same for all microbial genomes - lengths. In other words, being a large system with small-system statistics is a universal characteristic of microbial genomes. To summarize, the genomes: (a) have essentially identical sets of L_r 's and (b) have k -distributions that are emulated by model sequences generated using identical parameters (but with predetermined p values).

The model sequences are parameter-sensitive. If L_0 was significantly longer than 1 kb then no good model sequence could be found. This is unsurprising because L_0 cannot be much longer than the shortest L_r in Table 2. If, with $L_0=1$ kb, either \bar{l} or δ_l was changed by more than 10% from their optimal values of 25b and 11b respectively then the agreement between the genomic and model sequences would worsen noticeably.

Discussion

First we wish to make clear that although we have showed in Figs. 2, 3, 4 and 5 results that agree quite well with genomic data for all $k= 2$ to 9, it is far easier than not for our model to generate results that are good for one particular k and not for the other k 's. For example, in our first application of the model in which a much longer average duplicated segment length than 25 b was used, only 6-distributions were well reproduced but not the others [14].

In the spirit of simplicity no (point) mutations were imposed on the model sequences whose properties are shown here. This is because mutations (not accompanied by selection) randomize a sequence whereas we are looking for a way to stochastically generate model sequences with less randomness than that of a random sequence. If the model sequence were allowed to have too many mutations then a compensating mechanism would have to be found to de-randomize the sequence. We think such a more elaborate model exists but, in favor of simplicity and clarity - because we believe the widening of k -distributions is caused by duplication - and at the risk of some loss of reality, prefer to present the results of our minimal model at this stage.

In reality a fixation (of a mutation) is always the combined effect of mutation and selection and is therefore not random. However it is very difficult to model selection without ending in a situation where the result one gets is more or less what one has specifically ordered for. For instance one can presuppose that individual 3-mers are favored differently in a specific way by natural selection, devise a growth model by single mutation (more insertion than deletion) based on that supposition and get 3-distributions that agree well with data. As noted above, such a model would not yield good results for other k -distributions. Good results for all k -distributions will be obtained only if selection rules were given for all k -mers. Thus one would end with having an extremely detailed model with a very large number of parameters to be determined. Leaving aside

the question of what selection rules are to be devised such a model has two serious drawbacks: (a) It would generate genomes that are not universal but only those belonging to one class of species, those with relative occurrence frequencies of k -mers conforming to the selection rules. (b) With any reasonable value we assign to the respective rates for mutation and segment duplication, it would take the single mutation model orders of magnitude longer in time than the duplication model to produce sequences with the observed widths for the k -distributions. This implies that natural selection would select duplication for growth and reserve mutation for fine-tuning the outcome of such growth.

In any case the model sequences as given here can tolerate about one mutation per two duplication events: twenty thousand mutation fixations reduces the std of the k -distributions of the Class A model sequence by 4% (for $k=2$) to 10% (for $k=10$).

In bacterial genomes, typically about 12% of genes represent recent duplication events - 12% in *T. pallidum* [1], 11.2% in *H. influenzae* [15] and 12.8% in *V. cholerae* [16]. The model sequences presented here do not explain the pattern of all such duplications, many of which would involve segments up to several kb long. Work is underway to extend the model to account for the genomic pattern of repeat sequences of all lengths.

The generic statistical textual properties of eukaryotic genomes have also been examined and findings will be reported elsewhere. So much now is believed to obtain: when the great difference in length between microbial and eukaryotic genomes is accounted for, what is said here of the statistical textual properties of microbial genomes should hold true *mutatis mutandis* for eukaryotic genomes.

To be sure there will be many textual aspects of the generic microbial genome that the growth model proposed here will not be able to account for in detail. Nevertheless we believe the evidence presented here is sufficiently strong to support the following proposition: the ancestors of microbial genomes underwent a fundamental transition in their growth and evolution shortly after they had reached a length of not more than 1 kbp and by which time they had acquired a rudimentary duplication machinery, thereafter grew (and diverged) mainly by stochastic duplication of short segments whose lengths averaged to about 25b. Assuming this model to be substantially correct we mention some of its implications for biology and evolution.

Our results suggest that the base composition of a genome was essentially inherited from an ancestor whose own composition had been determined either randomly or by some unknown cause by

the time of the transition to growth-by-duplication. Subsequent compositional changes caused the duplications and by natural selection would have been relatively minor. If so, the base composition of a present-day genome should be close to being uniform over the entire genome because of the relatively small size of the ancestor genome - regardless of how it came into being - by comparison to present-day genomes. Indeed, this essentially holds true for genomes [6] (although coding regions often have a relatively richer GC content [3, 15, 17, 18]) and this phenomenon is of unknown biological significance.

