

The Length Of An Interval Of A Positive Integers Sequence Represented (Measured) By An Alternation Of The First Prime Numbers

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Abstract:

This paper is dedicated to analysis of a positive integers sequence represented as a periodic structure consisting of an alternation of prime numbers $\leq P$ (1 least prime factor >1 for any number). There was established the maximum possible length of alternation of the first prime odd numbers (from 3 to P_2) for any subsequent primorial period $=P\#$ (it has been proved that: any interval of a positive integers sequence may be represented (measured) as a rhythmic alternation of the first prime numbers from 2 up to certain P_2 inclusive (1 least prime factor >1 for any number) by one and only method). In this case the maximum length of any of the mentioned interval contains:

- no more than (P_1-1) odd numbers of such interval (int.odd num.);
- no more than (P_2-1) odd numbers of such interval inclusive of 1 odd number NON-divisible by the prime numbers $\leq P_2$;
- no more than (P_3-1) odd numbers of such interval inclusive of 2 odd numbers NON-divisible by the prime numbers $\leq P_2$.

Furthermore at an interval of the positive integers sequence from P_2^2 to P_3^2 :

- a). Difference between two adjacent prime numbers is $\leq 2P_1$.
- b). A variety (P_2-1) of odd numbers of the interval contains at least one prime number.
- c). A variety (P_3-1) of odd numbers of the interval contains at least two prime numbers.

Keywords: residue pairs, repeating sequences, prime numbers, a primorial, alternations.

1. INTRODUCTION

1. The principal law of arithmetic states that every integer may be represented as a product of prime numbers by one and only method [1,2,3,4,5]. It follows that a positive integers sequence (hereafter the p.i.s.) represented only by the least prime factors >1 may be represented as an alternation of prime numbers (1 least prime factor >1 for any p.i.s. number) by one and only method.
2. It's quite obvious that the p.i.s. represented by a periodically repeating table with a primorial period $=P\#$ is a rhythmic alternation of even numbers (as divisible by two) having repeating odd number sequences between them [3,6]. The mentioned odd numbers at the p.i.s. interval from 1 to $P\#$ contain $\varphi(P\#)$ of $\text{mod}(P\#)$ least residues pertaining to the reduced residue system modulo $=P\#$ [2]. (All odd numbers inclusive of residues are enantiomorphous with relation to the number $=P\#/2$ and repeat with the period $=P\#$) [6].
3. With account of paragraphs 1 and 2 we can draw a deduction that for any fixed value of primorial $=P\#$ the p.i.s. may be represented by one and only method as an alternation of the first prime numbers $\leq P$ (1 least prime factor >1 for any p.i.s. number) between which $\varphi(P\#)$ of the $\text{mod}(P\#)$ least residues (i.e. odd numbers non-divisible by prime numbers $\leq P$) is located. Data of $\varphi(P\#)$ residues "graduate" the p.i.s. into a countable periodic structure containing $\varphi(P\#)$ of the p.i.s. intervals having various length. Each of such p.i.s. intervals is represented by an alternation of the first prime odd numbers $\leq P$ (1 least prime factor ≥ 3 for a number). This structure is situated at the p.i.s. interval from 1 to $P\#$ in an ambidextrous manner against a symmetry point of number $=P\#/2$ and subsequently repeats without changes with the period of $=P\#$. (see Table1).

The paper [6] demonstrates that if any odd letter divisible by $\leq P$ is identified with account of one least prime factor selected from the limited set of the first prime numbers from 3 to P (inclusive) and any odd number which is non-divisible by any of $\leq P$ is denominated by a symbol like C_n or $(P\#-C_n)$ where C_n is a $\text{mod}(P\#)$ residue, then for each primorial period $=P\#$ an odd numbers sequence is represented by a periodic structure in a form of enantiomorphous alternations of the first prime numbers (from 3 up to P (inclusively), with one least factor for a number) with various lengths (of...~~ppppp~~... form) between which there is $\varphi(P\#)$ of indexed and mirror-like $\text{mod}(P\#)$ least residues represented like C_n and $(P\#-C_n)$.

1,3,5,7,3,11,13,C...~~ppCpCpppC,Cppp..pCpppp~~..(P#-C),13,11,3,7,5,3,(P#-1).

This structure is represented by one and only method at the interval of an odd numbers sequence from 1 to $P\#$ in an enantiomorphous manner against $=P\#/2$ number symmetry point and subsequently repeats without changes with $=P\#$ period (see Table 1).

Table 1.

1, 3, 5, 7, 3,C ₁ ..	pp	..C ₂ ..	pp	.. C _n ..	pp	P ₁ #-C _n	pp	P ₁ #-C ₁	5, 3, (P ₁ #-1)
(1+P ₁ #), 3, 5, 7, ..	C ₁ +P ₁ #	pp	C ₂ +P ₁ #	pp	C _n +P ₁ #	pp	2P ₁ #-C _n	pp	2P ₁ #-C ₁	5, 3, (2P ₁ #-1)
(1+2P ₁ #), 3, 5, ..	C ₁ +2P ₁ #	pp	C ₂ +2P ₁ #	pp	C _n +2P ₁ #	pp	3P ₁ #-C _n	pp	3P ₁ #-C ₁	5, 3, (3P ₁ #-1)
...	...	pp	...	pp	...	pp	...	pp
...	...	pp	...	pp	...	pp	P ₂ #-C _n	pp	P ₂ #-C ₁	5, 3, (P ₂ #-1)

2. THE MAXIMUM LENGTH OF THE FIRST PRIME NUMBERS ALTERNATION

In the paper [6] $\phi(P\#)$ of $\text{mod}(P\#)$ least residues located at the interval of a positive integers sequence from 1 to $P\#$ is represented as a combination of three groups of $\text{mod}(P\#)$ residue pairs with even differences =R:

- $\phi(P\#)$ of “adjacent” residues pairs N_{0.0} with pair differences expressed like $R=(C_2-C_1)$;
- $\phi(P\#)$ of “the next nearest” residue pairs N_{0.1} with pair differences expressed like: $R=(C_3-C_1)$;
- $\phi(P\#)$ of “the second next nearest” residue pairs N_{0.2} with pair differences expressed like: $R=(C_4-C_1)$.

