Examination of Genome Homogeneity in Prokaryotes Using Genomic Signatures

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Abstract

Background: DNA word frequencies, normalized for genomic AT content, are remarkably stable within prokaryotic genomes and are therefore said to reflect a “genomic signature.” The genomic signatures can be used to phylogenetically classify organisms from arbitrary sampled DNA. Genomic signatures can also be used to search for horizontally transferred DNA or DNA regions subjected to special selection forces. Thus, the stability of the genomic signature can be used as a measure of genomic homogeneity. The factors associated with the stability of the genomic signatures are not known, and this motivated us to investigate further. We analyzed the intra-genomic variance of genomic signatures based on AT content normalization (0th order Markov model) as well as genomic signatures normalized by smaller DNA words (1st and 2nd order Markov models) for 636 sequenced prokaryotic genomes. Regression models were fitted, with intra-genomic signature variance as the response variable, to a set of factors representing genomic properties such as genomic AT content, genome size, habitat, phylum, oxygen requirement, optimal growth temperature and oligonucleotide usage variance (OUV, a measure of oligonucleotide usage bias), measured as the variance between genomic tetranucleotide frequencies and Markov chain approximated tetranucleotide frequencies, as predictors.

Principal Findings: Regression analysis revealed that OUV was the most important factor ($p<0.001$) determining intra-genomic homogeneity as measured using genomic signatures. This means that the less random the oligonucleotide usage is in the sense of higher OUV, the more homogeneous the genome is in terms of the genomic signature. The other factors influencing variance in the genomic signature ($p<0.001$) were genomic AT content, phylum and oxygen requirement.

Conclusions: Genomic homogeneity in prokaryotes is intimately linked to genomic GC content, oligonucleotide usage bias (OUV) and aerobic metabolism, while oligonucleotide usage bias (OUV) is associated with genomic GC content, aerobicism and habitat.

Introduction

Analyses of the DNA composition in prokaryotes and eukaryotes have revealed important differences. While prokaryotes have, on average, a higher fraction of coding DNA than eukaryotes, the latter has a seemingly more advanced DNA composition with non-protein coding regions [1]. In addition, the DNA molecule in eukaryotic organisms is larger and nucleosomes are used to compact it introducing pronounced, long-range correlation effects not present in bacteria [2]. In bacteria however, small scale genomic DNA (i.e. genetic sections covering 200 bp) has a Brownian motion, or random walk reminiscent composition, in other words, the long-range correlation effects described above for eukaryotes are absent in microbial genomes [3]. The random walk-like base composition pattern found in prokaryotic genomes [1] indicates that statistical methods based on random walk methodology, also known as Markov chains, may be a useful tool to model and understand prokaryotic genome composition.

Markov chains describe a set of stochastic processes that all share the Markov property. This property states, in common terms, that the probability that an event occurs in the future is only dependent on the present and independent of any other events. In other words, Markov chains are, in general, only concerned with what happens in the last time step and not the previous history to predict a future event, hence the term “random walk” [4]. Markov chains can be extended to be made dependent on additional events, or time steps, allowing for short range correlation effects, i.e. short term memory, in the random walk process [4]. Short range correlated Markov chains are known as $n$th order Markov chains, where $n$ denotes the number of dependent time-steps, or events [4].

Markov chain theory has found many applications in biology and bioinformatics and are widely used in gene-finding [5], DNA sequence search [6], rRNA gene localization [7], and protein structure identification [8]. In this study, we used Markov chains to analyze prokaryotic genome composition. This was carried out by studying the genomic frequencies of small tuples of nucleotides known as oligonucleotides. Examples of genomic oligonucleotide...
frequencies include nearest neighbor frequencies (dinucleotide frequencies), codon frequencies (trinucleotides) and tuples of four nucleotides, known as tetranucleotide frequencies. Dinucleotide frequencies are associated with DNA structural features and base stacking energies [9]. Codons code for amino acids in all living organisms. Since there are 64 different codon combinations, but only 20 different amino acids, multiple codons can code for the same amino acid. Closely related species often prefer the same codons for specific amino acids [10]. There are however indications that codon preference is just as much driven by environmental factors as phylogeny [11–13]. Tetranucleotide patterns are influenced by biases from mono- to trinucleotide frequencies [14]. Moreover, tetranucleotide patterns with corresponding structural features are similarly distributed throughout prokaryotic genomes [15], and have also been found to carry a taxonomic signal [15–17]. As discussed above, prokaryotic DNA has been found to follow a short range correlated, random walk like pattern that can be modeled using Markov chain analysis.

To test the genomic sequences for random walk properties, or lack thereof, we computed the variance difference between genomic oligonucleotide frequencies and Markov chain approximated oligonucleotide frequencies. Lower variance between genomic oligonucleotide frequencies and Markov chain approximated oligonucleotide frequencies implies more random walk like properties. Due to the features described above for tetranucleotide frequencies, Markov chain analysis was used to approximate genomic tetranucleotide frequencies with the genomic frequencies of smaller DNA words (i.e. mono- to trinucleotide frequencies). Higher variance (squared difference) between genomic and approximated tetranucleotide frequencies is correlated with bias. Hence, stronger bias is in the present study taken to mean that the variance between genomic tetranucleotide frequencies and the Markov chain based random walk models is high. The more biased a genome is said to be, the more difficult it is to approximate the genomic tetranucleotide frequencies using random walk based methods such as Markov chains.

A zero’th order Markov chain (ZOM) approximates genomic oligonucleotide frequencies using the corresponding genomic nucleotide frequencies (see materials and methods for more details). For the ZOM-based approximation scheme, we assume that the lower variance between genomic and approximated tetranucleotide frequencies, the more mutated, or randomly composed, a genome is. Since each oligonucleotide frequency is approximated by the oligonucleotide’s corresponding nucleotide frequencies, the ZOM approximation assumes that each nucleotide, in the oligonucleotide that is being approximated, is independent of its neighbors.

Nearest-neighbor effects, or short range correlations, are important factors in both genomic DNA structure and DNA sequence and such effects are largely responsible for the bias in the ZOM variance model discussed above. For instance, nearest neighbor nucleotides are associated with base stacking energies [9], DNA helix structure [9] and DNA structure in general [18,19]. The three nucleotides in each codon are also dependent on each other, and this dependency is largely responsible for the preference of some codons over others that code for specific amino acids [10]. The dependencies between the nucleotides in each codon is thus strongly linked to codon usage bias in prokaryotic genomes [10]. Thus, it is clear that short range dependencies play an important role in genomic DNA composition.

