

# Both Chargaff Second Parity Rule and the Strand Symmetry Rule Are Imprecise

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**Abstract:** In order to check Chargaff Second Parity Rule, we find the strands are asymmetric in human DNA, this breaks the strand symmetry rule. We calculate the ratio between oligonucleotide ATGC and oligonucleotide CGTA, and we compare the sample sequence average ratio ATGC/CGTA and the complementary sequence average ratio ATGC/CGTA. we find evolution degree more bigger, then the strand symmetry deviation will be more bigger. sequence and its complementary strand sequence obviously have two different characters, include physical property, chemical property and biological property. It is very important, base on this asymmetry, we can find some new and special theories in biology to explain how chromosome communicates and works in the future. we also find, both leukemia and breast cancer are weakening the DNA's asymmetry degree. Here need more research and check, maybe we can find an easy diagnosing method to leukemia and breast cancer, if this result here is right at last, it will benefit to the world.

**Keywords:** ATGC/CGTA, Strand Asymmetry, Complementary Sequence, Evolutionary Forces

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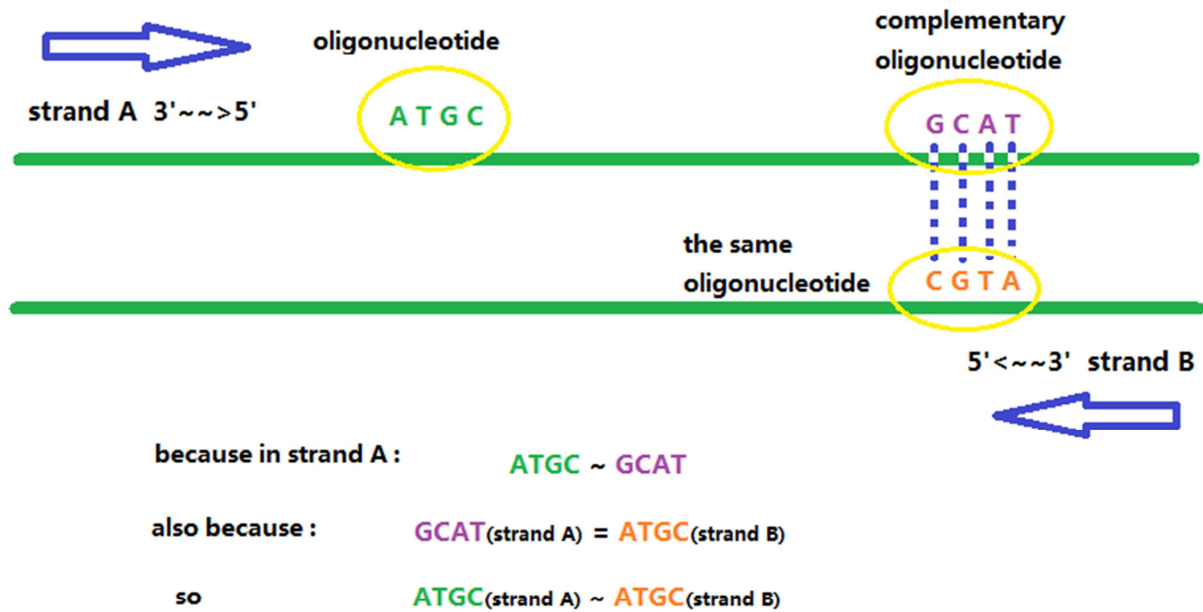
## 1. Introduction

Strand symmetry

Chargaff Second Parity Rule holds that both  $A \sim T$  and  $G \sim C$  are valid for each of the two DNA strands [7]. This describes only a global feature of the base composition in a single DNA strand [1]. It is discovered by Austrian born chemist Erwin Chargaff [2] [6]. Hence, this double-stranded DNA characteristic can also be called "symmetry of complementary DNA strands [3] [4]". Chargaff's second parity rule ordinarily considers only mononucleotides, which have been extensively studied. The strand symmetry rule also says that oligonucleotide such as ATGC and its complementary oligonucleotide GCAT, there is the same relation  $ATGC \sim GCAT$ .

