Gene expression from polynomial dynamics in the 2-adic information space

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February 4, 2008

Abstract

We perform geometrization of genetics by representing genetic information by points of the 4-adic information space. By well known theorem of number theory this space can also be represented as the 2-adic space. The process of DNA-reproduction is described by the action of a 4-adic (or equivalently 2-adic) dynamical system. As we know, the genes contain information for production of proteins. The genetic code is a degenerate map of codons to proteins. We model this map as functioning of a polynomial dynamical system. The purely mathematical problem under consideration is to find a dynamical system reproducing the degenerate structure of the genetic code. We present one of possible solutions of this problem.

1 Introduction

During last ten years there were found numerous applications of \( p \)-adic numbers outside the domain of number theory – in particular, in quantum physics, Beltrametti and Cassinelli, 1972, Volovich, 1987, Vladimirov et al, 1994, Khrennikov 1994, and theory of disordered systems, Avetisov et al, 1999a,b, 2002 a,b, Parisi and Sourlas, 2000,
Kozyrev et al, 2005, Khrennikov and Kozyrev, 2006 a,b. We pay attention to the series of papers, Khrennikov, 1997, 1998 a,b, 1999, 2000 a,b, and 2004 a,b in that p-adic information space was introduced and applied to information theory, cognitive and social sciences, psychology and neurophysiology, see also Pitkänen, 1998, Khrennikov and Nilsson, 2004. The main distinguishing feature of encoding of information by p-adic numbers is the possibility to encode the hierarchical structure of information through the ultrametric topology on the p-adic tree, cf. also with Voronkov, 2002 a,b. As was mentioned, this possibility was explored a lot in Khrennikov, 1997, 1998 a,b, 1999, 2000 a,b, and 2004 a,b. Recently it was pointed out that the same p-adic information space can be applied to mathematical modeling of gene expression, Dragovich, 2006, and Khrennikov 2006 a,b.

We apply this approach to genetics. Now we present schematically development of this model. DNA and RNA sequences are represented by 4-adic numbers. Nucleotides are mapped to digits in registers of 4-adic numbers: thymine - \( T = 0 \), cytosine - \( C = 1 \), adenine - \( A = 2 \), and guanine - \( G = 3 \). The U-nucleotide is represented (as well as \( T \)) by 0.[1]

The DNA and RNA sequences have the natural hierarchical structure: letters which are located at the beginning of a chain are considered as more important. This hierarchical structure coincides with the hierarchical structure of the 4-adic tree. Such a hierarchy can also be encoded by the 4-adic metric. The process of DNA-reproduction is described by the action of a 4-adical dynamical system. As we know, the genes contain information for production of proteins. The genetic code is a degenerate map of codons to proteins. We model this map as functioning of a polynomial 4-adical dynamical system. Proteins are associated with cycles of such a dynamical system. By well known theorem of number theory this dynamics can also be represented in the 2-adic space.

2 \( m \)-adic ultrametric spaces

The notion of a metric space is used in many applications for describing distances between objects. Let \( X \) be a set. A function \( \rho : X \times X \rightarrow \mathbb{R}_+ \) (where \( \mathbb{R}_+ \) is the set of positive real numbers) is said to be a metric if it has the following properties: \( \rho(x, y) = 0 \) iff \( x = y \).
y (non-degenerated); 2) \( \rho(x, y) = \rho(y, x) \) (symmetric); 3) \( \rho(x, y) \leq \rho(x, z) + \rho(z, y) \) (the triangle inequality). The pair \((X, \rho)\) is called a metric space.

We are interested in the following class of metric spaces \((X, \rho)\). Every point \(x\) has the infinite number of coordinates

\[
x = (\alpha_1, ..., \alpha_n, ...).
\]

Each coordinate yields the finite number of values,

\[
\alpha \in A_m = \{0, ..., m - 1\},
\]

where \(m > 1\) is a natural number, the base of the alphabet \(A_m\). The metric \(\rho\) should be so called ultrametric, i.e., satisfy the strong triangle inequality:

\[
\rho(x, y) \leq \max[\rho(x, z), \rho(z, y)], \ x, y, z \in X.
\]

The strong triangle inequality can be stated geometrically: each side of a triangle is at most as long as the longest one of the two other sides. It is impossible to imagine such a ‘triangle’ in the ordinary Euclidean space.

We denote the space of sequences (1), (2) by the symbol \(Z_m\). The standard ultrametric is introduced on this set in the following way. For two points

\[
x = (\alpha_0, \alpha_1, \alpha_2, ..., \alpha_n, ...), \ y = (\beta_0, \beta_1, \beta_2, ..., \beta_n, ...) \in Z_m,
\]

we set

\[
\rho_m(x, y) = \frac{1}{m^k} \text{ if } \alpha_j = \beta_j, j = 0, 1, ..., k - 1, \text{ and } \alpha_k \neq \beta_k.
\]

This is a metric and even an ultrametric. To find the distance \(\rho_m(x, y)\) between two strings of digits \(x\) and \(y\) we have to find the first position \(k\) such that strings have different digits at this position.