Dependence of nearest neighbor nucleotides in a random walk model can be modeled using a first or second order Markov chain. A first order Markov chain (FOM) approximates genomic oligonucleotide frequencies using the oligonucleotide’s corresponding mono- and dinucleotide frequencies. Hence, weak dependencies are incorporated into the FOM model by the use of genomic mono- and dinucleotide frequencies to approximate the frequencies of larger oligonucleotides as compared to only mononucleotide frequencies in the ZOM model. Even stronger neighboring effects, or short range correlations, are incorporated into the second order Markov chain (SOM), which uses di- and trinucleotide frequencies to approximate larger oligonucleotides.

The lower the variance is between genomic tetranucleotide frequencies and FOM and SOM based tetranucleotide frequency approximations, the stronger are the interactions of two and three neighboring nucleotides in the respective models. The variance tests measuring the random walk like behavior of the genomic DNA sequences are referred to as oligonucleotide usage variance (OUV) [14,15]. Hence, OUV is here a measure of tetranucleotide usage bias, measured as the variance between genomic tetranucleotide frequencies and Markov-chain approximated tetranucleotide frequencies. The higher the OUV value, the more biased (i.e. less random walk like) we say a genome is. Conversely, smaller OUV values are taken to mean that a genome has a more random walk or Brownian motion like sequence structure corresponding to the Markov model used. In other words, while FOM and SOM models emphasize dependence between 2 and 3 nucleotides in a DNA sequence, the ZOM model assumes no such dependencies at all. ZOM based approximations are thus assumed to better model random mutations in DNA sequences, while FOM and SOM based approximations are more suited to model neighboring dependencies and short range correlations, respectively. Figure 1 shows how OUV varies in two bacterial genomes, Bacillus cereus ATCC 14579 and Rhodopirellula baltica SH 1.

Figure 1. Oligonucleotide usage variance (OUV) in Bacillus cereus and Pirellula sp. The figure shows how tetranucleotide usage varies within the Bacillus cereus ATCC 14579 (grey line) and Rhodopirellula baltica SH 1 (black line) chromosomes. The vertical axis (OUV) is a measure of oligonucleotide usage variance. Higher OUV values indicate more biased tetranucleotide usage as compared to a randomly constructed DNA sequence with corresponding AT content. It can be seen that the R. baltica genome has, on average, more biased tetranucleotide usage than the B. cereus genome.

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The odds-ratio of genomic oligonucleotide frequencies divided by Markov chain approximated oligonucleotide frequencies, on arbitrary bulks of 50 kbp, has been shown to correspond remarkably well with known phylogenies for closely related organisms [20,21]. The discovered phylogenetic signal made Karlin and co-authors dub the odds-ratio of observed oligonucleotide frequencies divided by approximated oligonucleotide frequencies as “genomic signatures” [22]. The stable property of the odds-ratio between observed oligonucleotide frequencies and Markov chain approximated oligonucleotide frequencies in genomic DNA, was first discovered using a dinucleotide based zero’th order Markov chain [23]. Although this finding dates back to early 1960’s, it was Karlin and co-workers who discovered the more general validity of the method and called it a “genomic signature” [22]. Karlin and co-workers also tested an odds-ratio model based on a second order Markov chain model, but could not detect any improvement in performance compared to the ZOM-based odds-ratio model [20]. Subsequent studies have given a mixed picture regarding the genomic signature obtained with a SOM-based odds-ratio model compared to ZOM-based genomic signatures [16,24,25]. However, ZOM-, FOM- and SOM-based odds-ratios reflect taxonomical signals in prokaryotic genomes. The FOM-based odds-ratio model is especially suited to model nearest neighbor interactions between nucleotides, and may therefore be somewhat more biased towards base stacking energies than the ZOM model. Table 1 gives an overview of the different Markov chain models used in the present study together with the corresponding assumptions and biases.

Genomic signature variances within genomes can be measured using odds-ratios of genomic oligonucleotide frequencies divided by approximated oligonucleotide frequencies from smaller chunks of DNA, ranging from a few to a hundred kbps, and compared to the corresponding odds-ratios for the whole DNA sequence [25]. The genomic signature varies little within prokaryotic genomes [21,25]. However, variations of the genomic signature may be indicative of foreign DNA from plasmids, virus or the environment being integrated into a genome [26]. Variations in genomic signatures within prokaryotic genomes is therefore occasionally linked to virulence and pathogenicity islands [14,21,26]. Analysis of dinucleotide-based genomic signature variance within Thermotoga maritima revealed that correlation scores as high as \( r > 0.9 \) could be obtained between genomic signatures from 5 kbp sliding windows and whole chromosome based signatures [14]. Indeed, for the same genome and sliding window size tetranucleotide-based genomic signatures obtained correlation scores of \( r > 0.8 \) [14]. In the Bacillus subtilis genome the average correlation score was somewhat lower than the score obtained for T. maritima using tetranucleotide-based genomic signatures. Although both organisms are known to have acquired considerable amounts of foreign DNA [27,28], the average variance of the genomic signature within each genome varied considerably between the two genomes [14]. We shall refer to average variation measures of genomic signatures based on Pearson correlation as Pearson correlation-coefficient homogeneity tests (PCH). Figure 2 shows how the genomic signature, as measured using the PCH measure, varies within two genomes, Rhodopirellula baltica SH 1 and Bacillus cereus ATCC 14579.

**Table 1.** Assumptions of the Markov chain models and the corresponding reflected bias.

| Approximation model | Oligonucleotide(s) used in approximation | Assumptions | Bias |
|---------------------|-----------------------------------------|-------------|------|
| ZOM                 | mononucleotide frequencies               | no correlations between neighboring nucleotides | random mutations |
| FOM                 | mono- and dinucleotide frequencies       | correlations between neighboring nucleotides | base stacking energies |
| SOM                 | di- and trinucleotide frequencies        | Correlations between all adjacent nucleotides | base stacking energies, DNA structure, codon bias |

The table shows the different assumptions and biases associated with the corresponding Markov chain model used to approximate genomic oligonucleotide frequencies.

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**Figure 2.** Genomics signature variance in Bacillus cereus and Pirellula sp. The figure shows how the genomic signature varies within one of the most homogeneous chromosomes, Rhodopirellula baltica SH 1 (black line), and within one of the most heterogeneous chromosomes, Bacillus cereus ATCC 14579 (grey line). The vertical axis representing PCH, gives a measure of how homogeneous a genome is. The higher the PCH value, the more homogeneous the chromosome. It can be seen that PCH is both higher and with less variation in the R. baltica genome as compared to the B. cereus genome. While R. baltica is a slow growing GC rich bacterium with a relatively large genome (7 mbp), B. cereus is a fast growing AT rich bacterium with a genome of approximately 5.5 mbp.