In figure 1, we can get the relation  $ATGC(\text{strand A}) \sim ATGC(\text{strand B})$ , by the same way, we can get the relation about another oligonucleotide CGTA, between

sample sequence and its complementary sequence, there are the same relation  $CGTA(\text{strand A}) \sim CGTA(\text{strand B})$ , so there must be the relation, in strand A, the ratio  $ATGC/CGTA$  approximately equals to the ratio  $ATGC/CGTA$  in strand B. This result is based on strand symmetry rule, it means two strands in one chromosome have approximate properties, they are symmetry. But it is not the fact, when we check the sequence using human DNA, and we find evolution degree more bigger, then the deviation will be more bigger, although many scientists have found this phenomenon for many years, they always look for some method to modify the big deviation, they try to make the strand symmetry rule to perfect all the species. We think to human, the stand is not symmetric, it is asymmetric.



**That is to say : strand A and strand B are symmetric**

Figure 1. Analyze method to strand symmetry.

## 2. Method

See figure 2, segment a long sequence into many short segments with the same length, then, to every segment, calculate the number of oligonucleotide ATGC and the number of oligonucleotide CGTA. Then calculate the ratio ATGC/CGTA value for every segment. and give the average

ratio value for the whole sequence

By A~T, G~C, translate out the complementary strand sequence code, use method above in figure 2, calculate the ratio ATGC/CGTA value for every segment. and give the average ratio value for the complementary strand [9] [10] sequence

