# Modeling the distribution of primes in computable biomolecules 

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#### Abstract

Prime numbers are an important research area with application in computer security. The security of certain cryptographic schemes critical in information security lies in the difficulty of factoring large numbers into their prime factors. Determination of the distribution of prime numbers is an important unsolved problem in number theory. Biomolecules such as DNA have extended the domains of what is considered a standard computer model. This report investigated the distribution of prime numbers generated from viral DNA. The digits of Euler's number and Pi were found to be encoded between Bacteriophage T4 Watson-Crick DNA segments comprised of prime numbers.


Key words: Prime number, number theory, molecular computing, phage T4.

## INTRODUCTION

A prime number is a natural number larger than one which cannot be expressed as a product of two smaller natural numbers (Tao, 2007). The prime numbers less than 20 are $2,3,5,7,11,13,17$, and 19. Prime numbers, once thought to be of interest only to number theorists, have found application in computer science and technology, mainly in the protocols of information security and cryptography - with the development of public key cryptography (Rivest et al., 1978), whose security lies in the difficulty of factoring large numbers into their prime factors. The most common public key encryption algorithm is RSA, named after its developers Ron Rivest, Adi Shamir and Leonard Adleman (Rivest et al., 1978).
The standard computer model in computability theory is the Turing Machine (Turing, 1936). Deoxyribonucleic acid (DNA) has been used in the implementation of the Turing Machine (Rothemund, 1996; Qian et al., 2011), birthing the field of molecular computing (Lipton, 1995; Winfree, 1996; Quyang et al., 1997; Lagoudakis and LaBean, 2000; Braich et al., 2002; Rothemund et al., 2004). Molecular computing has brought biological molecules into the field of computer science and engineering. DNA computation also has potential application in fabrication tasks in nanotechnology (Cook et al., 2004; Barish et al., 2005) and in the design of digital logic circuits (Seelig et al., 2006).
Determining the distribution of prime numbers among natural numbers is an important unsolved problem in mathematical number theory (Tao, 2007). The question is
closely linked with the Riemann Hypothesis (Conrey, 2003), which predicts a precise formula for the probability distribution of primes. The distribution of 20,000 prime numbers generated from Bacteriophage T4 DNA was investigated, with the objective of determining their distribution. Euler's number (e) and $\mathrm{Pi}(\pi)$ are two of the most important mathematical constants and a part of Euler's identity: $e^{i \pi}+1=0$. The value of $e$ and $\pi$ to ten significant figures respectively are $\mathrm{e}=2.718281828$ and $\pi=3.141592653$, obtained from the Online Encyclopedia of Integer Sequence (Sequences A0011133 and A000796 respectively).

## MATERIALS AND METHODS

Bacteriophage T4 Genome (Miller et al., 2003) was sourced from GenBank, the institutional genome depository with accession number AF158101. Bacteriophage T4 represents the most understood model for modern genomics and proteomics; and its study has revealed many insights and paradigms in molecular biology. The numbers of each nucleotide base per Watson-Crick single strand DNA segments, comprising of ten bases each were counted and recorded in successive single strand segments of T4 phage DNA (single strand complement $1^{\prime}-99,180^{\prime}$ in the $3^{\prime}$ to $5^{\prime}$ direction). The prime numbers present as numbers of nucleotides were: 2, 3, 5 and 7; and the distances between them in 20,000 numbers generated from T4 Phage DNA was investigated. The frequency histogram of the distances was plotted with Microsoft ${ }^{8}$ Excel statistical package.T4 Phage Watson-Crick single strand DNA segments comprising only of prime numbers consist of the


Figure 1. Histogram showing the frequency distribution of the distances between prime numbers generated from T4 Phage DNA Watson-Crick units.
following combinations of nucleotide bases: 55, 37, 235 and 2233. The spatial distances between these prime segments were recorded and these distances traced out digits of the mathematical constants pi and e.

## RESULTS

The distribution of the 20,000 prime numbers generated from Bacteriophage T4 nucleotide bases followed a binomial distribution (Figure 1). The mean and standard deviation of a binomial random variable is expressed as: $\mu=n p$ and $\sqrt{ } n p(1-p)$. An understanding of the distribution of prime numbers among the natural numbers - a subject of the Riemann Hypothesis, is listed by the Clay Mathematics Institute as one the seven most important open questions in Mathematics and a Millennium Prize Problem (Sarnak, 2004). This work describes the distribution of prime numbers generated from a biomolecule, DNA. The secondary result of this investigation is that the distances between T4 Phage

Watson-Crick DNA segments comprised of prime numbers encoded 12 values of $e$ and 15 values of $\pi$ to ten significant figures (Table 1).