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The difference in average genomic signature variance between the bacteria discussed above motivated us to investigate genomic homogeneity in sequenced prokaryotic genomes by utilizing the stable property reflected by the Markov chain based genomic signature methods. The aim was to explore how genomic homogeneity, as measured by tetranucleotide-based genomic signatures, varied within all sequenced prokaryotic genomes, and whether this variance could be attributed to specific phylogenetic and environmental factors. Moreover, we wanted to examine the DNA compositional random walk like properties in each sequenced prokaryotic genome, and whether it could be linked to genomic homogeneity (PCH), and if it could be attributed to specific phylogenetic and environmental factors.

To model the factors affecting genomic homogeneity in prokaryotes, a linear regression analysis was used with PCH as the response variable with the predictor variables: growth temperature (a categorical factor classifying organisms as psychrophilic, mesophilic or thermophilic), AT content, chromosome size, habitat (a categorical factor describing the organisms habitat as aquatic, host-associated, multiple, specialized or terrestrial) and phyla, in addition to the corresponding Markov chain OUV.

| Table 2. OUV regression AIC/Coefficient of variation scores. |
|-----------------|--------------|---|---|---|-----------------|----------------|
|                | Constant Size | AT | Phyla | Oxygen | Habitat | Growth temperature | Transform |
| ZOM            | 1187         | 909 | 649 | 397 | 646 | 390 | log |
| ZOM orfs       | 1056         | 683 | 402 | 397 | 390 | 390 | log |
| FOM            | -4399        | -463 | -3515 | -3571 | -5715 | -5717 | log |
| FOM orfs       | -4204        | -4757 | -4954 | -4961 | -4961 | -4967 | log |
| SOM            | 961          | 542 | 324 | 314 | 308 | 295 | log |
| SOM orfs       | 2544         | 2511 | 2033 | 1766 | 1763 | 1757 | log |

Results of forward fitting regression models with the response variable in the leftmost column followed by the included predictors in the subsequent columns.

To examine factors influencing the random walk like behavior of genomic DNA sequences, a linear regression model was set up with ZOM, FOM and SOM OUV as response variables to the following predictor variables: growth temperature, AT content, chromosome size, habitat and phyla.

Separate models were fitted for whole chromosomes, including coding and non-coding regions, and open reading frames (orfs) to measure whether any differences in the PCH and OUV measures could be detected between coding and non-coding regions.

Results

OUV Regression Models

In Table 2 it can be seen that AT content and phyla were the strongest contributing factors in the OUV-based regression models. This means that the random walk like properties of genomic DNA in prokaryotes is, first and foremost, associated with genomic AT content (Figure 3) and phylogeny. The higher the genomic AT content, the more random walk like the genomic DNA sequence pattern tend to be. Oxygen requirement was

![Figure 3. Oligonucleotide usage variance (OUV) based on ZOM, FOM and SOM models.](https://doi.org/10.1371/journal.pone.0008113.g003)
2nd order Markov models (ZOM, FOM, and SOM respectively) are found in terms of AIC and associated with FOM and SOM OUV (affected by environmental conditions. Growth temperature was random walk like sequence structure in prokaryotic DNA is also all models but the FOM model (based random walk models. Habitat was associated with OUV for results from the regression model indicate that aerobic organisms (found to be associated with FOM and SOM orfs models it is one of many factors involved. Chromosome size was only temperature has an effect on genomic DNA composition, but that OUV measure (OUV measure) for both FOM and SOM models. The PCH regression AIC/Coefficient of variation scores. Hence, it is likely that growth (0.001) for both FOM and SOM models. From Table 2 it can be seen that the ZOM-based regression model explained the least observed variance (R^2 = 0.55), while the SOM model restricted to open reading frames explained the most variance (R^2 = 0.69). ZOM OUV compared to SOM OUV scores obtained the least associated of all measures with R^2 = 0.39, while FOM OUV compared to SOM OUV scores obtained the highest coefficient of determination of R^2 = 0.57. In summary, this indicates that the ZOM OUV model resembled the FOM OUV model more than the SOM OUV model.

PCH Regression Models

From Table 3 it can be seen that all Markov model based PCH regression models were influenced by AT content, respective order Markov model based OUV scores, and phyla. Thus, genomic DNA homogeneity as measured by the intra-genomic variance of Markov chain based genomic signatures increased with GC content and OUV. The more biased, i.e. less random walk like, the genomic DNA compositions was, the more homogeneous the genomic DNA sequence in terms of the Markov chain based genomic signature was found to be. Oxygen requirement was associated with increased genome homogeneity in all regression models except the ZOM model (p<0.001), while chromosome size was only found to be significant for the FOM orfs model. As was mentioned above, since chromosome size was only associated with the FOM orfs model, it is possible that the chromosome size confounds with AT content, or one of the other factors, and is thus found significant by the regression models. Habitat was found to improve the coefficient of determination (R^2) slightly but only for the ZOM and SOM orf regression models. It is therefore possible that habitat is confounding with another covariate, just as in the case for chromosome size. Most variance was explained by the

Table 3. PCH regression AIC/Coefficient of variation scores.

|            | Constant | Size | AT  | OUV | Phyla | Oxygen | Habitat | Transform |
|------------|----------|------|-----|-----|-------|--------|---------|-----------|
| ZOM orfs   | 728      | 1051 | 1492| 0.67| 0.77  | 1727   | 0.77    | 1730      | 0.77      |
| FOM orfs   | 828      | 1240 | 1629| 0.68| 0.74  | 1740   | 0.74    | 1753      | 0.74      |
| SOM orfs   | 1088     | 1364 | 1831| 0.8 | 0.82  | 1894   | 0.83    | 1920      | 0.83      |

Results of forward fitting regression models with the response variable in the leftmost column followed by the predictors used in the models.

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FOM and FOM orfs regression models \( R^2 = 0.83 \), while the least variance was explained by the SOM orfs model \( R^2 = 0.58 \). The orfs models were in general better, in terms of variance explained (Table 3), than the models based on whole chromosomes, and, from Figure 5, it can be seen that they in general obtained higher PCH scores.

The ZOM PCH compared to FOM PCH scores obtained a coefficient of determination score of \( R^2 = 0.38 \), while ZOM PCH compared to SOM PCH scores obtained the highest coefficient of determination with \( R^2 = 0.52 \). Hence, corresponding to the results obtained for the OUV values, ZOM PCH was more similar to FOM PCH than SOM PCH.

Both OUV and PCH based regression models were also tested with pathogenicity as a factor. This factor is assumed to give a weak indication of recombination or horizontal transfer [30,31], but was not found significant for any of the models and therefore removed.