Plot the ratio for the sequence and its complementary strand sequence

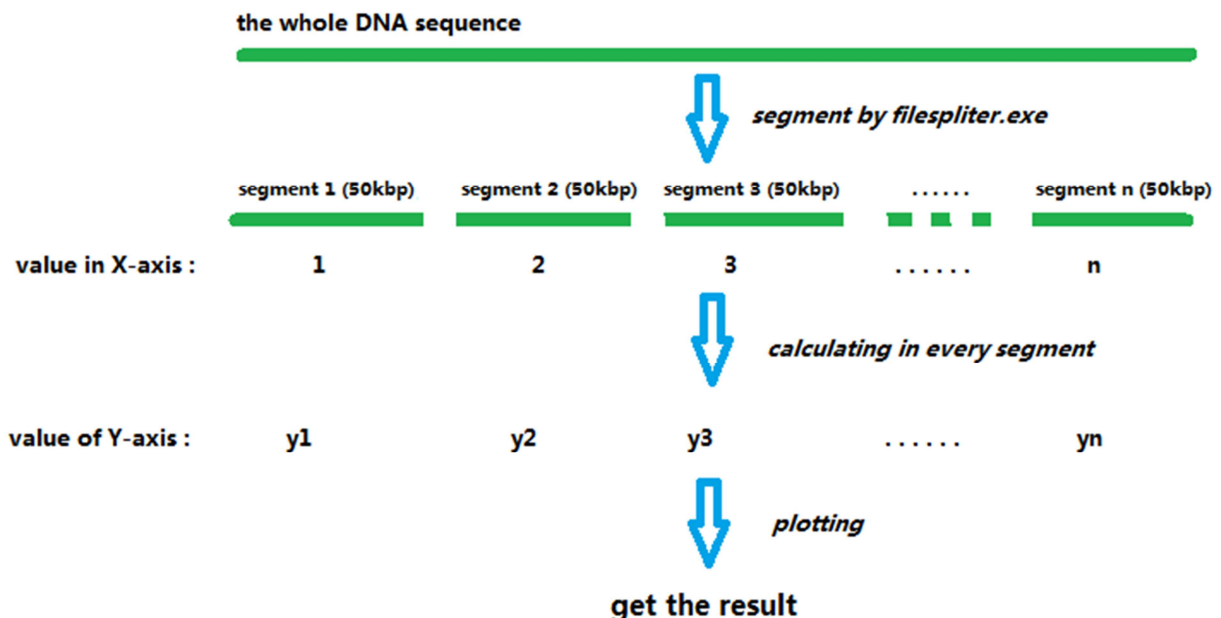


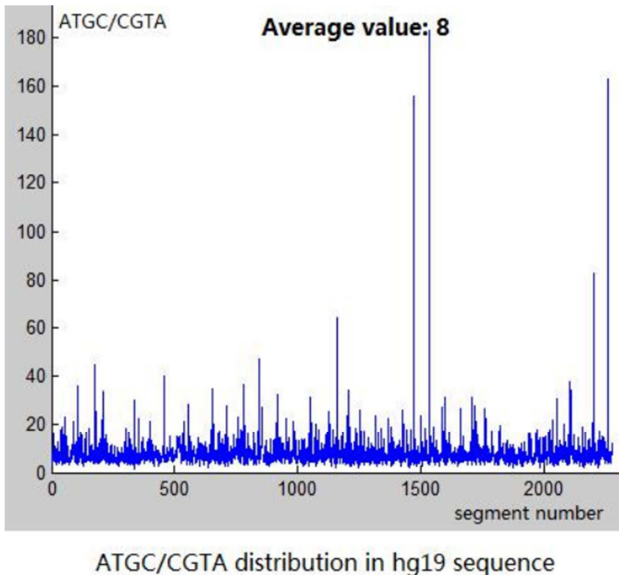
Figure 2. Calculate method.

## 3. Results

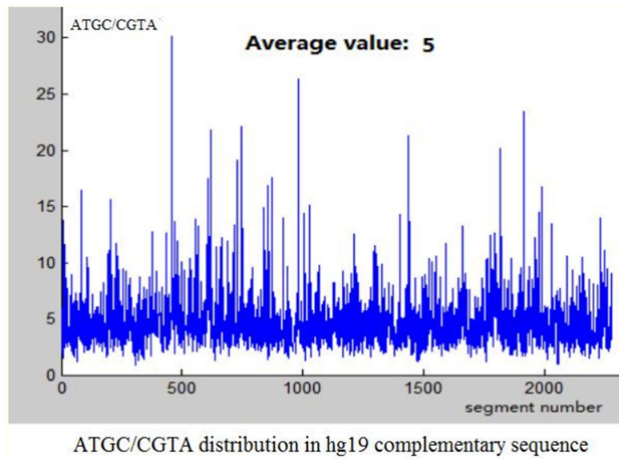
We use human DNA [8] sequence and mouse DNA sequence and fly DNA sequence to check strand symmetry,

compare two strands' ATGC/CGTA, we compare the sample sequence's ATGC/CGTA value with its complementary strand sequence's ATGC/CGTA value.