A genome of the order of 1 kbp long is far too short to encode enough proteins for DNA duplication. Setting the initial length of our model universal genome to not greater than 1 kbp at the point of transition to growth-by-duplication thus necessarily implies that the universal genome began its life in an RNA world, when there were no proteins and when RNAs had the dual roles of genotype and phenotype [19]. This view of the origin of life was advocated [20, 21, 22] even before RNA was discovered to exhibit self-splicing and enzymatic activities [23, 24]. Some RNA enzymes, or ribozymes, are very small; the hammerhead ribozyme is only 31 to 42 nucleotides (nt) long [25] and the hairpin ribozyme is only 50 nt long [26]. Hence we can infer with reasonable certainty that the 1 kbp initial universal genome was of sufficient size to encode the machinery necessary for sustained evolution and duplication (for many other issues of the RNA world see [27] for a review). Our model does not address the origin of this initial genome. The likelihood that it evolved from something arising spontaneously beforehand is enhanced by its short length and supported by the successful isolation of artificial ribozymes from pools of random RNA sequences *in vitro* [28]. The average duplicated segment length of 25b likely represents a good portion of the length of a typical ribozyme encoded in the early universal genome even if it is very short compared to a present-day gene that codes for an enzyme.

As mentioned earlier natural selection has not been explicitly included in our model not because it is unimportant in evolution, but rather because we believe it could not have played a lead role in generating the wide spectral width characteristic of genomes. On the other hand, the effect of natural selection is implicitly included in our model, so far as it is a model for evolution. Natural selection determines whether a change brought upon by segmental duplication becomes a fixation. Furthermore, natural selection fine-tunes the fixations for adaptation.

Returning to the issue we first raised in the introduction, the extreme low probability (less than

10^{-830}) that *T. pallidum* would have a single 3-mer (it has six) occurring more than 24,000 times in its genome, we believe the correct way of viewing the matter is the following. The probability is extremely low only if genomes grew and evolved mostly by single mutations. The probability is not at all low, indeed it is within the expected range, if genomes grew mostly by segmental duplication.

As a corollary of the above reasoning, we can consider that uneven codon usage may not have been the primary cause of the very broad distribution of the 3-mer counts now seen in genomes. It is much more likely that codons were evolutionary “spandrels” [29], that is to say, their rise as codes for proteins came as a consequence of an opportunistic evolutionary adaptation to the already-wide 3-distribution that had resulted from growth by duplication. Similarly, many of the highly under- or overrepresented oligonucleotides that now have biological functions might have originated as spandrels.

Our analysis presented here supports the view that statistical characteristics of present day genomes were already substantially determined by the characteristics of their ancestors by the time of their transition to growth by duplication; conversely, that statistical characteristics of genomes today can be regarded just in this manner as a basis from which to explore the nature and properties of early ancestral genomes; further analysis made along this line of reasoning may bring us a step nearer in understanding the universal ancestor [30].

Growth by duplication is in itself a brilliant strategy because it allowed the genome to utilize hard-to-come-by codes repeatedly, thereby increasing the rates of evolution and species diversion enormously. For this strategy to have worked, the length of the duplicated segments used and the typical length of coding sequences must match. This condition is likely met by our model because most ribozymes in the early universal genome must have been small. Was this strategy continued after the “early life” of the universal genome - after the rise of codons and proteins? If so, then, with proteins/enzymes much larger than the small ribozymes, the duplicated segments in the post-protein era must have been much longer than 25b for the strategy to have been effective. In higher organisms many repeat sequences with lengths ranging from 1 base to many kilobases are believed to have resulted from at least five modes of duplication, and about 50% - perhaps even more - of the human genome is composed of such duplications [17, 18]. Furthermore, as already mentioned, typically about 12% of genes in bacterial genomes represent recent duplication events. So certainly, the continuity of this strategy into the protein era is abundantly in evidence [31, 32]. In eventual

answers to questions such as why genes have been duplicated [33] at the high rate of about 1% per gene per million years [34], and why in all life forms so many duplicate genes are found [35, 36, 37], this growth strategy, if adopted universally in genomes, may be a simple and crucial, indeed a parsimonious part.