These $3\phi(P\#)$ of residue pairs N_{0.0,1,2} are located in an enantiomorphous manner against $(P\#)/2$ number and limit three groups of mirror-like alternations with various pairwise identical lengths. (I.e. alternation of the same length R leftwards = R rightwards with enantiomorphous arrangement of the same first prime numbers $\leq P$), see Table 2. Since in the mirror-like structure (which is symmetric about number $(P\#)/2$) any “lift-side” alternation limited by the corresponding residue pair of N_{0.2,1,0} type: R(on the left) $= (C_{2,3,4}-C_1)$ has an identical corresponding enantiomorphous “right-side” alternation (of the same first prime numbers) with the same length and the same difference of the pairs of N_{0.2,1,0} type: R(on the right) $= (P\#-C_1) - (P\#-C_{2,3,4}) = (C_{2,3,4}-C_1)$, there are two methods for setting up an alternation of the first prime numbers $\leq P$. Given that:

ALL alternations to the left of $(P\#)/2$ are set up by means of the leftwards-oriented Eratosthenes sieve towards number sequence increase with use of the descending odd numbers.	The alternations to the right of $(P\#)/2$ are set up by means of the rightward-oriented Eratosthenes sieve along the number sequence increase direction with use of ascending odd numbers.
An example of two methods of setting up enantiomorphous alternations of the first prime numbers $\leq P=11$ located in a repeating sequence from 1 to $11\# = 2310$	
..467, ◀ 469, 471, 473, 475, 477, 479.. $C_n, 7\text{-fold}, 3\text{-fold}, 11\text{-fold}, 5\text{-fold}, 3\text{-fold}, C_{n+1}$..1831, 1833, 1835, 1837, 1839, 1841▶, 1843 $(11\# - C_{n+1}), 3\text{-fold}, 5\text{-fold}, 11\text{-fold}, 3, 7, (11\# - C_n)$

Since the length of any alternation from C_1 to $C_{2,3,4}$ is determined by formula: $(R-2)/2$ of odd numbers of an interval (hereafter the int.odd num.) then subsequently any R will define the length of an alternation located at the interval from C_1 to $C_{2,3,4}$, where R is always even as represents difference between two residues $R=(C_{2,3,4}-C_1)$ and adopts a value from 2 to max value for a given $\text{mod}(P\#)$.

Table 2.

Table 2.	$3\varphi(P\#)$ of enantiomorphous alternations limited by pairs No. 0,1,2.
<u>$\varphi(P\#)$ of enantiomorphous pairs $N_{0,0}$ of “adjacent” $\text{mod}(P\#)$ residues with the differences of $R=(C_2-C_1)$ type.</u> $(C_1-1), (C_2-C_1), (C_3-C_2), (C_4-C_3), \dots (C_3-C_2), (C_2-C_1), (C_1-1), 2$, etc. $(C_1-1), (C_2-C_1) \dots$ Sum -R of all $-\varphi(P\#)$ residue pairs $N_{0,0}$ located at the interval from 1 to $P\#$ makes: $P\#$	
<u>$\varphi(P\#)$ of enantiomorphous pairs $N_{0,1}$ with the “next nearest” $\text{mod}(P\#)$ residue with the differences of $R=(C_3-C_1)$ type.</u> $(C_2-1), (C_4-C_2), (C_6-C_4), (C_8-C_5), \dots (C_6-C_4), (C_4-C_2), (C_2-1), (C_1+1)$, etc. $(C_3-C_1), \dots$ $(C_3-C_1), (C_5-C_3), (C_7-C_5), \dots (C_5-C_3), (C_3-C_1), (C_1+1)$, etc. $(C_2-1), (C_4-C_2), \dots$ Sum -R of all $-\varphi(P\#)$ residue pairs $N_{0,1}$ located at the interval from 1 to $P\#$ makes: $2(P\#)$	
<u>$\varphi(P\#)$ of enantiomorphous pairs $N_{0,2}$ with the “second next nearest” $\text{mod}(P\#)$ residue with the differences of $R=(C_4-C_1)$ type</u> $(C_3-1), (C_6-C_3), (C_9-C_6), \dots (C_6-C_3), (C_3-1), (C_2+1)$, etc. $(C_5-C_2), (C_8-C_5), \dots$ $(C_4-C_1), (C_7-C_4), (C_{10}-C_7), \dots (C_7-C_4), (C_4-C_1), (C_1+C_1)$ etc. $(C_4-C_1), (C_7-C_4), \dots$ $(C_5-C_2), (C_8-C_5), (C_{11}-C_8), \dots (C_8-C_5), (C_5-C_2), (C_2+1)$, etc. $(C_3-1), (C_6-C_3), \dots$ Sum -R of all $-\varphi(P\#)$ residue pairs $N_{0,2}$ located at the interval from 1 to $P\#$ makes: $3(P\#)$	

Taking for granted that the maximum-length alternation of the first prime numbers (from 3 to some P - inclusively) may be set up by one and only method, we shall obtain that for any fixed value of the primorial period $= (P\#)$ as a result of exclusion of all “left and right” pairs with equal differences (which limit enantiomorphously equal alternations) there is one and only non-repeating pair No.2 which limits enantiomorphously non-repeatable alternation of the first prime numbers $\leq P_1$ at the interval from 1 to $P_1\#$. I.e. the alternation which is set up by one and only method: from $(P_1\# - C_1)$ to $(P_1\# + C_1)$ with the difference $R = (P_1\# + C_1) - (P_1\# - C_1) = C_1 + C_1$, where $C_1 = P_2$ (since C_1 is the first prime number which is NOT divisible by $\leq P_1$). I.e. we’ve obtained a type of the maximum-length alternation of the first prime numbers $\leq P_1$ from $C_1 = (P_1\# - P_2) .. P_1 .. 3, 7, 5, 3, C_2 = (P_1\# - 1), C_3 = (P_1\# + 1), 3, 5, .. P_1 ..$ to $C_4 = (P_1\# + P_2)$

The rest multitude of enantiomorphous pairwise identical alternations (where $R_{left} = R_{right}$) CANNOT be of maximum length since they are set up by two different methods on the left and on the right from a symmetry point of number $= (P_1\#) / 2$ (which is in conflict with the assumed postulate).