**Discussion**

**OUV-Based Models and their Association with Genomic Signatures**

The Markov model based genomic signatures discussed here differentiate organisms in terms of the ratio of genomic tetranucleotide frequencies divided by Markov chain approximated tetranucleotide frequencies. OUV values, or the variance between genomic tetranucleotide frequencies and approximated tetranucleotide frequencies, are therefore strongly associated with genomic signatures, since the bias in tetranucleotide usage drives the genomic signature in the respective organism. Factors affecting Markov model approximated OUV values in prokaryotes were examined using regression analysis. The regression models revealed that OUV is more associated with AT content than phyla. The relationship between OUV and AT/GC content is most likely also confounded with factors not specified in the model, since genomic AT content has been associated with environment [11,12]. Habitat, a categorical factor describing the environment where the organisms are usually found, was divided into five branches: aquatic, host-associated, terrestrial, specialized (extremophiles) and multiple (same species found in many different environments). The regression models, except FOM OUV, improved with the inclusion of the habitat factor for all measures. It is assumed that the lack of significant association between the FOM OUV measure and habitat is due to the coarseness of the methods used. The same can be said for the categorical variable specifying oxygen requirement. The oxygen requirement variable describes aerobic, anaerobic and facultative lifestyles, and was found to be significantly improving all regression models except for the ZOM OUV model.

The coefficient of determination \( (R^2) \) is in general higher for all OUV models restricted to open reading frames, indicating that the variances in the regression models are better explained in the

![Figure 5. Markov chain model based PCH scores in prokaryotes.](https://www.plosone.org/doi/10.1371/journal.pone.0008113.g005)
coding regions. The oligonucleotide-based genomic signature methods require relatively large segments of DNA to give meaningful results, i.e., at least multiple kbp depending on the Markov model used [25]. The non-coding regions were therefore not separated from the chromosomes analyzed. Hence, differences between coding and non-coding regions was measured as the difference between chromosomes, containing both coding and non-coding regions, and predicted open reading frames. It is interesting to note that AT content explains more variance in the OUV models than phyla. An explanation may be that the genomic DNA composition of prokaryotes is more sensitive to changes in conditions affecting mononucleotide frequencies than phyla. In other words, phyla could provide prokaryotic genomes with a sense of ‘inertia’ (or memory) while environmental factors affecting base composition may be responsible for inducing more rapid genomic changes. For instance, nitrogen is more abundant in GC rich genomes meaning that changes in nitrogen levels may affect the base composition in such genomes severely [32]. Similar trends have been observed for oxygen and aerobic bacteria, in the sense that the genomes of aerobic bacteria tend to be more GC rich [33]. In general, it has been shown, using sequenced genomes, that the environment affects the base composition in bacteria [11], and that the resulting change is relatively fast [12].

GC rich genomes were found to be more strongly biased in terms of OUV than AT rich genomes in the sense that AT rich genomes had, on average, a more random walk like DNA composition. Lower OUV scores mean less bias which, in turn, implies increased independence between the adjacent nucleotides and therefore more random genomic sequence patterns, presumably due to increased mutation rates [14]. This is supported by the observation that intracellular bacteria having undergone genome reduction tend to lose DNA repair genes and become AT rich [34–36]. This appears to happen to free living genomes as well when the amount of available nutrition changes. An example of the latter can be found in different strains of the ocean living bacterium Prochlorococcus marinus. Some of the P. marinus strains that live in the upper high light layer of the ocean tend to have smaller genomes than strains living in the nutrition rich low light areas [37]. Although only slightly, AT content was associated with habitat for host-associated and terrestrial environments (p<0.001), but aquatic, multiple (bacteria found in different environments) and specialized habitats (extremophiles) were not found significant. Oxygen requirement was also associated with AT content, but only slightly for anaerobic and facultative oxygen requirement (p<0.001). In contrast, growth temperature was not significantly (p>0.5) associated with AT content. It should be emphasized that global genomic data is necessarily “noisy”, and many of the environmental influences are assumed to affect particular areas of the genome and in distinct patterns [38]. Examinations of environmental influences on more specific genomic regions will, however, require the use of different methods than those employed here. It is conceivable that such methods should be based on nucleotides rather than oligonucleotides for an increase in sensitivity [39,40].

The SOM OUV method has also been used to approximate oligonucleotide frequencies in E. coli [41,42]. The SOM method was found to be inferior to similar methods allowing gaps [42]. Our findings indicate that the quality of the oligonucleotide approximations in prokaryotes depend, most importantly, on AT content. Thus, since AT rich genomes tended to be less biased, in terms of random walk like sequence patterns, than GC rich genomes, it may indicate that AT rich genomes are more concentrated, that is, dependencies between nucleotides are more short ranged, and therefore easier to approximate.

**Variance of Genomic Signatures within Genomes**

The principal motivation for this work was to examine prokaryotic genome homogeneity using Markov chain based genomic signatures. Figure 6 shows how the genomic signature changes within an E. coli K-12 genome. The ZOM PCH measure obtained higher scores than the FOM PCH measure, which, in turn, obtained higher scores than the SOM PCH measure. It can be seen that PCH scores increase with wider sliding windows [29].

The regression models indicate that all PCH methods are influenced by AT content and phyla, but most of all, corresponding Markov chain model OUV scores. Thus, genomic homogeneity, as measured using Markov chain based genomic signatures, is positively correlated with bias in genomic tetranucleotide patterns in the sense that the less random walk like the DNA composition of a genome is, the more homogeneous the genome is.

The FOM PCH based regression model obtained a coefficient of determination higher than the other Markov-chain based PCH models. In other words, FOM PCH was the best regression model in terms of variance explained. Although the reason for this is not known, it has been shown that mono- and dinucleotide frequencies to a large degree determine genome wide codon usage bias, and that the codon bias can be determined from intergenic regions as well [43]. Codon bias is therefore found to be, first and foremost, determined by forces inducing mutations on the whole genome and only secondary by factors related to specific genes [43]. The SOM PCH based models obtained R² values lower than those of both ZOM and FOM PCH models. The low PCH scores obtained with the SOM-based measures may indicate that the lower R² values obtained with the SOM PCH regression models may be caused by the increased genetic ‘noise’ found in these models.

The correlation between OUV and PCH scores means that random walk like DNA composition is strongly associated with intra-genomic heterogeneity, as measured by the different Markov model based genomic signatures. All PCH models, except for the ZOM PCH model, improved significantly with the inclusion of the oxygen requirement factor, although only slightly in terms of AIC and R². This result may indicate that oxygen requirement affects DNA composition in prokaryotes on many levels. Oxygen requirement did not reach the same significance level in the ZOM PCH model (p = 0.08) as the other models.