Materials and Methods

Complete microbial genome sequences

Complete microbial genome sequences are obtained from GenBank [38]. The names, GenBank codes, lengths and base compositions of the genomes are listed in Table 3; p_{AT} is the combined probability of A and T in the genome, and p is the greater of p_{AT} and $1 - p_{AT}$. The 25 Class A genomes are given in the top half of the table and the 28 Class C genomes in the bottom half. Counting of k -mers is done by reading through a k -base wide overlapping sliding window. Counts are normalized to per 1 Mb and variation in genomic base composition is compensated for by dividing the actual genomic counts by the factor $L(p/\bar{p})^m((1-p)/(1-\bar{p}))^{k-m}$, where p is the greater of the joint AT or CG probability, $\bar{p} = 0.5$ ($\bar{p} = 0.7$) for Class A (Class C) genomes and m is the total number of AT bases (or CG) in each k -mer.

Generation of model sequence

A random sequence of length L_0 with a given base composition is first generated. Thereafter the sequence is altered by single mutations (replacements only) and duplications, with a fixed average mutation to duplication event ratio. In duplication events, a segment of length l , chosen according to the Erlang probability density function $f(l) = 1/(\sigma n!)(l/\sigma)^n e^{-l/\sigma}$, is copied from one site and pasted onto another site, both randomly selected. In the above, n is an integer and σ is a length scale in bases. The function gives a mean duplicated segment length $\bar{l} = (n+1)\sigma$ with std $\delta_l = (n+1)^{1/2}\sigma$. The values $n = 0$ to 8 and selected values for σ from 3 to 15,000 were used. In the text, the model sequences used to compare with genomic sequences were generated with $L_0 = 1000$, $n = 4$, $\sigma = 5$ and without mutation events. This model has $\bar{l} = 25$ and $\delta_l = 11.2$. There is nothing special about the Erlang function except that it was a simple generalize function of the exponential function - that we used in the first instnace - and that it provided a simple setting for discrete parameter search: after we realized \bar{l} needed to be less than 50, we scanned \bar{l} in intervals of 5 and n in intervals

Table 4: Standard deviations of k -distributions from from $p \approx 0.7$ sequences: column 2, for the genome of *M. jannaschii*; column 3, averaged over 28 $p \approx 0.7$ Class C genomes; column 4, for a $p = 0.7$ random sequence; column 5, for a $p = 0.7$ model sequence. All genomic stds are normalized to correspond to a $p = 0.7$ sequence (see Methods).

k	<i>M. jan.</i>	Class C Genomes	Random	Model
2	38,700	37,300±5,900	36,700	36,700
3	12,600	12,200±2,060	11,700	11,800
4	3,930	3,830±680	3,520	3,580
5	1,180	1,150±220	1,020	1,060
6	347	339±69	292	311
7	101	100±22	82.8	91.8
8	29.5	29.3±6.8	23.3	27.6
9	8.62	8.58±2.13	6.68	8.74
10	2.60	2.60±0.67	2.01	2.99

of 1. Nevertheless, when $f(l)$ is replaced by a Gaussian distribution with the same values for \bar{l} and δ_l , respectively, less satisfactory results are obtained. Fine-tuning to find the best parameters was not attempted.

The following are some examples that gave very good k -distributions for specific k -mers but not generally; all were generated with $L_0 = 1000$ and $n = 0$: for 6-mer, $\sigma = 13,000 \pm 2,000$ and on average 0.04σ mutations per duplication (these parameters also work for genomes with biased base compositions) [14]; for 2-mer, $\sigma = 50$, no mutation; for 5-mer, $\sigma = 30$, no mutation; for 9-mer, $\sigma = 15$, no mutation.

Sequences with highly biased compositions

The standard deviation (std) in the k -distribution of a sequence with a significantly biased base composition is essentially determined by the value of p . This is because when p is large (i.e., significantly greater than 0.5), the k -distribution of even a random sequence is spread out, as is seen in the cyan curves of the (B) and (C) panels in Fig. 1. There the sharp peaks occur at the mean frequencies \bar{f}_m of subsets of k -mers with m AT's (called m -sets), $m=0$ to k :

$$\bar{f}_m = \bar{f} 2^k p^m (1-p)^{k-m}, \quad m = 0, 1, \dots, k \quad (1)$$

where $\bar{f} = 10^6 4^{-k}$ is the overall mean. When p is away from 0.5 it is possible for \bar{f}_m to be much greater or much less than \bar{f} .