The difference of two max. $\text{mod}(P_1\#)$ residues for this maximum “second next nearest” residue pair is as follows: $R = (C_4 - C_1) = (P_1\# + P_2) - (P_1\# - P_2) = P_2 + P_2 = 2P_2$. The length of interval of alternation for this “second next nearest” residue pair makes $(R - 2) / 2 = (P_2 - 1)$ int.odd num.

3. CORRELATION OF THE MAXIMUM LENGTHS OF ALTERNATIONS

Therefore we are aware of the value of the maximum-length alternation of the first prime numbers within the maximally long “second next nearest” residue pair No.2 for any fixed value of $(P\#)$. Consequently it becomes quite obvious that the limits of an alternation length, i.e. the length limits of pairs No.1 and No.0 unknown to us will be shorter than the maximum length of pair No.2 in the ratios as shown in Table 3.

Table 3. Correlations of the maximum lengths of alternations

Maximum difference =R of residue pairs No.0 of $C_1 \dots C_2$ type	<	Maximum difference =R of residue pairs No.1 of $C_1 \dots C_2 \dots C_3$ type	<	Known maximum difference =R of residue pairs No.2 of $C_1 \dots C_2 \dots C_3 \dots C_4$ type
$\max = (C_2 - C_1) \text{mod}(P_1\#)$	<	$\max R = (C_3 - C_1) \text{mod}(P_1\#)$	<	$\max R = (C_4 - C_1) \text{mod}(P_1\#) = 2P_2$
$\max = (C_2 - C_1) \text{mod}(P_2\#)$	<	$\max R = (C_3 - C_1) \text{mod}(P_2\#)$	<	$\max R = (C_4 - C_1) \text{mod}(P_2\#) = 2P_3$
$\max = (C_2 - C_1) \text{mod}(P_3\#)$	<	$\max R = (C_3 - C_1) \text{mod}(P_3\#)$	<	$\max R = (C_4 - C_1) \text{mod}(P_3\#) = 2P_4$
...	<	...	<	...
$\max = (C_2 - C_1) \text{mod}(P_y\#)$	<	$\max R = (C_3 - C_1) \text{mod}(P_y\#)$	<	$\max R = (C_4 - C_1) \text{mod}(P_y\#) = 2P_{y+1}$

In order to determine the values of max R of pairs $N_{o.1}$ and $N_{o.0}$ let's consider the order of the pairs setting up within the interval from $\text{mod}(P_1\#)$ to $\text{mod}(P_2\#)$, i.e. alternations from $\leq P_1$ to $\leq P_2$.

4. REPETITION OF PAIRS AND ALTERNATIONS

within the interval from $\text{mod}(P_1\#)$ to $\text{mod}(P_2\#)$ (see Table 4) Table 1 clearly shows that during transition from $\text{mod}(P_1\#)$ to $\text{mod}(P_2\#)$ $\varphi(P_1\#)$ of the residues of the primorial period $=P_1\#$ repeats P_2 times precisely. At that the number divisible by P_2 NOT being a $\text{mod}(P_2\#)$ residue “passes through” all of the $\varphi(P_1\#)$ residue columns and replaces one residue in each column. Having expanded the interval of the positive integers sequence from 1 до $P_2\#$ into a single line we obtain: $\varphi(P_1\#) \cdot (P_2 \text{ lines}) - \varphi(P_1\#)$ (divisible by P_2) $= \varphi(P_1\#)(P_2 - 1) = \varphi(P_2\#) \text{ mod}(P_2\#)$ residues. It is also obvious that during transition from $\text{mod}(P_1\#)$ to $\text{mod}(P_2\#)$ (i.e. rearrangement of alternations from $\leq P_1$ to $\leq P_2$) each of $3\varphi(P_1\#) \text{ mod}(P_1\#)$ residue pairs No. 0,1,2 (alternations $\leq P_1$) repeats P_2 times exactly (each pair $N_{o.0,1,2}$ in its column consisting of P_2 lines, see Fig.1). At that:

<p> $C_1 \dots \dots \dots \text{ppp} \dots \text{ppp} \dots \dots \dots C_{2,3,4}$ $C_1 + P_1\# \dots \text{ppp} \dots \text{ppp} \dots P_1\# + C_{2,3,4}$ $C_1 + 2P_1\# \dots \text{ppp} \dots \text{ppp} \dots 2P_1\# + C_{2,3,4}$ $\dots \dots \text{ppp} \dots \text{ppp} \dots \dots$ $C_1 + P_2\# \dots \text{ppp} \dots \text{ppp} \dots P_2\# + C_{2,3,4}$ Fig.1 Column P_2 pairs repetition. P_2 alternations of constant length=R. </p>	<p> The number divisible by P_2 NOT being a $\text{mod}(P_2\#)$ residue “passes through” all of the $3\varphi(P_1\#)$ columns of pairs (see Fig.1) and every time “replaces” in alternation of each P_2 times repeated pair NO MORE than ONE number (see Fig. 1). I.e. in the column of each pair (Fig. 1) the number divisible by P_2 rearranges each P_2 times repeated pair by $\text{mod}(P_2\#)$ by “replacing” once in each P_2 line every $C_{1,2,3,4}$ residue or 1 number of alternation $\leq P_1$. Since the length of alternation of any $\text{mod}(P_1\#)$ residue pair $N_{o.0,1,2}$ is shorter than $(P_2 - 1)$ int. odd num. </p>	
<p>In addition the composition of the alternation remains unchangeable as long as in the canonical form of any number (subject to alternation) only the least prime numbers are taken into consideration. Therefore by means of exclusion of 2,3,4 residues we'll obtain the repetition (R) for $\text{mod}(P_2\#)$ pairs represented as a repetition of alternations of the same first prime numbers. For alternations $\leq P_2$</p>		
<p> $(P_2 - 2)$ repetitions $R = \text{const}$ for pairs $N_{o.0}$. </p>	<p> $(P_2 - 3)$ repetitions $R = \text{const}$ for pairs $N_{o.1}$. </p>	<p> $(P_2 - 4)$ repetitions $R = \text{const}$ for pairs $N_{o.2}$. </p>