A small, but significant, improvement to the ZOM and SOM PCH orfs models was observed with the inclusion of the habitat factor. Chromosome size was only found to improve the FOM PCH orfs model. These results mean that chromosomal homogeneity, in terms of variance in the Markov model based genomic signatures, is associated with, first and foremost, corresponding ZOM, FOM and SOM OUV scores followed by AT content and phyla, with oxygen requirement influencing chromosomal homogeneity to a lesser degree.

Although all Markov-chain based PCH measures, and particularly the SOM PCH model, are fairly crude in measuring average chromosomal homogeneity it was of some surprise to note the substantial improvement to the models by the inclusion of AT content as a factor. All statistical models improved considerably in terms of both AIC and R² scores. This was unexpected since the variance of genomic signatures within genomes has usually been associated with foreign genetic elements like phages and pathogenicity islands [21]. The finding that global AT content is an important factor associated with how the genomic signatures vary within genomes can be seen from tables 4–9, where the high PCH scoring genomes tend to have lower AT content than the low PCH scoring genomes. The strong association with the corresponding OUV values may be a consequence of selective forces. Indeed, AT content is associated with phyla in the sense that
Figure 6. *E. coli K-12* profiles based on ZOM, FOM and SOM PCH measures. Plots of genomic signatures based on ZOM (red line), FOM (green line), or SOM (blue line) models compared with tetranucleotide-based signatures from a 10 kbp sliding window, overlapping every 5 kbp. Higher PCH (vertical axis) mean greater intra-chromosomal homogeneity. The low dips located close to genomic positions (horizontal axis) 2.1 mbp and 2.8 mbp indicate prophage DNA.

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similar species and strains tend to have similar AT content. However, all statistical PCH models indicated that AT content contributed more to the regression models than phyla. It should be noted that the above mentioned results are trends with a varying proportion of unexplained variance, i.e. exceptions do occur. In addition, the selection of sequenced genomes is in turn biased both by genome size and interest.

Genomic OUV and PCH Scores as Measures of Selection Forces

It is reasonable to think that OUV mirrors, although somewhat crudely, the sum of selective forces acting on an organism’s genomic DNA. Low OUV scores implies that the observed genomic DNA composition is closer to a model assuming, in the simplest case (ZOM), only similar mononucleotide frequencies. Thus, the more similar the genomic DNA composition, measured as mononucleotide frequency approximated tetranucleotide frequencies, is to corresponding mononucleotide frequencies, the weaker selective forces are assumed to have been acting on the genome. It has also been noted in several articles [34,36], that genomes in a stable environment, such as in a nutrition providing cell, tend to lose DNA repair genes with the implication that genomes mutate, particularly from cytosine to thymine on the lagging strand [44], leading subsequently to many defective genes and, ultimately, reduced genomes [34]. To reverse the processes of genome reduction, stronger selection forces must act on the genome. There are not many examples of genome expansion known to the authors, however Ehrlichia ruminantium and Frankia sp. strain EAN1pec are assumed to be affected by stronger selection forces due to their alleged genome increase [45,46]. The strong association between OUV and PCH scores may indicate that strong selection forces, i.e. high OUV and PCH scores, have a high impact on an organism’s DNA sequence which results in higher chromosomal homogeneity. This may explain the association between AT content and OUV/PCH scores, which, furthermore, may imply that genomic amelioration rates [47] are linked to AT content.

In summary, homogeneity in prokaryotic genomes, measured using genomic signatures, is highly associated, in order of importance, with bias in DNA composition, as measured by the

| Table 4. Highest ZOM PCH scoring genera. |
|------------------------------------------|
| Name                                     | NCBI accession number | ZOM PCH | AT  | Size mbp | ZOM OUV/Z-scores (log) | Oxygen | Habitat    | Growth temperature |
|------------------------------------------|-----------------------|---------|-----|----------|------------------------|--------|------------|-------------------|
| Candidatus Korarchaeum cryptofilum strain OPF8 | NC 010482             | 0.96    | 0.51| 1.59     | 4.32E-006/0.96         | Anaerobic | Specialized | Thermophilic      |
| *Rhodopirellula baltica* SH 1            | NC 005027             | 0.96    | 0.45| 7.15     | 3.59E-006/0.63         | Aerobic | Aquatic    | Mesophilic        |
| *Wolinella succinogenes*                 | NC 005090             | 0.96    | 0.52| 2.11     | 4.61E-006/1.07         | Aerobic | Host associated | Mesophilic        |
| *Dichelobacter nodosus* strain VCS1703A | NC 009446             | 0.96    | 0.56| 1.39     | 6.26E-006/1.7          | Anaerobic | Host associated | Mesophilic        |
| *Leptospira borgpetersenii* serovar Hardjo-bovis strain JB197 | NC 008510             | 0.96    | 0.6  | 3.58     | 5.08E-006/1.25         | Aerobic | Host associated | Mesophilic        |

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| Table 5. Lowest ZOM PCH scoring genera. |
|------------------------------------------|
| Name                                     | NCBI accession number | ZOM PCH | AT  | Size mbp | ZOM OUV/Z-scores (log) | Oxygen | Habitat    | Growth temperature |
|------------------------------------------|-----------------------|---------|-----|----------|------------------------|--------|------------|-------------------|
| *Buchnera aphidicola*                    | NC 004545             | 0.73    | 0.75| 0.62     | 1.99E-006/-0.41        | Facultative | Host associated | Mesophilic        |
| *Staphylococcus epidermidis* strain RP62A | NC 002976             | 0.73    | 0.68| 2.62     | 7.62E-007/-2.11        | Facultative | Host associated | Mesophilic        |
| Candidatus Blochmannia floridanus        | NC 005061             | 0.75    | 0.73| 0.71     | 9.18E-007/-1.78        | Aerobic | Specialized | Mesophilic        |
| *Bacillus cereus* strain ATCC 1479       | NC 004722             | 0.77    | 0.65| 5.22     | 1.24E-006/-1.31        | Facultative | Multiple     | Mesophilic        |
| *Finegoldia magna* strain ATCC 29328     | NC 010376             | 0.78    | 0.68| 1.8      | 2.47E-006/-0.03        | Anaerobic | Multiple     | Mesophilic        |