For a random sequence the distribution within a m -set is a Poisson distribution with mean \bar{f}_m . If the widths of such distributions are ignored then the std for the entire k -distribution is

$$\Delta_k(p) = \bar{f} \left[2^k \left(p^2 + (1-p)^2 \right)^k - 1 \right]^{1/2} \quad (2)$$

Table 5: Mean frequency and standard deviation of k -distribution for m -sets from $p \approx 0.7$ sequences: column 2, mean frequency \bar{f}_m for the set; column 3, std (and its own std) averaged over 50 $p = 0.7$ random sequences; column 4, std averaged over 28 Class C genomes; column 5, std of $p = 0.7$ model sequence (see Methods).

k, m	\bar{f}_m	Standard deviation		
		Class C genomes	Random	Model
2,1	52,500	6,381±1,674	168±58	2,555
3,2	18,375	3,736±1,038	120±20	1,851
4,2	2,756	1,142±246	51.6±4.6	688
5,3	964	452±92.2	30.8±1.5	296
6,3	145	92.6±19.9	12.0±0.28	92.3
7,4	50.6	36.6±7.7	7.12±0.10	50.6
8,4	7.60	7.44±1.57	2.76±0.02	9.93
9,5	2.65	3.05±0.61	1.63±0.01	4.69
9,7	14.5	11.3±2.87	3.80±0.03	12.1
10,6	0.93	1.33±0.28	0.97±0.00	2.28
10,8	5.06	4.66±1.18	2.25±0.01	5.79

$\Delta_k(p)$ is zero at $p=0.5$ but grows rapidly when $2p$ deviates from 1. This means that for a random sequence the std is given by the Poissonian value $\bar{f}^{1/2}$ when $2p \approx 1$ but is given by Δ_k when $\max\{2p, 1/2p\}$ is significantly greater than 1. This is verified by data shown in Table 4, where the stds for the genome *M. jannaschii*, those averaged over 28 Class C genomes, for a $p=0.7$ random sequence, and for a $p=0.7$ model sequence are given. The genomic results are normalized - by dividing the frequency of every k -mer by a factor $(L/10^6)(p/0.7)^m((1-p)/0.3)^{k-m}$ - to those for a sequence 10^6 bases long with exactly $p=0.7$; L is the actual length of the genome. The entries in the table are very accurately given by Eq. (2): $\Delta_k(0.7) = 36,700, 11,700, 3,520, 1,020, 293, 82.5, 23, 6.4$ and 1.8 for $k = 2$ to 10 , respectively. Thus for sequences with highly biased base compositions the std of the entire k -distribution is not sensitive to details of the sequence that we are interested in.

k -distributions of m -sets

Such details show up in widths of the distributions of m -sets. In a random sequence the distribution of such a set is still approximately Poissonian, with its std approximately equal to the mean frequency \bar{f}_m . The total number of k -mers in an m -set is $N_m = 2^k \binom{k}{m} \bar{f}_m$ giving $\sum_m N_m = 10^6$, where $\binom{k}{m}$ is the binomial. Table 5 shows for some m -sets: the mean frequency (column 2); std averaged over 28 Class C genomes (\pm its own std) (column 3); std averaged over 50 random sequences (column 4); std for a $p = 0.7$ model sequence. In computing the genomic stds, the genomic k -mer frequencies per 1 Mb are first normalized to correspond to a sequence with $p=0.7$,

then another overall normalization is made to set the total number of k -mers in the m -set to N_m . This guarantees the genomic mean frequency of the k -mers in the m -set to be \bar{f}_m . In Table 5 it is noticed that for $k=2$ and 3 the std for the random sequence is less than $\bar{f}_m^{1/2}$ as would be expected of a Poisson distribution. This reflects the fact that we have ignored a binomial factor that would reduce the std. Nevertheless in each case the std of average genomic k -distribution is either greater or much greater (for the smaller k 's) than the std of a random sequence. The relation between the stds of genomic and random sequences is now similar to that seen in Table 1 for the Class A genomes. The stds for the model sequence are in general agreement with the genomic values but has a k -dependence that is slightly too weak. Model sequences that fit the data better can be found but that is not the primary purpose of the present study.

Computation of L_r

Denote the average genomic std for an m -set by $\Delta_{k,m}$ and that for random sequences by $\Delta'_{k,m}$, then the statistical length for the “universal” $p = 0.7$ genome is defined as the weighted average

$$L_r = L \sum_{m=0}^k \frac{N_m}{L} \left(\frac{\Delta'_{k,m}}{\Delta_{k,m}} \right)^2 \quad (3)$$

Errors for L_r are similarly computed. The results are given in column 3 of Table 2.

Presentation of data

In Figs. 3 and 5 the curves shown are the result of a small amount of forward and backward averaging - to remove excessive fluctuations. In Figs. 2 and 4 data bunching was used to produce the towers shown.

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