<p>By exclusion of two residues $C_{1,2}$ we'll obtain (P_2-2) of repetitions of alternations (of the same first prime numbers) with the constant length $=R$. Total number of repetitions of pairs No. 0 (alternations $\leq P_2$) will make $\varphi(P_1\#)(P_2-2)$ for $\text{mod}(P_2\#)$.</p>	<p>By exclusion of three residues $C_{1,2,3}$ we'll obtain (P_2-3) of repetitions of alternations (of the same first prime numbers) with the constant length $=R$. Total number of repetitions of pairs No. 1 (alternations $\leq P_2$) will make $\varphi(P_1\#)(P_2-3)$ for $\text{mod}(P_2\#)$.</p>	<p>By exclusion of four residues $C_{1,2,3,4}$ we'll obtain (P_2-4) of repetitions of alternations (of the same first prime numbers) with the constant length $=R$. Total number of repetitions of pairs No. 2 (alternations $\leq P_2$) will make $\varphi(P_1\#)(P_2-4)$ for $\text{mod}(P_2\#)$.</p>
<p>Sum of differences $=R$ of the repeating pairs No.0 = $P_1\#*(P_2-2)$. where: $P_1\#$ - sum R of pairs from 1 to $P_1\#$.</p>	<p>Sum of differences $=R$ of the repeating pairs No.1 = $2P_1\#*(P_2-3)$. where: $2P_1\#$ - sum R of pairs from 1 to $P_1\#$.</p>	<p>Sum of differences $=R$ of the repeating pairs No.2 = $3P_1\#*(P_2-4)$ where: $3P_1\#$ - sum R of pairs from 1 to $P_1\#$.</p>

5. CHAIN OF REARRANGEMENT OF PAIRS AND ALTERNATIONS

from $\text{mod}(P_1\#)$ to $\text{mod}(P_2\#)$ The rest $\text{mod}(P_1\#)$ residue pairs, i.e. alternations $\leq P_1$ (with residues "replaced" by a number divisible by P_2) are being rearranged to $\text{mod}(P_2\#)$ as follows:

<p>The order of "replacement" of residue C_2 among all $\varphi(P_1\#)$ pairs $N_{0,1}$ of $\text{mod}(P_1\#)$ residues, where: R of pairs $N_{0,1}=(C_3-C_1) \leq P_1$</p>	<p>The order of "replacement" of residues C_2 and C_3 among all $\varphi(P_1\#)$ pairs $N_{0,2}$ of $\text{mod}(P_1\#)$ residue pairs $N_{0,2}=(C_4-C_1) \leq P_2$</p>	<p>"New" pairs $N_{0,2}$ among $\varphi(P_1\#)$ pairs of $\text{mod}(P_1\#)$ residues, where R of "new" pairs $N_{0,2}=(C_4-C_1) \leq P_3$</p>
<p>C_1 1 C_3 1 C_5 1 ... C_n</p>	<p>C_1 1 2 C_4 2 1 C_7 ... C_n</p>	<p>C_1 1 2 3 C_5 C_n</p>
<p>C_2 1 C_4 1 C_6 1 ...</p>	<p>C_2 2 1 C_5 1 2 C_8 ...</p>	<p>C_2 2 3 1 C_6</p>
	<p>C_3 1 2 C_6 2 1 ...</p>	<p>C_3 3 1 2 C_7 ...</p>
		<p>C_4 1 2 3 C_8</p>
<p>Any residue $=C_n$ "replaced" by a number divisible by P_2 rearranges ONE, TWO, THREE other pairs in the corresponding column from $\text{mod}(P_1\#)$ to $\text{mod}(P_2\#)$, i.e. rearranges alternations from $\leq P_1$ to $\leq P_2$, at the same time:</p>		

<p>Pairs No.1 are rearranged into pairs No.0, at that the pairs (alternations) length remains unchanged: $R = \text{const.}$</p> <p>In other words as a result of “replacement” of the residue $=C_2$ each $\text{mod}(P_1\#)$ residue pair No. 1 (alternations $\leq P_1$) is being rearranged into 1 pair No. 0 of $\text{mod}(P_2\#)$ residues along with “transfer” of the length of every alternation from pairs No. 1 to PAIRS No.0. All $\varphi(P_1\#)$ of enantiomorphous pairs No.1 of $\text{mod}(P_1\#)$ residues (alternations $\leq P_1$) are being rearranged in a chain-like manner into $\varphi(P_1\#)$ of enantiomorphous PAIRS No.0 of $\text{mod}(P_2\#)$ residues (alternations $\leq P_2$), where: $\varphi(P_1\#) = \varphi(P_2\#) - \varphi(P_1\#)(P_2 - 2)$.</p> <p>$\varphi(P_2\#)$ – total number of pairs No.0 from at the interval from 1 to $P_2\#$. At that only two max pairs No.1 of $\text{mod}(P_1\#)$ residues with the length of $(P_1 - 1)$ int.odd num. can be rearranged into two enantiomorphous max pairs No.0 of $\text{mod}(P_2\#)$ residues with the length of $= (P_1 - 1)$ int.odd num. (alternations $\leq P_2$) since the rest of the pairs in the chain have shorter length then the maximum one.</p>	<p>Two pairs No.2 of this column are being rearranged into 2 pairs No.1, at that the pairs (alternations) length remains unchanged: $R = \text{const.}$</p> <p>In other words as a result of one-time “replacement” of every of 2 residues $=C_{2,3}$ each pair No.2 of $\text{mod}(P_1\#)$ residues (alternations $\leq P_1$) is being rearranged into 2 enantiomorphous pairs No.1 of $\text{mod}(P_2\#)$ residues (alternations $\leq P_2$) along with “transfer” of the length of every alternation from pairs No.2 to PAIRS No.1. All $\varphi(P_1\#)$ of pairs No.2 of $\text{mod}(P_1\#)$ residues (alternations $\leq P_1$), are being rearranged in a chain-like manner into $2\varphi(P_1\#)$ of PAIRS No.1 of $\text{mod}(P_2\#)$ residues (alternations $\leq P_2$), where: $3\varphi(P_1\#) = 2\varphi(P_2\#) - \varphi(P_1\#)(P_2 - 3)$.</p> <p>$\varphi(P_2\#)$ – total number of pairs No.1 at the interval from 1 to $P_2\#$. At that only one max pair No.2 of $\text{mod}(P_1\#)$ residues with the length of $(P_2 - 1)$ int.odd num. can be rearranged into 2 enantiomorphous max pairs No.1 of $\text{mod}(P_2\#)$ residues with the length of $= (P_2 - 1)$ int.odd num. (alternations $\leq P_2$) since the rest of the pairs in the chain have shorter length then the maximum one.</p>	<p>THREE other pairs of this column are being rearranged into three “new” pairs No.2. as the length = R (i.e. alternations) of these “new” pairs grows. I.e. as a result of “replacement” of max. residues C_1 and C_4 there are being formed $3\varphi(P_1\#)$ “new” “longer” alternations $\leq P_2$ (pairs No.2) of $\text{mod}(P_2\#)$ residues. Simultaneously the length of these alternations $\leq P_2$ grows up to the known value $(P_3 - 1)$ int.odd num., where: $3\varphi(P_1\#) = \varphi(P_2\#) - \varphi(P_1\#)(P_2 - 4)$, where: $\varphi(P_2\#)$ – total number of pairs No.2 at the interval from 1 to $P_2\#$.</p>
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Sum of differences - R of the chain of the rearranged pairs No.0 for mod($P_2\#$): $2P_1\# = P_2\# - (P_1\#)(P_2 - 2)$, where $P_2\#$ - sum R of pairs No.0 at the interval from 1 to $P_2\#$.	Sum of differences -R of the chain of the rearranged pairs No.1 for mod($P_2\#$): $3 * 2P_1\# =$ $= 2P_2\# - 2P_1\#(P_2 - 3)$, where $2P_2\#$ - sum R of pairs No.1 at the interval from 1 to $P_2\#$.	Sum of differences -R of "new" pairs of residues No.2 for mod($P_2\#$): $4 * 3P_1\# =$ $= 3P_2\# - 3P_1\#(P_2 - 4)$, where $3P_2\#$ - sum R of pairs No.2 at the interval from 1 to $P_2\#$.
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6. FORMULA OF MAXIMUM PAIRS AND ALTERNATIONS NO.1 AND NO.2 (Table 5)