Here is human's DNA sequence is hg19 sequence

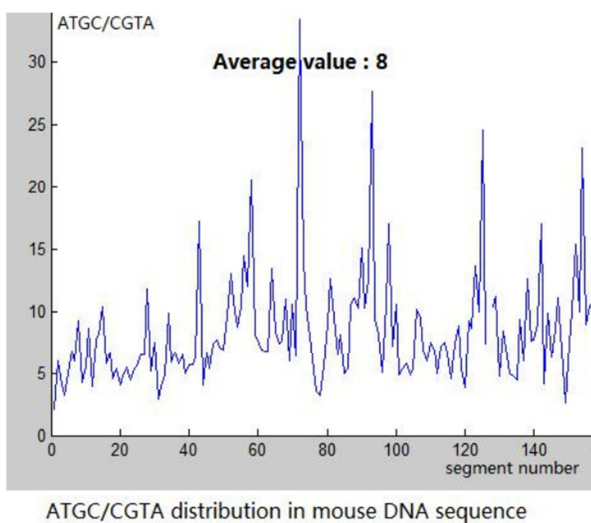


**Figure 3.** Human healthy DNA.

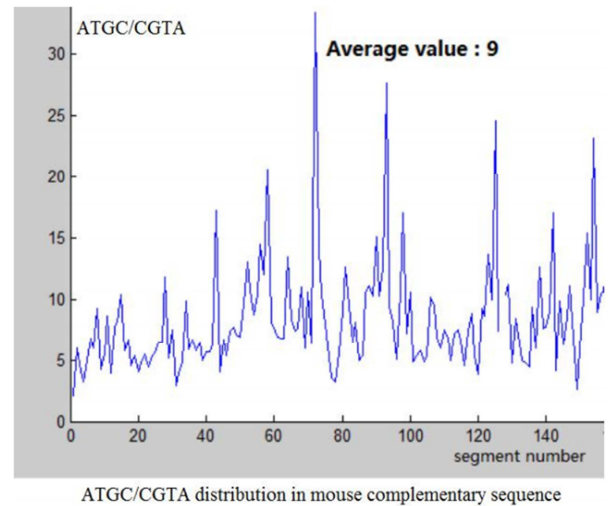


**Figure 4.** Human healthy DNA complementary sequence.

Then, we do the same analysis on a mouse's DNA, the sequence is from [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov), the GenBank: NC\_008802.1

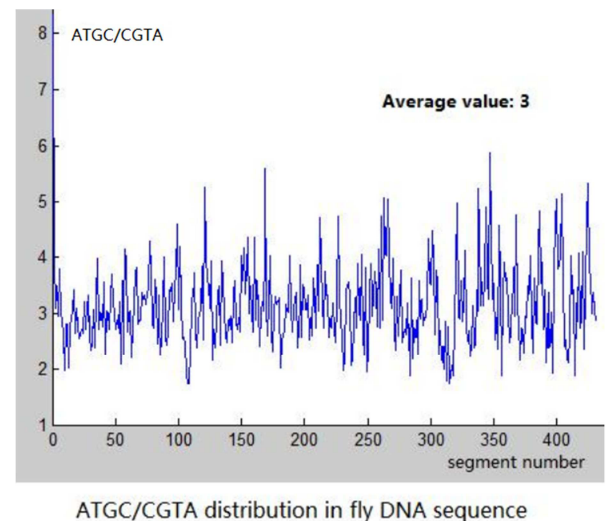


**Figure 5.** Mouse DNA.

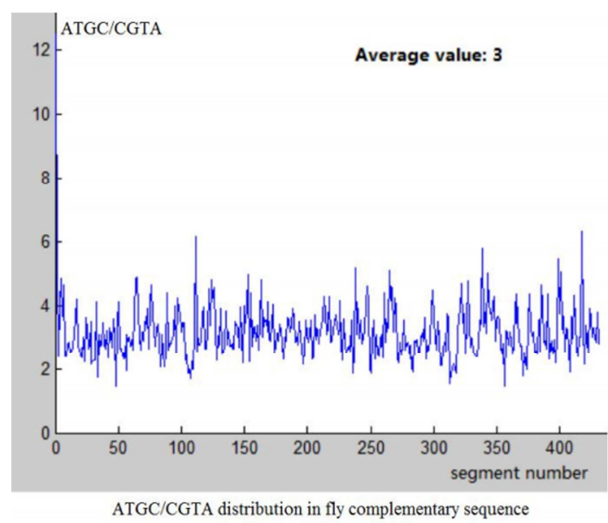


**Figure 6.** Mouse DNA complementary sequence.

Next, we do the same analysis on a fly's DNA, the sequence is from [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov), the GenBank: CP012523.1



**Figure 7.** Fly DNA.



**Figure 8.** Fly DNA complementary sequence.

Compare the above data using the following

**Table 1.** Asymmetry degree and Evolution degree.

Species	Sequence ATGC/CGTA	Complementary sequence ATGC/CGTA	Ratio (big/small)	Asymmetry degree	Evolution degree
fly	3	3	1.0	low	low
mouse	9	8	1.1	middle	middle
human	8	5	1.6	high	high