Geometrically we can imagine a system of \(m\)-adic integers (which will be the mathematical basis of our cognitive models) as a homogeneous tree with \(m\)-branches splitting at each vertex. The distance between mental states is determined by the length of their common root: close mental states have a long common root. The corresponding geometry strongly differs from the ordinary Euclidean geometry.
Figure 1: The 2-adic tree

Let \((X, \rho)\) be an arbitrary ultrametric space. For \(r \in \mathbb{R}_+, a \in X\), we set

\[
U_r(a) = \{x \in X : \rho(x, a) \leq r\}, \quad U_r^-(a) = \{x \in X : \rho(x, a) < r\}.
\]

These are balls of radius \(r\) with center \(a\). Balls have the following properties:

1) Let \(U\) and \(V\) be two balls in \(X\). Then there are only two possibilities: (a) balls are ordered by inclusion (i.e., \(U \subset V\) or \(V \subset U\)); (b) balls are disjoint\(^2\).

2) Each point of a ball may serve as a center.

3) In some ultrametric spaces a ball may have infinitely many radii.

Let \(m > 1\) be the fixed natural number. We consider the \(m\)-adic metric space \((\mathbb{Z}_m, \rho_m)\). This metric space has the natural algebraic structure.

A point \(x = (\alpha_0, \alpha_1, \alpha_2, \ldots, \alpha_n, \ldots)\) of the space \(\mathbb{Z}_m\) can identified with a so called \(m\)-adic number:

\[
x = \alpha_0 \alpha_1 \ldots \alpha_k \ldots \equiv \alpha_0 + \alpha_1 m + \ldots + \alpha_k m^k + \ldots.
\]

The series converges in the metric space \(\mathbb{Z}_m\). In particular, a finite string \(x = \alpha_0 \alpha_1 \ldots \alpha_k\) can be identified with the natural number

\[
x = \alpha_0 + \alpha_1 m + \ldots + \alpha_k m^k.
\]

It is possible to introduce algebraic operations on the set of \(m\)-adic numbers \(\mathbb{Z}_m\), namely addition, subtraction, and multiplication. These

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\(^2\)There is the third possibility in the Euclidean space.
operations are natural extensions by the $m$-adic continuity of the standard operations on the set of natural numbers $\mathbb{N} = \{0, 1, 2, 3, \ldots\}$.

3 Mental information space

We shall use the following mathematical model for mental information space:

(1) Set-structure: The set of mental states $X_{\text{mental}}$ has the structure of the $m$-adic tree: $X_{\text{mental}} = \mathbb{Z}_m$.

(2) Topology: Two mental states $x$ and $y$ are close if they have sufficiently long common root. This topology is described by the metric $\rho_m$.

In our mathematical model, mental space is represented as the metric space $(\mathbb{Z}_m, \rho_m)$.

4 Genetic information space

Genetic information space arises as a special case of mental information spaces.

4.1 4-adic encoding of nucleotides

We shall use the following mathematical model for genetic information space. We choose the 4-adic representation for DNA and RNA:

$T = 0, C = 1, A = 2, G = 3$

and

$U = 0, C = 1, A = 2, G = 3$.

An arbitrary gene in a DNA-sequence is encoded by a 4-adic integer, for example:

$ATCGTA... \rightarrow 201302... = 2 + 4^2 + 3 \cdot 4^3 + 2 \cdot 4^5 + ...$

Of course, biologically realizable sequences are finite (but very long). Thus they correspond to natural numbers. But in a mathematical model we can use even infinitely long genetic sequences. Denote this space by the symbol $X_{\text{genetic}}$. This space has the following distinguishing features:
(a) **Set-structure:** The set of genetic states $X_{\text{genetic}}$ has the structure of the 4-adic tree: $X_{\text{genetic}} = \mathbb{Z}_4$.

(b) **Topology:** Two genetic states $x$ and $y$ are close if they have sufficiently long common root\(^3\). This topology is described by the metric $ρ_4$.

(c) **Dynamics:** Information processing on the level of genetic states is described by 4-adic dynamical systems. In the simplest case of the discrete-time dynamics these are iteration of a map

$$f : \mathbb{Z}_4 \to \mathbb{Z}_4.$$  

(d) **Hierarchical structure:** The coding system which is used our model for recording vectors of information generates a hierarchical structure between digits of these vectors – between nucleotides in the gene-sequence. Thus if $x = (α_1, α_2, ..., α_n, ...)$, $α_j = 0, 1, 2, 3$ is an information vector which presents genetic information then digits $α_j$ have different weights. The digit $α_0$ is the most important, $α_1$ dominates over $α_2, ..., α_n, ...$, and so on.