It follows from paragraphs 4 and 5 that:

- 6.1. Within the transition from mod($P_1\#$) to mod($P_2\#$) there are only two methods of rearranging alternations and pairs, namely as a repetition of R-pairs (par.4) and as a chain of rearrangements (par. 5).
- 6.2. Rearrangement involving increase of the maximum lengths of pairs and alternations =R is possible only by the chain-like rearrangement of pairs (par. 5).

Therefore for any fixed value of module = mod($P_1\#$) the p.i.s. interval from 1 to $P_1\#$ contains $\varphi(P_1\#)$ of mod($P_1\#$) residue pairs No.2 limiting alternations of the first prime numbers $\leq P_1$ among which there is one and only pair No. 2 located at the interval from $(P_1\# - P_2)$ to $(P_1\# + P_2)$ and having difference $R = (P_1\# + P_2) - (P_1\# - P_2) = P_2 + P_2 = 2P_2$ which limits the maximum-length alternation of the first prime numbers $\leq P_1$ amount of $(R - 2)/2 = (2P_2 - 2)/2 = (P_2 - 1)$ odd numbers.

Subsequently (as per par. 5) we'll obtain that by replacing every residue C_2 or C_3 by a P_2 -fold number in the chain of every of $\varphi(P_1\#)$ of rearranged pairs No.2 of mod($P_1\#$) residues we get $2\varphi(P_1\#)$ of pairs No.1 for mod($P_2\#$). At the same time from the single P_2 -times repeated alternation $\leq P_1$ which is limited by the maximum mod($P_1\#$) residue pair No.2 with the length of $(P_2 - 1)$ int.odd num. we can get at the most two enantiomorphous maximum pairs No.1 of mod($P_2\#$) residues which limit two enantiomorphous alternations $\leq P_2$ with the length of $(P_2 - 1)$ int.odd num. According to formula P_2 -fold and C_2 numbers are defined as follows: $(nP_1\# \pm 1)$ and $(P_2 - n)P_1\# \pm 1$, where: n - an integer $< P_2 / 2$. The rest pairs of the chain of the rearranged pairs No.2 have shorter length than the max. one $= (P_2 - 1)$ int.odd num.(see par.5.)

By further replacement of the remaining residue C_2 in the chain of every rearranged mod($P_2\#$) residue pairs No.1 among $\varphi(P_2\#)$ by a P_3 -fold number we'll get $\varphi(P_2\#)$ of pairs No.0 for mod($P_3\#$), inclusive of precisely two symmetric mod($P_3\#$) residue pairs No.0 limiting two enantiomorphous alternations of the first prime numbers $\leq P_3$ with the length of $= (P_2 - 1)$ of odd numbers. According to formula P_3 -fold and P_4 -fold numbers are defined as follows: $(nP_1\# \pm 1)$ and $(P_2P_3 - n)P_1\# \pm 1$, where : n - an integer $< P_3P_2/2$. The rest pairs of the chain of the rearranged pairs No.1 have shorter length than the max. one $= (P_2 - 1)$ of the interval odd numbers (see par.5).

Therefore in the course of chain of rearrangement of pairs from No.2 to No.1 and from No.1 to No.0 we've got the formulas for determining the composition of the

maximum lengths of alternations and preservation of permanence of the mentioned limit values, i.e. of the differences of the residue pairs, for three successive growing modulo values: from $\text{mod}(P_1\#)$ to $\text{mod}(P_2\#)$ and to $\text{mod}(P_3\#)$.

In other words all $\varphi(P_1\#)$ of the rearranged $\text{mod}(P_1\#)$ pairs No.2 (where $R \leq 2P_2$) repeat in a chain-like manner as follows: $2\varphi(P_1\#)$ of $\text{mod}(P_2\#)$ pairs No.1 (where $R \leq 2P_2$). And subsequently all $\varphi(P_2\#)$ for the rearranged $\text{mod}(P_2\#)$ pairs No.1 (where $R \leq 2P_2$) repeat in a chain-like manner as follows: $\varphi(P_2\#)$ of $\text{mod}(P_3\#)$ residue pairs No.0 (where $R \leq 2P_2$).

Data from paragraph 6 are summarized in Tables 4,5,6.

