

Universal Recursive Crossing Science Of Genetic Kind

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Abstract

In this research investigation, the author presents a novel method called ‘*Universal Recursive Crossing Science Of Genetic Kind*’. This method outlays how Genetic Crossing happens for the Asexual and Heterosexual kind.

Theory

Firstly, we consider the entire Genome of say any Human Being and we call all ‘*Unique Segments*’ of Sequences (as variables numbered from 1 through as many needed by the aforementioned Genome). For example, say if we have four bases, namely Adenine (A), Cytosine (C), Thymine (T), Guanine (G) and therefore for the double helical DNA type we can have 12 combinations slated below:

A-C

A-T

A-G

C-T

C-A

C-G

T-A

T-C

T-G

G-A

G-C

G-T

Now, these 12 combinations can be further arranged in $12!$ (i.e., 12 factorial) ways. Therefore, we can have $12!$ Unique Segments of sequences to which we assign $12!$ number of variables for all the $12!$ Arrangements mentioned before. We now consider the Crossing Method synonymous with any scheme of generation of Sequence of Primes [1], [2] (the algebra slated in [2] is not discussed in this example, however one can read it for better inertia of comprehension of this research problem) wherein we first consider a Cartesian

Cross Product of each of the aforementioned variables, i.e., Unique Segments with themselves. We then also create a set equivalent to the addition of these ordered pair values of the $12! \times 12!$ number of Unique Segments thusly found by the aforementioned Cross Product. Upon such addition, we also distill and/ or reduce them to a fashion wherein each of such additioned aspect variable is actually a 'm' times (the originally considered 12 pairs sequence) where 'm=($12! \times 12!$)' goes from 1 through a number prescribed by the limits of the Human Genome for this situation of algebraic operation. Therefore, now we can actually perform deduction of the set of crossed and ordered pairs added set from this set of 'm' times (the originally considered 12 pairs sequence).

It is possible that some of the Unique Segments gotten by the aforementioned additions may not be reducible as describe above. Therefore, for these Unique Segments we use the Sequence Of Primes of 3rd Order Space and implement the crossing procedure (see [2]) commensurate with the algorithmic scheme for generating the Sequence Of Primes of 3rd Order Space. Again, among the residual Unique Segments that were non-reducible in the above already once detailed fashion some and/ or all of them may be reducible if we implement the same procedure again using the algorithmic scheme for generating the Sequence Of Primes of 4th Order Space and so on so forth infinitely. At each of the levels we also perform the necessary deductions of the already detailed kind to get the final Cross Product Set which will be a Union of Cross Product elements (Unique Segments) gotten (after performing the necessary aforementioned kind deductions) Sets, each gotten via the algorithmic scheme of generation of Sequence Of Primes of 2nd , 3rd , 4th ,(and so on so forth until we have no more such residual elements (Unique Segments) Ordered Spaces.

This gives us the Pure Self Cross of Asexual kind of the Human Genome. In a similar fashion, one can consider Hetero-Sexual kind crosses of the Human Genome kind.

References

- 1.<http://www.vixra.org/abs/1502.0100>
'The Prime Sequence Generating Algorithm'.

2.<http://www.vixra.org/abs/1509.0291>

'The Prime Sequence's (Of Higher Order Space's) Generating Algorithm'.

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Note

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