### 4.2 Transcription-map

Transcription is the process of copying a gene into RNA. This is the first step of turning a gene into protein (although not all transcriptions lead to proteins). In our coding system transcription is simply the identity map from $\mathbb{Z}_4 \to \mathbb{Z}_4$ (since the $T$ and $U$ nucleotides are represented by the same digit).

### 5 Genetic code

#### 5.1 Encoding of proteins by codons

In the genetic code proteins are encoded by *codons* – blocks of the length 3 in the gene transcription. Each codon contains information for producing of a single amino acid. By using our 4-adic coding system we can rewrite the table of the genetic code, see, e.g., Wikipedia, 2006. We collect amino acids in families with respect to a number of codons which are used to encode an amino acid:

\(^3\)Thus the first SNP (single nucleotide polymorphism) distinguishes two genetic states.
(1). Met: 203; Trp: 033;
(2). Asn: 220, 221; Asp: 320, 321; Cys: 030, 031; Gln: 122, 123; Glu: 322, 323; His: 120, 121; Lys: 222, 223; Phe: 000, 001; Tyr: 020, 021;
(3) Ile: 200, 201, 202; Stop: 023, 032, 022;
(4). Ala: 310, 311, 312, 313; Gly: 330, 331, 332, 333; Pro: 110, 111, 112, 113; Thr: 210, 211, 212, 213; Val: 300, 301, 302, 303;
(6). Arg: 130, 131, 132, 133, 232, 233;
Leu: 002, 003, 100, 101, 102, 103;
Ser: 010, 011, 012, 023, 230, 231;

5.2 Codon-map
First we consider the standard left-shift:
\[ s_l(α_0α_1α_2...) = α_1α_2... \]
We also consider the following cutoff-map
\[ c_3(α_0α_1α_2...) = α_0α_1α_2. \]
Then the representation by codons of the gene-expression is given by the \( c_3 \)-projections of the iterations of the left-shift:
\[ x_n = c_3(s_l^{3(n-1)}(x)). \]

6 2-adic encoding of proteins
The 4-adic encoding can be easily transformed into the 2-adic encoding just by using the 2-adic representation of the genetic alphabet:
2-adic code: U=00, A=01, C=10, G=11;
We again collect amino acids in families with respect to a number of codons which are used to encode an amino acid:
(1). Met: 010011; Trp: 001111;
(2). Asn: 010100, 010110; Asp: 110100, 110110; Cys: 001100, 001110; Gln: 100101, 100111; Glu: 110101, 110111; His: 100100, 100110;
Lys: 010101, 010111; Phe: 000000, 000010; Tyr: 000100, 000110;
(3). Ile: 010000, 010010, 010001; Stop: 000111, 001101, 000101;
(4). Ala: 110100, 110101, 110110, 110111;
Gly: 111100, 111110, 111101, 111111;
Pro: 101000, 101010, 101001, 101011;
Thr: 011000, 011010, 011001, 011011;
Val: 110000, 110010, 110001, 110011;
(6). Arg: 011100, 011101, 011101, 011111, 101110, 101111;
Leu: 000001, 000011, 100000, 100010, 100001, 100011;
Ser: 001000, 001010, 001001, 000111, 011100, 011110.

7 Dynamical model for degeneracy of the genetic code

We shall use study dynamical systems corresponding to maps:

\[ Z_m \rightarrow Z_m, x \rightarrow f(x). \]  \hspace{1cm} (5)

As usual, we study the behaviour of iterations \( x_n = f^n(x_0), x_0 \in \mathbb{Z}_p \),
where \( f^n(x) = f \circ \ldots \circ f(x) = f(\ldots(f(f(x))\ldots), \) the result of \( n \) successive
applications of the map \( f \). We shall use the standard terminology of
the theory of dynamical systems. If \( f(x_0) = x_0 \) then \( x_0 \) is a fixed point.
If \( x_n = x_0 \) for some \( n = 1, 2, \ldots \) we say that \( x_0 \) is a periodic point.
If \( n \) is the smallest natural number with this property then \( n \)
is said to be the period of \( x_0 \). We denote the corresponding cycle by
\( \gamma = (x_0, x_1, \ldots, x_{n-1}) \). In particular, the fixed point \( x_0 \) is the periodic
point of period 1. Obviously \( x_0 \) is a fixed point of the iterated map \( f^n \) if \( x_0 \) is a periodic point of period \( n \).

Simplest dynamical laws are given by monomial functions \( f_s(x) = x^s, s = 2, 3, \ldots \) (each branch of the \( p \)-adic tree is multiplied by itself \( s \)
times producing a new branch).