## 4. Discussion

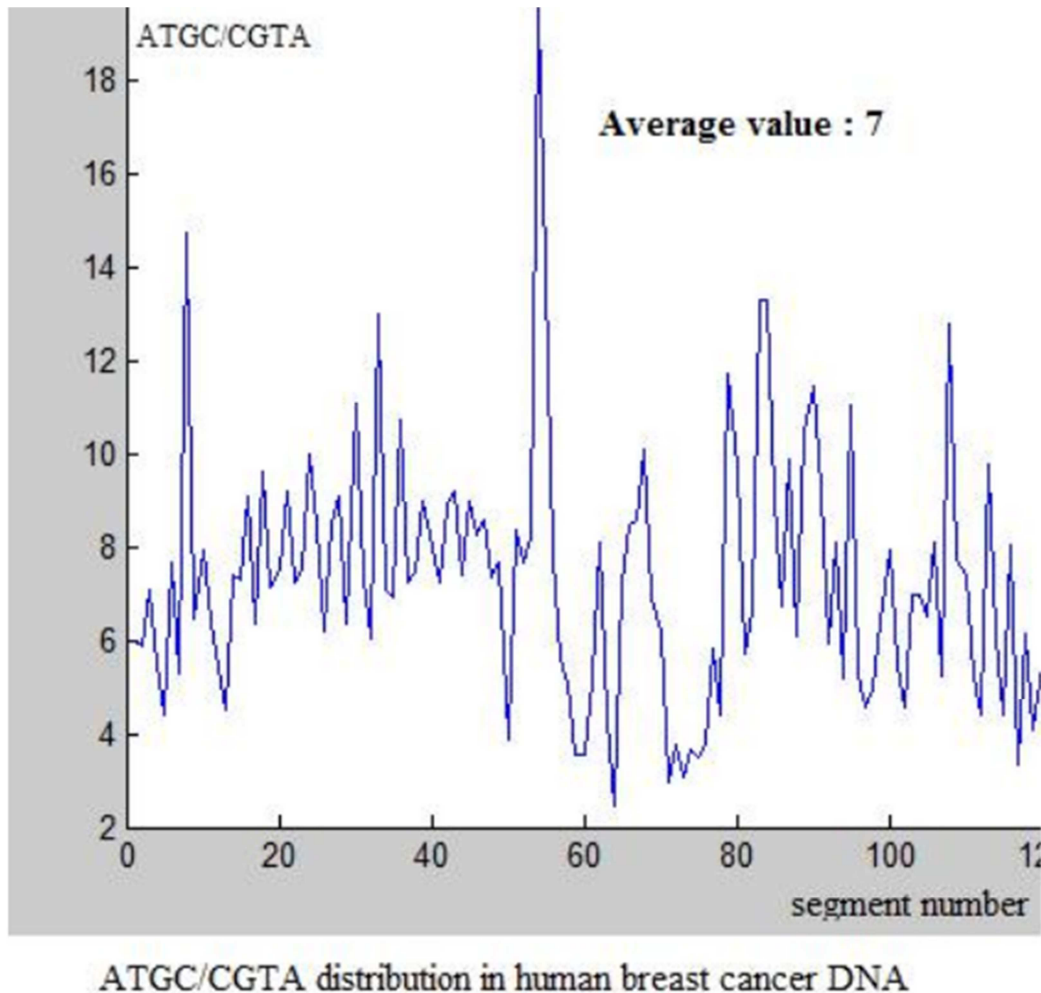
First, we can find, both Chargaff Second Parity Rule and the Strand Symmetry Rule do not perfect to human DNA, *in human chromosome, sequence and its complementary strand sequence obviously have two different characters, include physical property, chemical property and biological property.* It is very important, based on this asymmetry, we can find some new and special theories in biology to explain how chromosome communicates and works in the future.