## DISCUSSION AND CONCLUSION

The principal finding of this work is that the distribution of prime numbers in DNA follows a binomial distribution. The study of the nature of prime numbers is of importance in computer security (Tao, 2007). Secondarily, the efforts directed at computing the values of mathematical constants such as pi and e (Shanks and Wrench, 1962; Wei et al., 1996; Bailey et al., 1997) permits us two ways of making sense of the encoding of the two mathematical constants within DNA molecules. On the one hand, there is merit in attributing this to pure chance; on the other hand, it might point to non-trivial behaviour in DNA molecules, which is not a surprise given the new role of DNA molecules in computing.

Table 1. Spatial distances of digits of $e$ and $\pi$ as encoded between the distances of Watson-Crick units of T4 DNA comprised of prime numbers.

| Spatial distances of digits of e |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| e | $\mathbf{e}_{1}$ | $\mathbf{e}_{2}$ | $\mathbf{e}_{3}$ | $\mathrm{e}_{4}$ | $\mathbf{e}_{5}$ | $\mathbf{e}_{6}$ | $\mathbf{e}_{7}$ | $\mathrm{e}_{8}$ | $\mathrm{e}_{9}$ | $\mathbf{e}_{10}$ |  |  |  | $\mathbf{e}_{12}$ |  |
| 2 | 26 | 170 | 270 | 410 | 620 | 702 | 780 | 896 | 1014 | 1173 |  | 01 |  | 1571 |  |
| 7 | 35 | 175 | 280 | 428 | 630 | 714 | 789 | 915 | 1032 | 1174 |  | 19 |  | 1575 |  |
| 1 | 36 | 183 | 281 | 431 | 633 | 723 | 814 | 921 | 1039 | 1178 |  | 20 |  | 1579 |  |
| 8 | 69 | 196 | 293 | 571 | 635 | 731 | 865 | 929 | 1047 | 1191 |  | 27 |  | 1589 |  |
| 2 | 90 | 202 | 300 | 572 | 650 | 735 | 866 | 931 | 1049 | 1204 |  | 66 |  | 1594 |  |
| 8 | 103 | 222 | 308 | 585 | 661 | 750 | 867 | 955 | 1080 | 1205 |  | 79 |  | 1621 |  |
| 1 | 105 | 225 | 320 | 593 | 662 | 753 | 879 | 959 | 1082 | 1208 |  | 84 |  | 1623 |  |
| 8 | 122 | 258 | 348 | 595 | 686 | 758 | 881 | 995 | 1135 | 1338 |  | 22 |  | 1635 |  |
| 2 | 130 | 261 | 351 | 613 | 687 | 760 | 885 | 1003 | 1136 | 1354 |  | 26 |  | 1636 |  |
| 8 | 168 | 265 | 378 | 619 | 700 | 776 | 890 | 1007 | 1161 | 1398 |  | 59 |  | 1642 |  |
| Spatial distances of digits of $\pi$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T | $\Pi_{1}$ | $\pi{ }^{2}$ | $\pi_{3}$ | T 4 | T 5 | T 6 | $\mathrm{T}_{7}$ | T 8 | T9 | $\Pi_{10}$ | $\Pi_{11}$ | $\pi_{12}$ | $\Pi_{13}$ | $\Pi_{14}$ | $\Pi_{15}$ |
| 3 | 23 | 161 | 238 | 429 | 525 | 665 | 786 | 982 | 1072 | 1146 | 1207 | 1358 | 1443 | 1498 | 1596 |
| 1 | 27 | 163 | 240 | 431 | 539 | 675 | 814 | 984 | 1078 | 1153 | 1208 | 1365 | 1448 | 1519 | 1601 |
| 4 | 37 | 179 | 288 | 433 | 545 | 688 | 818 | 987 | 1086 | 1155 | 1216 | 1369 | 1449 | 1530 | 1619 |
| 1 | 40 | 183 | 295 | 437 | 548 | 689 | 834 | 1002 | 1090 | 1157 | 1219 | 1376 | 1453 | 1532 | 1623 |
| 5 | 57 | 190 | 297 | 447 | 559 | 694 | 839 | 1008 | 1092 | 1158 | 1234 | 1379 | 1469 | 1535 | 1627 |
| 9 | 109 | 195 | 337 | 455 | 601 | 742 | 883 | 1040 | 1102 | 1177 | 1258 | 1411 | 1473 | 1561 | 1683 |
| 2 | 119 | 202 | 351 | 458 | 613 | 744 | 885 | 1049 | 1113 | 1190 | 1282 | 1412 | 1478 | 1571 | 1689 |
| 6 | 123 | 207 | 385 | 463 | 616 | 763 | 965 | 1057 | 1116 | 1195 | 1350 | 1413 | 1483 | 1576 | 1690 |
| 5 | 135 | 224 | 401 | 512 | 618 | 768 | 976 | 1061 | 1137 | 1196 | 1352 | 1437 | 1490 | 1580 | 1691 |
| 3 | 147 | 227 | 402 | 513 | 654 | 782 | 979 | 1070 | 1144 | 1198 | 1355 | 1441 | 1491 | 1583 | 1706 |