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| Table 6. Highest FOM PCH scoring genera. |
|------------------------------------------|
| Name                                     | NCBI accession number | FOM PCH | AT  | Size mbp | FOM OUV/Z score (log) | Oxygen | Habitat    | Growth temperature |
|------------------------------------------|-----------------------|---------|-----|----------|----------------------|--------|------------|-------------------|
| *Caldivirga maquiltingensis* strain IC-167 | NC 009954             | 0.92    | 0.57| 2.08     | 2.36E-006/1.95        | Aerobic | Specialized | Thermophilic      |
| *Helicobacter acinonychis* strain Sheeba  | NC 008229             | 0.92    | 0.62| 1.55     | 1.28E-006/0.87        | Aerobic | Host associated | Mesophilic        |
| *Dehalococcoides* strain CBDB1           | NC 007356             | 0.91    | 0.53| 1.4      | 1.36E-006/0.98        | Aerobic | Multiple     | Mesophilic        |
| *Pyrobaculum aerophilum*                 | NC 003364             | 0.91    | 0.49| 2.22     | 1.32E-006/0.93        | Facultative | Aquatic     | Thermophilic      |
| *Ignicoccus hospitalis* strain KIN41     | NC 009976             | 0.91    | 0.43| 1.36     | 1.5E-006/1.15         | Anaerobic | Aquatic     | Thermophilic      |

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OUV measure, AT content, phyla and oxygen requirement. All Markov-chain based genomic signatures were found to be associated with AT/GC content, with the implication that the more GC rich and higher OUV a genome has, the more homogeneous is the genome. In other words, GC rich genomes tend to be more homogeneous than AT rich. This result was not expected since genomic signatures are known to be sensitive to foreign genetic elements. Other factors such as habitat and oxygen requirement were also significant factors for the different models, and the genomic signatures were more stable in coding regions than in non-coding regions.

### Materials and Methods

All 636 genomes, consisting of 694 prokaryotic chromosomes, were downloaded from the NCBI database [48] [http://www.ncbi.nlm.nih.gov/genomes/lproks.cgi]. Genomic properties and information about the different organisms were also obtained from the NCBI website [48]. Regression analyses and data visualization was performed with R [49], and computer programs were made according to the guidelines described below. DNA sequences were analyzed in the 5' → 3' direction. All data used in the analyses, can be found as supporting information (File S1).

### Notation

Using the notation from Karlin and co-workers [20], the ZOM, FOM and SOM based functions are represented by the following formulas:

\[
\rho_{XYZW}(f) = \frac{f_{XYZW}}{f_{X} f_{YZ} f_{ZW}} \quad \text{(ZOM)}
\]

\[
\xi_{XYZW}(f) = \frac{f_{X} f_{YZ} f_{X} f_{YZ} f_{X} f_{ZW}}{\text{(FOM)}}
\]

\[
\eta_{XYZW}(f) = \frac{f_{XYZW} f_{X} f_{YZ} f_{X} f_{YZ} f_{X}}{\text{(SOM)}}
\]

\( f \) is the DNA sequence while \( f_{XYZW} \) indicates the frequency of oligo

### Table 7. Lowest FOM PCH scoring genera.

| Name                        | NCBI accession number | FOM PCH | AT  | Size mbp | FOM OUV/Z score (log) | Oxygen   | Habitat            | Growth temperature |
|-----------------------------|-----------------------|---------|-----|----------|-----------------------|----------|---------------------|--------------------|
| Fusobacterium nucleatum     | NC 003454             | 0.46    | 0.73| 2.17     | 8.88E-007/0.23        | Anaerobic| Host associated     | Mesophilic         |
| Mycoplasma penetrans        | NC 004432             | 0.46    | 0.74| 1.36     | 3.87E-007/-1.23       | Facultative| Host associated     | Mesophilic         |
| Borrelia afzelii strain PKo | NC 008277             | 0.53    | 0.72| 0.91     | 3.69E-007/-1.31       | Aerobic  | Host associated     | Mesophilic         |
| Parachlamydia sp. strain UWE25 | NC 005861         | 0.55    | 0.65| 2.41     | 8.98E-008/-3.05       | Aerobic  | Host associated     | Mesophilic         |
| Clostridium difficile strain 630 | NC 009089        | 0.56    | 0.71| 4.29     | 6.34E-007/-0.36       | Anaerobic| Multiple            | Mesophilic         |

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### Table 8. Highest SOM PCH scoring genera.

| Name                        | NCBI accession number | SOM PCH | AT  | Size mbp | SOM OUV/Z score (log) | Oxygen   | Habitat            | Growth temperature |
|-----------------------------|-----------------------|---------|-----|----------|-----------------------|----------|---------------------|--------------------|
| Helicobacter acinonychis strain Sheeba | NC 008229       | 0.87    | 0.62| 1.55     | 4.12E-007/1.31        | Aerobic  | Host associated     | Mesophilic         |
| Thermoproteus neutrophilus strain V24sta | NC 010525      | 0.86    | 0.4 | 1.77     | 8.74E-007/2.88        | Anaerobic| Specialized         | Thermophilic       |
| Ignicoccus hospitalis strain KIN41 | NC 009776        | 0.86    | 0.43| 1.3      | 4.79E-007/1.63        | Anaerobic| Aquatic             | Thermophilic       |
| Methanococcus aeolicus strain Nankai-3 | NC 009635       | 0.84    | 0.7 | 1.57     | 3.22E-007/0.8         | Anaerobic| Aquatic             | Mesophilic         |
| Methanoculleus marisnigri strain JR1 | NC 009051       | 0.84    | 0.38| 2.48     | 5.3E-006/1.84        | Anaerobic| Aquatic             | Mesophilic         |

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### Table 9. Lowest SOM PCH scoring genera.

| Name                        | NCBI accession number | SOM PCH | AT  | Size mbp | SOM OUV/Z score (log) | Oxygen   | Habitat            | Growth temperature |
|-----------------------------|-----------------------|---------|-----|----------|-----------------------|----------|---------------------|--------------------|
| Kineococcus radiotolerans strain SRS30216 | NC 009664       | 0.27    | 0.26| 4.76     | 7.84E-007/2.65        | Aerobic  | Multiple            | Mesophilic         |
| Mycoplasma penetrans        | NC 004432             | 0.4     | 0.74| 1.36     | 1.95E-007/-0.24       | Facultative| Host associated     | Mesophilic         |
| Ehrlichia ruminantium strain Gardel | NC 006831        | 0.4     | 0.72| 1.5      | 1.7E-007/0.53        | Aerobic  | Host associated     | Mesophilic         |
| Nocardioides sp. strain J5614 | NC 008699        | 0.43    | 0.28| 4.99     | 4.85E-007/1.65        | Aerobic  | Multiple            | Mesophilic         |
| Fusobacterium nucleatum     | NC 003454             | 0.44    | 0.73| 2.17     | 2.81E-007/0.52        | Anaerobic| Host associated     | Mesophilic         |

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The correlation scores between each sliding window and the whole average value for each chromosome was in turn calculated from signatures to signatures obtained from a non-overlapping sliding within each chromosome by comparing whole-chromosome ZOM, FOM and SOM-based genomic signatures were examined with the correlation formula. Thus, the variance of the different based on the ZOM, FOM and SOM measures above together different genomes, an average correlation score was calculated this comparison was carried out using the FOM model, and the sums are taken over every possible tetranucleotide combination XYZW.