7. CONCLUSION

It follows from the principal law of arithmetic and primorial periodicity of the positive integers sequence that any p.i.s. interval may be presented by one and only method as an alternation of the first prime numbers $\leq P_2$ (1 least prime factor >1 for any p.i.s. number) which are arranged from 1 to $(P_2\#)$ and repeat with the period $= (P_2\#)$.

This paper allows coming to a conclusion that alternation of the first prime odd numbers from 3 to P_2 (inclusively) has a limited length:

- no more than (P_1-1) odd numbers of such interval (int.odd num.);
- no more than (P_2-1) odd numbers of such interval inclusive of 1 odd number NON-divisible by the prime numbers $\leq P_2$;
- no more than (P_3-1) odd numbers of such interval inclusive of 2 odd numbers NON-divisible by the prime numbers $\leq P_2$.

Hence it appears that any interval of a positive integers sequence may be represented (measured) by one and only method as a rhythmic alternation of the first prime numbers from 2 up to certain P_2 inclusive (1 least prime factor >1 for any number). In this case the maximum length of any of the mentioned interval contains:

- no more than (P_1-1) odd numbers of such interval (int.odd num.);
- no more than (P_2-1) odd numbers of such interval inclusive of 1 odd number NON-divisible by the prime numbers $\leq P_2$;
- no more than (P_3-1) odd numbers of such interval inclusive of 2 odd numbers NON-divisible by the prime numbers $\leq P_2$.

Furthermore at an interval of the positive integers sequence from P_2^2 to P_3^2 :

- a) Difference between two adjacent prime numbers $\leq 2P_1$.
- b) A variety (P_2-1) of odd numbers of the interval contains at least one prime number.
- c) A variety (P_3-1) of odd numbers of the interval contains at least two prime numbers.

CONFLICT OF INTERESTS

The author confirms that the given data do not contain any conflict of interests.

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Chain of rearrangement of alternations and 3 groups of residue pairs with constant maximum pairs difference ($\max R = \text{const}$)									
Table 4.	Pairs No.0+chain No.1 (C_2 excluded)			Pairs No.1+chain No.2 (C_{2-3} excluded)			Pairs No.2+«new» with known R		
	Repetition of pairs No.0 mod $P_1\#$	Chain of pairs No.1 mod $P_1\#$	Pairs No.0 total mod $P_2\#$	Repetition of pairs No.1 mod $P_1\#$	Chain of pairs No.2 mod $P_1\#$	Pairs No.1 total mod $P_2\#$	Repetition of pairs No.2 mod $P_1\#$	New pairs No.2 mod $P_1\#$	Pairs No.2 total mod $P_2\#$
Rearrangement of 3 groups of pairs from mod $P_0\#$ to mod $P_1\#$ at the interval from 1 to $P_1\#$. (Rearrangement of alternations to $\leq P_1$)									
Number of pairs on new mod $P_1\#$ Differences $-R$ of these pairs	$\varphi(P_0\#)(P_1-2)$ ($R \leq 2P_0$)	$+\varphi(P_0\#)$ $R \leq 2P_0$	$=\varphi(P_1\#)$ $R \leq 2P_0$	$\varphi(P_0\#)(P_1-3)$ $R \leq 2P_0$	$+2\varphi(P_0\#)$ $R \leq 2P_1$	$=\varphi(P_1\#)$ $R \leq 2P_1$	$\varphi(P_0\#)(P_1-4)$ $R \leq 2P_1$	$+3\varphi(P_0\#)$ $R \leq 2P_2$	$=\varphi(P_1\#)$ $R \leq 2P_2$
Sum R of pairs mod $P_1\#$ Alternation structure	$P_0\#*(P_1-2)$ (from 3 to P_1) Incl. of 2 pairs $\max R = 2P_0$	$+2P_0\#$	$=P_1\#$	$2P_0\#*(P_1-3)$ (from 3 to P_1) Incl. of 2 pairs $\max R = 2P_1$	$+3*2P_0\#$	$=2P_1\#$	$3P_0\#*(P_1-4)$ (from 3 to P_1) Incl. of 1 pair $\max R = 2P_2$	$+4*3P_0\#$	$=3P_1\#$
Rearrangement of 3 groups of pairs from mod $P_1\#$ to mod $P_2\#$ at the interval from 1 to $P_2\#$. (Rearrangement of alternations to $\leq P_2$)									
Number of pairs on new mod $P_2\#$ Differences $-R$ of these pairs	$\varphi(P_1\#)(P_2-2)$ $R \leq 2P_0$	$+\varphi(P_1\#)$ $R \leq 2P_1$	$=\varphi(P_2\#)$ $R \leq 2P_1$	$\varphi(P_1\#)(P_2-3)$ $R \leq 2P_1$	$+2\varphi(P_1\#)$ $R \leq 2P_2$	$=\varphi(P_2\#)$ $R \leq 2P_2$	$\varphi(P_1\#)(P_2-4)$ $R \leq 2P_2$	$+3\varphi(P_1\#)$ $R \leq 2P_3$	$=\varphi(P_2\#)$ $R \leq 2P_3$
Sum R of pairs mod $P_2\#$	$P_1\#*(P_2-2)$	$+2P_1\#$	$=P_2\#$	$2P_1\#*(P_2-3)$	$+3*2P_1\#$	$=2P_2\#$	$3P_1\#*(P_2-4)$	$+4*3P_1\#$	$=3P_2\#$

