



Article

Random Worms: Evidence of Random and Nonrandom Processes in the Chromosomal Structure of Archaea, Bacteria and Eukaryotes

In Table 1 we list the number of genes per string (n/s) and then the 3 standard deviation range for each entry. When we compare the string lengths observed with the expected range for the coin-flip model, we see significant deviations from that in Table 1 among the archaea and bacteria. ... The clear conclusion is that this random model totally fails to account for the bacterial data.

Genome	Model 1		# Genes	# Strings		3 Standard Deviation Range
	Strain	Domain	n	s	n/s	
Mycoplasma genitalium	G-37	Bacteria	522	86	6.07	1.73–2.26
Bacillus subtilis	168	Bacteria	4222	1092	3.78	1.91–2.09
Escherichia coli	K12	Bacteria	4405	1292	3.41	1.91–2.09
Escherichia coli	157:H7	Bacteria	5410	1472	3.68	1.91–2.08
Vibrio cholerae 1	N16961	Bacteria	2769	876	3.16	1.88–2.11
Vibrio cholerae 2	N16961	Bacteria	1115	398	2.80	1.82–2.17
Aeropyrum pernix	K1	Archaea	2746	1612	1.70	1.88–2.11
Archaeoglobus fulgidus	DSM4304	Archaea	2486	738	3.37	1.87–2.12
Campylobacter jejuni		Bacteria	4102	1094	3.75	1.91–2.09
Plasmid F		Bacteria	111	32	3.47	1.43–2.57
	Chromosome					
Saccharomyces cerevisiae	1	Eukaryote	112	62	1.80	1.43–2.57
Saccharomyces cerevisiae	2	Eukaryote	446	237	1.88	1.72–2.28
Saccharomyces cerevisiae	3	Eukaryote	186	84	2.21	1.56–2.44
Saccharomyces cerevisiae	4	Eukaryote	856	467	1.83	1.79–2.21
Saccharomyces cerevisiae	5	Eukaryote	309	151	2.04	1.66–2.34
Saccharomyces cerevisiae	6	Eukaryote	145	72	2.01	1.50–2.50
Saccharomyces cerevisiae	7	Eukaryote	609	319	1.91	1.76–2.24
Saccharomyces cerevisiae	8	Eukaryote	295	149	1.97	1.65–2.35
Saccharomyces cerevisiae	9	Eukaryote	233	126	1.84	1.61–2.39
Saccharomyces cerevisiae	10	Eukaryote	416	220	1.89	1.71–2.29
Saccharomyces cerevisiae	11	Eukaryote	355	189	1.87	1.68–2.32
Saccharomyces cerevisiae	12	Eukaryote	571	313	1.82	1.75–2.25
Saccharomyces cerevisiae	13	Eukaryote	513	273	1.88	1.74–2.26
Saccharomyces cerevisiae	14	Eukaryote	438	225	1.94	1.71–2.29
Saccharomyces cerevisiae	15	Eukaryote	597	319	1.87	1.75–2.25
Saccharomyces cerevisiae	16	Eukaryote	519	289	1.79	1.74–2.25
Caenorhabditis elegans	1	Eukaryote	2411	1140	2.11	1.88–2.12
Caenorhabditis elegans	2	Eukaryote	2962	1384	2.14	1.89–2.11
Caenorhabditis elegans	3	Eukaryote	1788	834	2.14	1.85–2.14
Caenorhabditis elegans	4	Eukaryote	2453	1149	2.13	1.87–2.12
Caenorhabditis elegans	5	Eukaryote	4325	1961	2.20	1.91–2.09
Caenorhabditis elegans	X	Eukaryote	2643	1208	2.18	1.88–2.11
	What are called Scaffolds					
Drosophila melanogaster	1	Eukaryote	1119	594	1.88	1.82–2.17
Drosophila melanogaster	2	Eukaryote	672	378	1.77	1.76–2.23
Drosophila melanogaster	3	Eukaryote	596	297	2.00	1.75–2.24
Drosophila melanogaster	4	Eukaryote	1034	555	1.86	1.81–2.18
Drosophila melanogaster	5	Eukaryote	1699	910	1.86	1.85–2.14
Drosophila melanogaster	6	Eukaryote	116	66	1.75	1.44–2.55
Drosophila melanogaster	7	Eukaryote	28	15	1.86	0.86–3.13
Drosophila melanogaster	8	Eukaryote	568	313	1.81	1.74–2.25
Drosophila melanogaster	9	Eukaryote	286	174	1.64	1.64–2.35
Drosophila melanogaster	10	Eukaryote	264	148	1.78	1.63–2.36
Drosophila melanogaster	11	Eukaryote	1756	952	1.84	1.85–2.14
Drosophila melanogaster	12	Eukaryote	142	80	1.77	1.50–2.50
Drosophila melanogaster	13	Eukaryote	2953	1593	1.86	1.90–2.11
Drosophila melanogaster	14	Eukaryote	48	24	2.00	1.14–2.86
Drosophila melanogaster	15	Eukaryote	86	44	1.95	1.35–2.65
Drosophila melanogaster	16	Eukaryote	63	28	2.25	1.24–2.76
Drosophila melanogaster	17	Eukaryote	1787	978	1.83	1.85–2.14
Drosophila melanogaster	18	Eukaryote	53	28	1.89	1.18–2.82
Drosophila melanogaster	19	Eukaryote	30	17	1.76	0.90–3.10

Table 1. Genome Data.