To measure how the genomic signature changed within the different genomes, an average correlation was calculated based on the ZOM, FOM and SOM measures above together with the correlation formula. Thus, the variance of the different ZOM, FOM and SOM-based genomic signatures were examined within each chromosome by comparing whole-chromosome signatures to signatures obtained from a non-overlapping sliding window of 20 kbps using the Pearson correlation formula. The average value for each chromosome was in turn calculated from the correlation scores between each sliding window and the whole chromosome signature.

The maximum number of sliding windows $S$ is given by:

$$S = \frac{\text{size of DNA string}}{\text{sliding window size}}$$

The ZOM, FOM and SOM based OUV measures calculate the variance between observed and approximated oligonucleotide frequencies:

$$OUV_{ZOM}(f) = \frac{1}{N} \sum_{i=1}^{N} \left( \frac{f_{XYZW}(f) - \bar{f}_{XYZW}}{\bar{f}_{XYZW}} \right)^2, N \geq 4^d = 256, 1 \leq i \leq N \ (ZOM \ OUV)$$

$$OUV_{FOM}(f) = \frac{1}{N} \sum_{i=1}^{N} \left( \frac{f_{XYZW}(f) - \bar{f}_{XYZW}}{\bar{f}_{XYZW}} \right)^2, N \geq 4^d = 256, 1 \leq i \leq N \ (FOM \ OUV)$$

$$OUV_{SOM}(f) = \frac{1}{N} \sum_{i=1}^{N} \left( \frac{f_{XYZW}(f) - \bar{f}_{XYZW}}{\bar{f}_{XYZW}} \right)^2, N \geq 4^d = 256, 1 \leq i \leq N \ (SOM \ OUV)$$

Regression Analysis

The models measuring associations between OUV values as response functions and chromosome size, AT content, phyla, habitat, oxygen requirement and growth temperature as predictors, were all based on transformed 'linear' regression analysis:

$$E \left( (Y_{OUV})^2 \right) = \text{Size} + \text{Size}^2 + \text{AT} + \text{AT}^2 + \text{Phyla}$$

$$+ \text{Oxygen requirement} + \text{Habitat} + \text{Growth temp}$$

All PCH models were on a similar form, but with OUV included as a factor:

$$E \left( (Y_{PCH})^2 \right) = \text{Size} + \text{Size}^2 + \text{AT} + \text{AT}^2 + \text{OUV} + \text{OUV}^2$$

$$+ \text{Phyla} + \text{Oxygen requirement} + \text{Habitat}$$

All regression equations explained in this work were transformed on the left hand side with the $\lambda$ coefficient found using Box-Cox estimation [50] to conform as much as possible to the underlying hypothesis of normally distributed residuals. Phyla, oxygen requirement, habitat and growth temperature were all categorical variables, while PCH, Size, AT and OUV were numerical variables.

The results obtained must be considered as coarse as there is some expected co-linearity between predictors like OUV, AT content and chromosome size [14,15,29,51]. In addition, the computed oligonucleotide frequencies were all obtained by counting overlapping oligonucleotides, thereby adding considerable ‘noise’ to any potential genomic signal. The quality of the models was assessed using the Akaike information criterion (AIC) and the coefficient of determination ($R^2$). Factors were added forwardly to the models and deleted if $p>0.001$. The Z-scores, i.e. ($\bar{z}$-$\mu$)/$\sigma$, in tables 4–9 are based on transformed OUV values.

Supporting Information

File S1 Main dataset. An Excel file containing the data used to generate the results in the paper

Found at: doi:10.1371/journal.pone.0008113.s001 (0.26 MB XLS)

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Author Contributions

Conceived and designed the experiments: JB. Performed the experiments: JB. Analyzed the data: JB ES. Wrote the paper: JB.