Our basic idea is associate with the genetic code some polynomial

\[ f_{\text{genetic}}(x) = a_0 + a_1x + \ldots + a_nx^n, x \in \mathbb{Z}_m, \]

where depending on the choice of the coding system \( m = 4, 2 \).

Such a polynomial encodes amino acids in the following way. The set of codons (which are considered as 2-adic numbers) is split by this
polynomial into groups of cycles. Each cycle encodes one amino acid, so:

Amino acids are coded by cycles of this polynomial.

Our model cannot explain the origin of such a coding polynomial. Its origin can be a consequence of biological evolution or just purely information features of the genetic system. Since we do not know the (e.g., biological) background inducing a coding polynomial \( f_{\text{genetic}}(x) \). We are not able to choose it in the unique way. In this note we propose one of possible solutions of the problem of finding of a coding polynomial.

We shall use the well known Mahler’s polynomials. To proceed in this way, we choose the 2-adic genetic coding. The \( m = 2 \) is a prime number and the system of 2-adic integers \( \mathbb{Z}_2 \) can be extended to the field of 2-adic numbers \( \mathbb{Q}_2 \). We recall that in a number field one can use all arithmetic operations: addition, subtraction, multiplication and division. We need these operations to define a Mahler’s polynomial (the main problem is division). It would be a map \( f_{\text{genetic}} : \mathbb{Z}_2 \rightarrow \mathbb{Q}_2 \) having the structure of cycles corresponding to the genetic code of amino acids.

Let we know values of some function \( f : \mathbb{Z}_2 \rightarrow \mathbb{Q}_2 \) in points \( j = 0, 1, ..., n \). Then its \( n \)th Mahler coefficient is defined by

\[
a_n = \sum_{j=0}^{n} (-1)^{n-j} \binom{n}{j} f(j).
\]

The corresponding Mahler’s polynomial has the form:

\[
F_n(x) = \sum_{k=0}^{n} a_k \binom{x}{k},
\]

where the binomial polynomial

\[
\binom{x}{k} = \frac{x(x-1)(x-2)...(x-k+1)}{k!}
\]

The crucial is that

\[
f(j) = F_n(j), j = 0, 1, ..., n.
\]

Coming back to the genetic code, we see that there are 64 different points-codons. Thus we need a Mahler polynomial of degree 63 such that
Met : f(010011) = 010011; Trp : f(001111) = 001111;
Asn : f(010100) = 010110, f(010110) = 010100;
Asp : f(110100) = 110110, f(110110) = 110100, ...
Ser : f(001000) = 001010, f(001010) = 001001, f(001001) = 000111,
f(000111) = 011100, f(011100) = 011110, f(011110) = 001000.

8 Representation of gene code through dynamics of fuzzy cycles

By using the 2-adic coding we can represent each codon with a 2-adic ball of the radius $r = 1/64$ with center in the corresponding 2-adic word. For example, $010011 \rightarrow U_{1/64}(010011)$. This is the set of all 2-adic sequences such that the first sixth digits coincides with the codon word 010011. Thus the amino acid Met can be represented by the ball $U_{1/64}(010011)$ and Trp by $U_{1/64}(001111)$. But Asn by the union of two balls: $U_{1/64}(010100) \cup U_{1/64}(010110)$ and, e.g., Ser by the union of sixth balls

$$U_{1/64}(001000) \cup U_{1/64}(001010) \cup U_{1/64}(001001) \cup U_{1/64}(000111) \cup U_{1/64}(011100) \cup U_{1/64}(011110).$$

We remark that in Dragovich, 2006, there was considered a 5-adic model to explain the origin of the gene code. In this model 5-adic balls were used to classify codons.

In Khrennikov, 1997, there were also considered fuzzy cycles, cycles of balls,

$$U_{r_1}(a_1) \rightarrow U_{r_2}(a_2) \rightarrow \cdots \rightarrow U_{r_k}(a_k) \rightarrow U_{r_1}(a_1).$$

We can easily define the notion of attractor fuzzy cycle and Siegel fuzzy cycle. The basin of attraction of a fuzzy cycle is a set of all points which are attracted by such a cycle.

As we have seen in Dubischar et al, 1999, and Khrennikov and Nilsson, 2004, consideration of fuzzy cycles is a more natural, since they are stable with respect to noise (ordinary cycles can be easily
disturbed by noisy perturbations). Now we consider a model in that the “genetic polynomial” $f_{\text{genetic}}(x)$ encodes amino acids in the following way: *Amino acids are coded by fuzzy cycles of this polynomial.* However, at the moment we do not have mathematical examples of simple polynomials having the structure of fuzzy cycles corresponding to the genetic code. We shall continue the study of this problem in one of our following papers.

**Conclusion.** We have seen that the genetic code has a natural $4$-adic (or $2$-adic) structure. Gene expression could be coupled to a dynamical system in the genetic information space.

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