Here we also give the answer to question: “Did

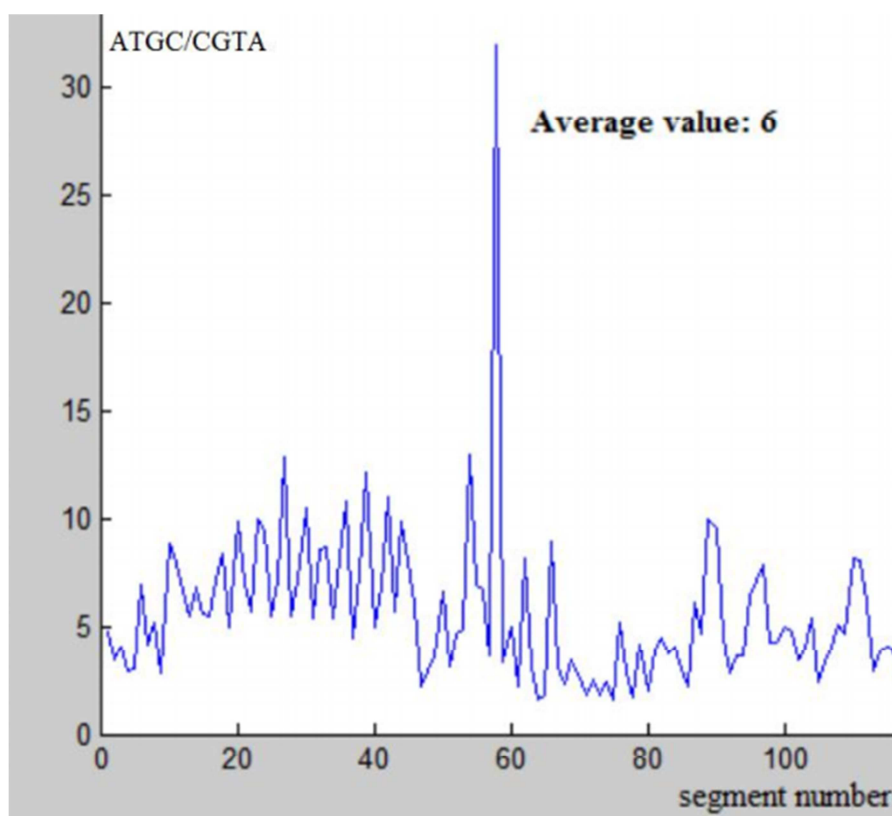
evolutionary forces select for the Chargaff ratios in single DNA strands, with equality of complementary oligonucleotide frequencies being an automatic consequence? Alternatively, did evolutionary forces select for equality of complementary oligonucleotide [5] frequencies, with the Chargaff ratios being an automatic consequence?” Evolutionary forces select for the Chargaff ratios in single DNA strands.

## 5. More Application

Next we do the same analysis on human breast cancer’s DNA, the sequence is from [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)