References

1. Ussery D, Soumpasis DM, Brunak S, Staerfeldt HH, Worning P, et al. (2002) Bias of purine stretches in sequenced chromosomes. Comput Chem 26(5): 531–541.
2. Vaillant C, Audit B, Thermes C, Arneodo A (2006) Formation and positioning of nucleosomes: Effect of sequence-dependent long-range correlated structural disorder. Eur Phys J E Soft Matter 19(3): 263–277.
3. Garcia JA, Bartumeus F, Roche D, Giraldo J, Stanley HE, et al. (2008) Ecophysiological significance of scale-dependent patterns in prokaryotic genomes unveiled by a combination of statistic and genometric analyses. Nucleic Acids Res 36(9): 2950–2965.
4. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. J Mol Biol 215(3): 403–410.
5. Ewens WJ, Grant GR (2001) Statistical methods in bioinformatics. Springer.
6. Lagesen K, Hallin P, Rodland EA, Staerfeldt HH, Rognes T, et al. (2007) RNAmer: Consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res 35(9): 3100–3108.
7. Eidhammer I, Jonassen I, Taylor WR (2004) Protein bioinformatics. Wiley.
8. Sinden RR (1994) DNA structure and function. Academic Press.
9. Sharp PM, Li WH (1987) The codon adaptation index—A measure of directional bias of purine stretches in sequenced chromosomes. Comput Chem 26(5): 531–541.
10. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. J Mol Biol 215(3): 403–410.
11. Chen LL, Zhang CT (2003) Seven GC-rich microbial genomes adopt similar codon usage patterns regardless of their phylogenetic lineages. Biochim Biophys Res Commun 306(0006-291; 1): 310–317.
12. Foerstner KU, von MC, Hooper SD, Bork P (2005) Environments shape the nucleotide composition of genomes. EMBO Rep 6:149-221; 12: 1208-1213.
13. Willenbrock H, Friis C, Juncker AS, Usery DW (2006) An environmental signature for 323 microbial genomes based on codon adaptation indices. Genome Biol 7(12): R114.
14. Bohlin J, Skjerve E, Usery DW (2008) Investigations of oligonucleotide usage variance within and between prokaryotes. PLoS Comput Biol 4(4): e1000057.
15. Reva ON, Tummler B (2004) Global features of sequences of bacterial chromosomes, plasmids and phages revealed by analysis of oligonucleotide usage patterns. BMC Bioinformatics 5: 90.
16. Pride DT, Meinersmann RJ, Wassenaa TM, Blaser MJ (2003) Evolutionary implications of microbial genome tetranucleotide frequency biases. Genome Res 13(2): 145-158.
17. Pride DT, Wassenaa TM, Ghose C, Blaser MJ (2006) Evidence of host-virus co-evolution in tetranucleotide usage patterns of bacteriophages and eukaryotic viruses. BMC Genomics 7: 8.
18. Packer MJ, Hunter CA (1998) Sequence-dependent DNA structure: The role of the sugar-phosphate backbone. J Mol Biol 280(5): 407-420.
19. Packer MJ, Dauncey MP, Hunter CA (2000) Sequence-dependent DNA structure: Dinucleotide conformational maps. J Mol Biol 295(1): 71-83.
20. Kurlin S, Mravek J, Campbell AM (1997) Compositional biases of bacterial genomes and evolutionary implications. J Bacteriol 179(12): 3899-3913.
21. Kurlin S (1998) Global dinucleotide signatures and analysis of genomic heterogeneity. Curr Opin Microbiol 1(3): 390-610.
22. Kurlin S, Burge C (1995) Dinucleotide relative abundance extremes: A genomic signature. Trends Genet 11(7): 283-290.
23. Josse J, KAISER AD, KORNBERG A (1961) Enzymatic synthesis of deoxyribonucleic acid. VIII. frequencies of nearest neighbor base sequences in deoxyribonucleic acid. J Biol Chem 236: 864-875.
24. Teeling H, Meyerderieks A, Bauer M, Amann R, Glockner FO (2004) Application of tetranucleotide frequencies for the assignment of genomic fragments. Environ Microbiol 6(9): 938-947.
25. Bohlin J, Skjerve E, Usery DW (2008) Reliability and applications of statistical methods based on oligonucleotide frequencies in bacterial and archaeal genomes. BMC Genomics 9: 104.
26. Baran RH, Ke H (2008) Detecting horizontally transferred and essential genes based on dinucleotide relative abundance. DNA Res 15(3): 267-276.
27. Nelson KE, Clayton RA, Gill SR, Gwinn ML, Dodson RJ, et al. (1999) Evidence for lateral gene transfer between archaea and bacteria from genome sequence of thermotoga maritima. Nature 399(6734): 323-329.
28. Kunst F, Ogasawara N, Moszer I, Albertini AM, Alloni G, et al. (1997) The complete genome sequence of the gram-positive bacterium bacillus subtilis. Nature 390(6657): 249-256.
29. Mitchell D (2007) GC content and genome length in chargaff compliant genomes. Biochem Biophys Res Commun 353(5): 207-210.
30. Fournier PE, Drancourt M, Raoult D (2007) Bacterial genome sequencing and its use in infectious diseases. 7(11): 711-723.
31. Fournier PE, Wren BW (2007) Bacterial pathogenomics. Nature 449(7164): 835-842.
32. McEwan CE, Gathereh D, McEwan NR (1998) Nitrogen-fixing aerobic bacteria have higher genomic GC content than non-fixing species within the same genus. Hereditas 129(2): 173-178.
33. Naya H, Romero H, Zavala A, Alvarez B, Musto H (2002) Aerobiosis increases the genomic guanine plus cytosine content (GC%) in prokaryotes. J Mol Evol 55(5): 260-264.
34. Moran NA (2002) Microbial minimalism: Genome reduction in bacterial pathogens. Cell 108(5): 503-506.
35. Gonzalez-Valero L, Rocha EP, Latore A, Silva FJ (2007) Reconstructing the ancestor of mycobacterium leprae: The dynamics of gene loss and genome reduction. Genome Res 17(8): 1178-1183.
36. Rocha EP, Danchin A (2002) Base composition bias might result from competition for metabolic resources. Trends Genet 18(6): 291-294.
37. Dufresne A, Garzarek I, Partenky F (2005) Accelerated evolution associated with genome reduction in a free-living prokaryote. Genome Biol 6(2): R14.
38. Koobay-Avraham L, Hoshi S, Boidiho A (2006) Involvement of DNA curvature in intergenic regions of prokaryotes. Nucleic Acids Res 34(10): 2316-2327.
39. Allen TE, Price ND, Joyce AR, Palsson BO (2006) Long-range periodic patterns in microbial genomes indicate significant multi-scale chromosomal organization. PLoS Comput Biol 2(1): e2.
40. Kulkarni OC, Vigneshwar R, Jayaraman VK, Kulkarni BD (2005) Identification of coding and non-coding sequences using local horder exponent formalism. Bioinformatics 21(20): 3818-3823.
41. Phillips GJ, Arnold J, Ivarie R (1987) Mono- through hexanucleotide composition of the escherichia coli genome: A markov chain analysis. Nucleic Acids Res 15(6): 2611-2626.
42. Elhaj J (2001) Determination of bias in the relative abundance of oligonucleotides in DNA sequences. J Comput Biol 8(2): 151-175.
43. Chen SL, Lee W, Hottes AK, Shapiro L, McAdams HH (2004) Codon usage between genomes is constrained by genome-wide mutational processes. Proc Natl Acad Sci U S A 101(10): 3480-3485.
44. Woring P, Jensen LJ, Hallin PF, Stenderfeld HH, Usery DW (2006) Origin of replication in circular prokaryotic chromosomes. Environ Microbiol 8(2): 353-361.
45. Normand P, Lapierre P, Tiss LS, Gogarten JP, Alloiso N, et al. (2007) Genome characteristics of facultatively symbiotic frankia sp. strains reflect host range and host plant biogeography. Genome Res 17(1): 7-15.
46. Collins NE, Lieberberg J, de Villiers EP, Bratton KA, Louise E, et al. (2003) The genome of the heartwater agent ehrlichia ruminantium contains multiple tandem repeats of actively variable copy number. Proc Natl Acad Sci U S A 102(3): 838-843.
47. Lawrence JG, Ochman H (1997) Amplification of bacterial genomes: Rates of change and exchange. J Mol Evol 44(4): 383-397.
48. National Center for BI. (2007) http://www.ncbi.nlm.nih.gov/Genomes/.
49. R Development CT. (2007) R: A language and environment for statistical computing. (2).
50. Box GEP (1964) An analysis of transformations. Journal of the Royal Statistical Society. Series B (Methodological), Vol. 26, no. 2, 262(2): 211-254.
51. Musto H, Naya H, Zavala A, Romero H, Valin-F v, et al. (2006) Genomic GC level, optimal growth temperature, and genome size in prokaryotes. Biochem Biophys Res Commun 347(0006-291): 1-3.