## REFERENCES

Bailey D, Borweinand P, Plouffe S (1997). On the Rapid Computation of Various Polylogarithmic constants. Math. Comput., 66: 903-913.
Barish RD, Rothemund PWK, Winfree E (2005). Two computational primitives for algorithmic self-assembly: Copying and counting. Nano Lett., 5: 2586-2592.
Braich RS, Chelyapov N, Johnson C, Rothemund PWK, Adleman L (2002). Solution of a 20 -variable 3 -SAT Problem on a DNA Computer. Science, 296: 499-502.
Conrey JB (2003).The Riemann Hypothesis. Notices Am. Math. Soc., 50: 341-353.
Cook M, Rothemund PWK, Winfree E (2004). Self-assembled circuit patterns. In Chen J and Reif J (eds), DNA Computers, volume 9. Lect. Notes Comput. Sci., 2943, Berlin Heidelberg, Springer-Verlag, pp. 91-107.
Lagoudakis MG, LaBean TH (2000). 2-D DNA self-assembly for satisfiability. In Winfree E and Gifford DK (eds) DNA Based Computers V, volume 54 of DIMACS, Providence, RI. American Mathematical Society, pp. 141-154.
Lipton RJ (1995). DNA solution of hard computational problems. Science, 268: 542-545.
Miller ES, Kutter E, Mosig G, Arisaka F, Kunisawa T, Ruger W (2003). Bacteriophage T4. Microbiol. Mol. Biol. Rev., 67: 86-156
Qian L, Soloveichik D, Winfree E (2011). Efficient Turing-Universal computation with DNA polymers. (Eds: Sakakibara Y. and Mi Y.) In DNA 16, Lect. Notes Comput. Sci., 6518: 123-140.
Quyang Q, Kaplan PD, Liu S, Libchaber A (1997). DNA solution of maximal clique problem. Science, 278: 446-449.
Rothemund PWK (1996). A DNA and restriction enzyme implementation of Turing Machines. In Lipton RJ and Baum EB (eds) DNA Based Computers, volume 27 of DIMACS, Providence, RI, 1996. American Mathematical Society, pp. 75-120.

Rothemund PWK, Papakakis N, Winfree E (2004). Algorithmic selfassembly of DNA Sierpinski triangles. PLoS Biol., 2: 424-436.
Rivest R, Shamir A, Adleman L (1978). A method for obtaining digital signatures and Public-Key Cryptosystems. Commun. ACM., 21(2): 120-126.
Sarnak P (2004). Problems of the Millennium: The Riemann Hypothesis. Clay Mathematics Institute, p. 1.
Seelig G, Soloveichik D, Zhang DY, Winfree E (2006). Enzyme-free nucleic acid logic circuits. Science, 314: 1585-1588.
Shanks D, Wrench JW (1962). Calculation of Pi to 100,000 decimals. Math. Comput., 16: 76-79.
Tao T (2007). Structure and randomness in the prime numbers: A small collection of results in number theory. UCLA Science Colloquium, pp. 2, 24, 18.
Turing A (1936). On computable numbers with an application to the entscheidnungsproblem. Proc. London Math. Soc., 42(2): 230-265.
Wei GY, Yang ZG, Sun JC, Li JK (1996). The computation of Pi to 10,000,000 decimal digits. J. Numer. Methods Comput. Appl., 17: 7881.

Winfree E (1996). On the computational power of DNA annealing and ligation. In R. J. Lipton RJ and Baum EB (eds) DNA Based Computers, volume 27 of DIMACS, Providence, RI, 1996. American Mathematical Society, pp. 199-221.