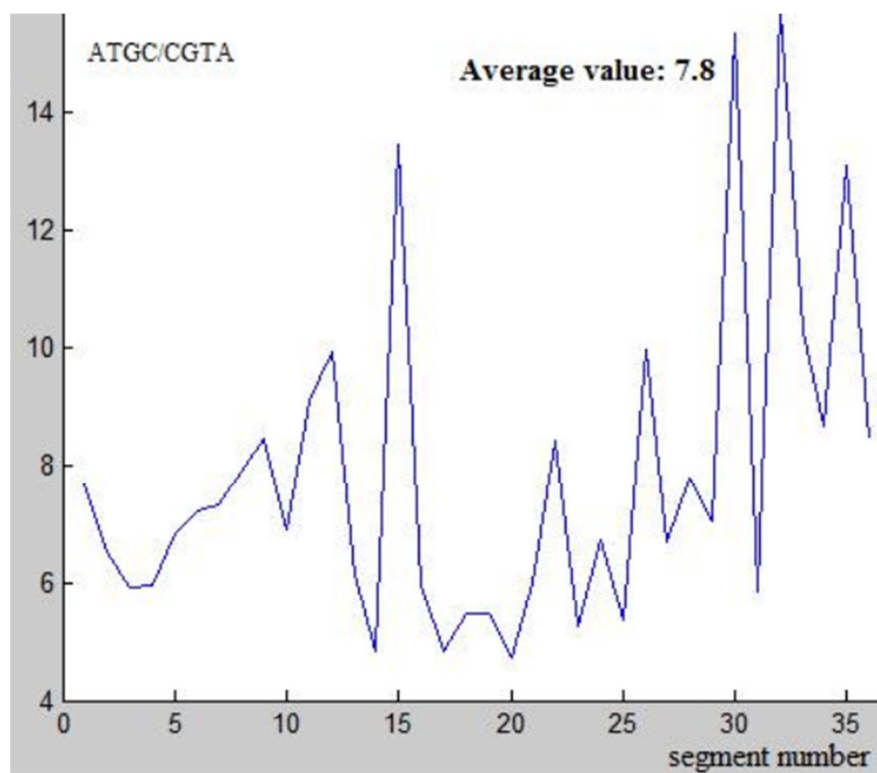
**Figure 9.** Human breast cancer DNA.



ATGC/CGTA distribution in human breast cancer complementary sequence

**Figure 10.** Human breast cancer DNA complementary sequence.

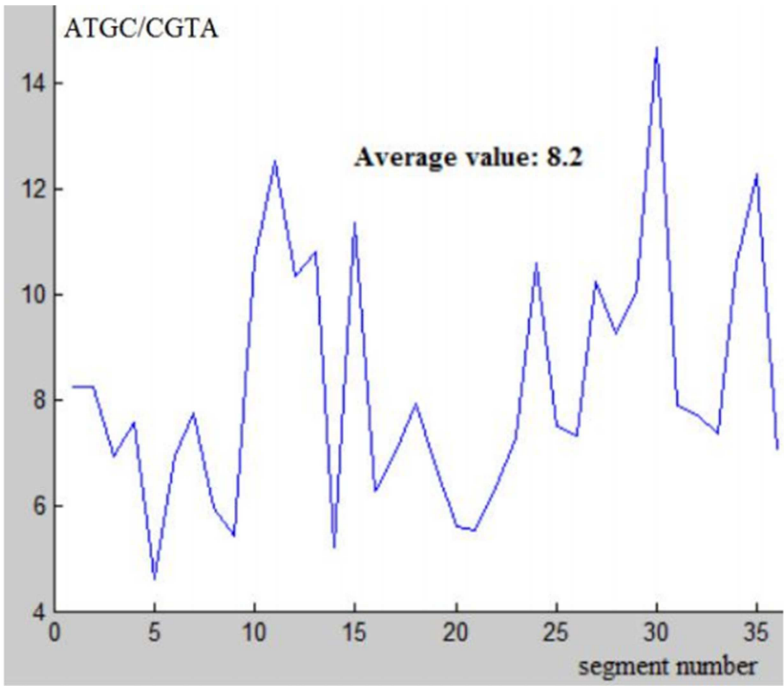
Next we do the same analysis on human leukemia's DNA, the sequence is from [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)



ATGC/CGTA distribution in leukemia DNA

**Figure 11.** Human leukemia DNA.





ATGC/CGTA distribution in human leukemia complementary sequence

Figure 12. Human leukemia DNA complementary sequence.

Compare the above data using the following

Table 2. Cancer and Asymmetry degree.

Species	Sequence ATGC/CGTA	Complementary sequence ATGC/CGTA	Ratio (big/small)	Asymmetry degree
Human healthy DNA	8	5	1.6	high
Homo Leukemia	8.2	7.8	1.05	lower
Homo breast cancer	7	6	1.17	low

Both leukemia and breast cancer are weakening the DNA’s asymmetry degree. Here need more research and check, maybe we can find an easy diagnosing method to leukemia and breast cancer, if my result here is right at last, it will benefit to the world, thanks to other researchers!

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