Alternation structure	(from 3 to P_2). Incl. of 2 pairs $\max R=2P_1$	(from 3 to P_2) Incl. of 2 pairs $\max R=2P_2$	(from 3 to P_2) Incl. of 1 pair $\max R=2P_3$
Rearrangement of 3 groups of pairs from $\text{mod } P_2\#$ to $\text{mod } P_3\#$ at the interval from 1 to $P_3\#$. (Rearrangement of alternations to $\leq P_3$)			
Number of pairs on new $\text{mod } P_3\#$	$\varphi(P_2\#)(P_3--2)$	$+\varphi(P_2\#)$ $R \leq 2P_2$	$=\varphi(P_3\#)$ $R \leq 2P_2$
Differences $-R$ of these pairs	$R \leq 2P_1$		
Sum R of pairs $\text{mod } P_3\#$	$P_2\#*(P_3--2)$	$+2P_2\#$	$=P_3\#$
Alternation structure	(from 3 to P_3). Incl. of 2 pairs $\max R=2P_2$	(from 3 to P_3) Incl. of 2 pairs $\max R=2P_3$	(from 3 to P_3) Incl. of 1 pair $\max R=2P_4$
Rearrangement of 3 groups of pairs from $\text{mod } P_3\#$ to $\text{mod } P_4\#$ at the interval from 1 to $P_4\#$. (Rearrangement of alternations to $\leq P_4$)			
Number of pairs on new $\text{mod } P_4\#$	$\varphi(P_3\#)(P_4--2)$	$+\varphi(P_3\#)$ $R \leq 2P_3$	$=\varphi(P_4\#)$ $R \leq 2P_3$
Differences $-R$ of these pairs	$R \leq 2P_2$		
Sum R of pairs $\text{mod } P_4\#$	$P_3\#*(P_4--2)$	$+2P_3\#$	$=P_4\#$
Alternation structure	(from 3 to P_4). Incl. of 2 pairs $\max R=2P_3$	(from 3 to P_4) Incl. of 2 pairs $\max R=2P_4$	(from 3 to P_4) Incl. of 2 pairs $\max R=2P_5$
Rearrangement of alternations and 3 groups of residue pairs from $\text{mod } P_1\#$ to $\text{mod } P_2\#$.	$\varphi(P_1\#)$ of $\text{mod } P_1\#$ pairs No.0 repeat (P_2--2) times (at $R \leq 2P_0$). $+\varphi(P_1\#)$ of pairs No.1 (with increase to $\text{mod } P_2\#$ with constant $R \leq 2P_1$) result in: $:=\varphi(P_2\#)$ of $\text{mod } P_2\#$ pairs No.0 (where $R \leq 2P_1$)	$\varphi(P_1\#)$ of $\text{mod } P_1\#$ pairs No.1 repeat (P_2--3) times (at $R \leq 2P_1$). $+2\varphi(P_1\#)$ of pairs No.2 (with increase to $\text{mod } P_2\#$ with constant $R \leq 2P_2$) result in: $\varphi(P_2\#)$ of $\text{mod } P_2\#$ pairs No.1 (where $R \leq 2P_2$)	$\varphi(P_1\#)$ of $\text{mod } P_1\#$ pairs No.2 repeat (P_2--4) times (at $R \leq 2P_2$) + (new) $3\varphi(P_1\#)$ of $\text{mod } P_2\#$ pairs No.2 (with known $R \leq 2P_3$) result in: $:=\varphi(P_2\#)$ of $\text{mod } P_2\#$ pairs No.2 (where $R \leq 2P_3$)

... etc. according to the increasing values of modulo $\equiv \text{mod } P\#$... where: $P\#$ - primorial, $P_0 < P_1 < P_2 < P_3 < P_4 < P_5$ – consecutive prime numbers.

Table 5.	Numerical examples of maximum-length alternations of the first prime numbers within the max. pairs No.0, No.1, No.2		
The form of maximum-length alternations of the first prime numbers ≤ 7 (within 5 max pairs of $\text{mod}(7\#)$ residues at the interval from 1 to $7\# = 210$)			
$C_1=1, 3, \text{ fold-}(5,7), 3, 11= C_2$ $\text{maxR}=2*5C_1=199, 201, \text{ fold-}(7,5), 207,$ $209=C_2$ $\text{fold-}(5,7) \text{ is } (n3\# \pm 1) \text{ and } (5*7--n)3\# \pm 1. n=1 < 5*7/2$	$C_1=83,85,87, C_2=89, 91=7*13, \dots, 95, C_3=97.$ $\text{maxR}=2*7$ $C_1=113, 115, 117, 119=7*17, C_2=121, 123, 125,$ $C_3=127$ $\text{fold-}(7, C_2) \text{ is } (n5\# \pm 1) \text{ and } (7--n)5\# \pm 1. \text{ where:}$ $n=3 < 7/2$	$C_1, \text{ fold-}3, 7, 5, 3, C_2, C_3, 3, 5, 7, 3, C_4.$ $199, 201, \dots, 207, 209, 211, 213, 215, 217, 219, 221$ $\text{further recur. with pe-}$ $\text{riod } 7\#. \text{maxR}=2*11$	
The form of maximum-length alternations of the first prime numbers ≤ 11 (within 5 max pairs of $\text{mod}(11\#)$ residues at the interval from 1 to $11\# = 2310$)			
$113, 5, 3, \text{ fold-}$ $(7=119, 11=121), 3, 5, 127=C_2. \text{maxR}=2*7$ $C_1=2183, 5, 3, \text{ fold-}$ $(11=2189, 7=2191), 3, 5, 2197=C_2$ $\text{fold-}(7, 11) \text{ is } (n5\# \pm 1), (7*11--n)5\# \pm 1.$ $n=4 < 7*11/2$	$199, 3, \dots, 3, 11*19=209, C_2=211, 3, \dots, 3, 221=C_3. \text{maxR}$ $=2*11$ $C_1=2089, 3, 7, 5, 3, C_2=2099, 11*191, 3, 5, 7, 3,$ $2111=C_3$ $\text{fold-}(11, C_2) \text{ is } (n7\# \pm 1) \text{ and } (11--n)7\# \pm 1. \text{ where:}$ $n=1 < 11/2$	$C_1, 11, 3, 7, 5, 3, \text{ fold-}$ $(C_2, C_3), 3, 5, 7, 3, 11, C_4$ $2297, \text{ fold-}$ $11, 3, \dots, 3, 2309, 2311, 3, 5, \dots, 11, 2323$ $\text{further recurrence period } 11\#.$ $\text{maxR}=2*13$	
The form of maximum-length alternations of the first prime numbers ≤ 13 (within 5 max pairs of $\text{mod}(13\#)$ residues at the interval from 1 to $13\# = 30030$)			

<p>9439,...$\frac{9449}{11*859}$, $\frac{9451}{13*727}$, 3,5,7,3, 9461. $\max R=2*11$ $C_1=20569,$ $\frac{20579}{13*1583}$, $\frac{20581}{11*1871}$.....20591=C_2 fold-(11,13)is(n7#±1),(11*13--n)7#±1.n=45<11*13/2</p>	<p>$C_1=6917,$ $\frac{6929}{13*533}$$C_2=6931,3,..11,6943=C_3.$ $\max R=2*13$ $C_1=23087,11,..,3,C_2=23099,$ $\frac{23101}{13*1777},3,5,..,11,23$ $113=C_3$ fold -(13,C_2) is (n11#±1),(13--n)11#±1 where:n=3<13/2</p>	<p>$C_1,3,13,11,3,7,5,3,C_2$ $C_3,3,5,7,3,11,13,3,C_4$ 30013,3,13,..3,30029,30031,3,..,13,3,30 047 further recurrence with period 13#. $\max R=2*17$</p>
<p>The form of maximum-length alternations of the first prime numbers≤17 (within 5 max pairs of mod(17#) residues at the interval from 1 to 17#=510510)</p>		
<p>217127..$\frac{217139}{13*16703}$, $\frac{217141}{17*12773}$..217153. $\max R=2*13$ 293357, $\frac{293369}{17*17257}$, $\frac{293371}{13*22567}$..3, 2933 $83=C_2$ fold-(13,17)is(n11#±1),(13*17--n)11#±1. n=94<13*17/2</p>	<p>$C_1=60043,..,C_2,$ $\frac{60061}{17*3533}$...13,3,60077=C_3 $\max R=2*17$ $C_1=450433,3,..,3,$ $\frac{450449}{17*26497},C_2=450451,$ $3,..,450467=C_3$ fold-(17,C_2)is (n13#±1)and(17--n)13#±1.where: n=2<17/2</p>	<p>$C_1,17,..,7,5,3,$ $C_2,C_3,$ 3,5,7,3,11,13,3,17,C_4 510491, 17,..3, 510509,510511, 3,..,17,510529 further recurrence with period 17#. $\max R=2*19$</p>
<p>The form of maximum-length alternations of the first prime numbers≤19 (within 5 max pairs of mod(19#) residues at the interval from 1 to 19#=9699690)</p>		
<p>60043,..,$\frac{60059}{19*3161}$, $\frac{60061}{17*3533}$...60077. $\max R=2*17$ 9639613,..3, $\frac{9639629}{17*567037}$, $\frac{9639631}{19*507349}$, 3,.., 9639647 fold-(17,19)is(n13#±1),(17*19--n)13#±1.n=2<17*19/2</p>	<p>510491,..,$C_2,$ $\frac{510511}{19*26869}$, 3,5,..,3,17,510529. $\max R=2*19$ $C_1=9189161,17,3,..,3,$ $\frac{9189179}{19*483641},C_2,..,3,17,$ $9189199=C_3$ fold-(19,C_2) is(n17#±1) and(19--n)17#±1.where n=1<19/2</p>	<p>$C_1,3,19,..,3,$ $C_2,C_3,$ 3,5,7,3,11,13,3,17,19,3,C_4 9699667, 3,..3, 9699689,9699691, 3..19,3,9699713 further recurrence with period 19#. $\max R=2*23$</p>

Table 6.	The form of maximum-length alternations of the first prime numbers $\leq P_2$ (within 5 max pairs of $\text{mod}(P_2\#)$ residues from 1 to $P_2\#$)		
<p>Two “enantiomorphous” max “adjacent” pairs $N_{0,0} \text{ mod } P_2\#$ residues with difference: $(C_2 - C_1) = \max R = 2 * P_1$ $C_1, \dots, 5, 3, (P_2 \text{ and } P_1)\text{-fold}, 3, 5, 7, 3, 11, 13, 3, \dots, C_2.$ $(P_2\# - C_2), 5, 3, (P_1, P_2)\text{-fold}, 3, 5, 7, \dots, (P_2\# - C_1)$ fold $-(P_1, P_2)$ is $(nP_{0\#} \pm 1), (P_1 P_2 - n)P_{0\#} \pm 1, n < (P_1 * P_2) / 2$</p>	<p>Two “enantiomorphous” “next nearest” max pairs No.1 of $\text{mod } P_2\#$ residues with difference: $(C_3 - C_1) = \max R = 2 * P_2$ $C_1, \dots, P_1, \dots, 3, 7, 5, 3, (C_2, P_2)\text{-fold}, 3, 5, \dots, 17, 19, 3, \dots, P_1, \dots, C_3$ $(P_2\# - C_3), \dots, 5, 3, (P_2, C_2)\text{-fold}, 3, 5, 7, \dots, (P_2\# - C_1)$ fold $-(P_2 \text{ and } C_2)$ is $(nP_{1\#} \pm 1)$ and $(P_2 - n)P_{1\#} \pm 1, n < P_2 / 2$</p>	<p>One “second next nearest” max pair No.2 of $\text{mod } P_2\#$ residues with difference: $(C_4 - C_1) = \max R = 2 * P_3$ $C_1, \dots, P_2, \dots, P_1, \dots, C_2, C_3, 3, 5, 7, 3, \dots, P_1, \dots, P_2, \dots, C_4$ $(C_2 \text{ and } C_3)$ - fold is: $(P_2\# \pm 1).$... etc. with repetition period $= P_2\#$</p>	
<p>The chain of pairs $N_{0,2}$ of $\text{mod}(P_1\#)$ residues (one of the residues (C_2 or C_3) excluded) contains 2 enantiomorphous pairs No.1 of $\text{mod}(P_1\#)$ residues (alternation of the first primes $\leq P_2$) with the length $= (P_2 - 1)$ int. odd num., defined by the formula: $(P_2, C_2)\text{-fold}$ is: $(nP_{1\#} \pm 1)$ and $(P_2 - n)P_{1\#} \pm 1$, where: n-integer $< P_2 / 2$. The chain of $P_1 P_2$ pairs $N_{0,2}$ of $\text{mod}(P_0\#)$ residues (one of the residues (C_2 or C_3) excluded) contains $2P_1$ enantiomorphous pairs $N_{0,1}$ with the max length $= (P_1 - 1)$ int. odd num. (alternations $\leq P_1$) among which only 2 pairs of $N_{0,0}$ (alternat. $\leq P_2$) are defined by the formula: $(P_2, C_2)\text{-fold}$ is: $(nP_{0\#} \pm 1)$ and $(P_1 P_2 - n)P_{0\#}$, where: n-integer $< (P_1 * P_2) / 2$.</p>			