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BIOCOMPUTERS 4

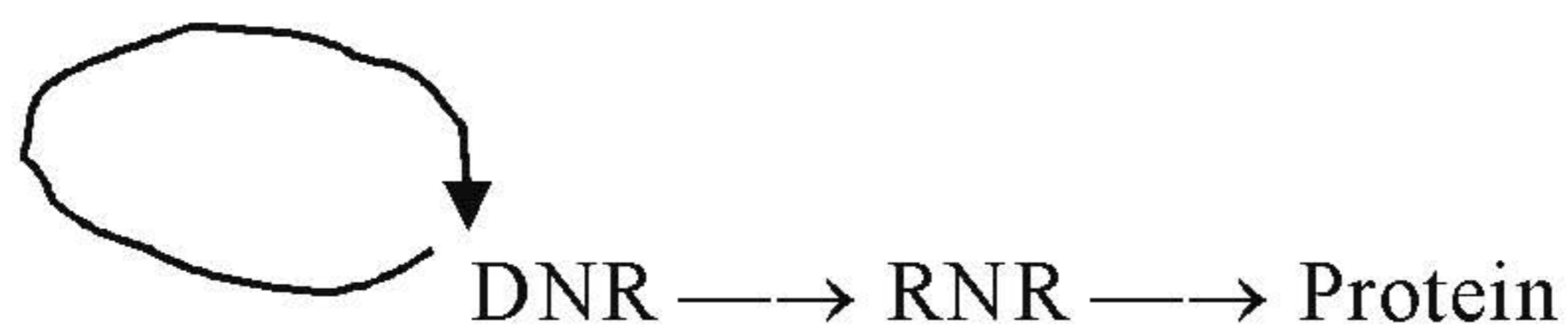
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We reformulate the notion of 2-Linear Cell Automata for biological computing in a manner that may be implemented the concrete biochemical synthesis. The main theorems are the theorem 1 and theorem 2 can characteristic 2-Linear Cell Automata in a linear algorithmic types. The main result given here is the concrete biochemical model of biological computing, carried out in chapter 4. Our mathematical techniques also consider ensemble methodic. It is the article is continuous of [1–3].

Keywords: computer, genome, cellular automata, matroid, category, DNA, RNA.

1. Introduction

For all genetic information in system



we have g-LCA universal design. Everything that has been said so far can be formulated mathematics' abstractly whenever a suitable notion of biological-genetic terminology is available. By [3–6], it follows that 2-Linear Cell Automata (g-LCA) is isomorphic g-LCA universal design.

Classical Computer Science modeless real phenomena aid of differential equations for examples and other continuous methods. To construct a biological computing structure associated with a specific combinatorial class, it is useful to introduce the following terminology (see detailed in [8]).

Let $\Delta = (V(\Delta), E(\Delta))$ is a digraph, where $V(\Delta)$ is the setpoint and $E(\Delta)$ is the setarrow of Δ . A digraph Δ (3) is called an *orforest* if Δ not contains an *orloop*. Moreover, a digraph

$$\Lambda = (V(\Lambda), E(\Lambda)),$$

is called a *straightedge* if $V(\Lambda) = [0, 1, 2, \dots, n]$ and $E(\Lambda) \subseteq \{(i-1, i)\}, i \in [1, n]$. Also, a *linear orgraph* is called a orgraph $\Gamma = (V, E)$ such that there exists a surjective map

$$\mathcal{C}: \Gamma \longrightarrow \Lambda,$$

where Λ is a straightedge and a restriction of the map on diwalk L^{\rightarrow} is injective map, where L^{\rightarrow} is a suborgraph Γ .

The following theorem was first in [3, 5].

Proposition 1. 2-Linear Cell Automata of DNA-RNA -Automata is a linear diforest.

Further, let $\Delta = (V, E)$ is cell digraph (6), $V^h \subseteq V, V^y \subseteq V$, and $D(\Delta)$ is the set of all directed walk $I^{\rightarrow}(v_1, v_{n+1}) = v_1 e_1 v_2 e_2 v_3 \dots e_n v_{n+1}$, where $v_1 \in V^h, v_{n+1} \in V^y$. There is given a map

$$\psi: E \longrightarrow (\Xi, \Xi \times \Xi).$$

The set Ξ is called an *arrows cell (a-cell)*. V^h and V^y are called an *input* and an *output*. Sekstant

$$CL = (\Gamma, \Xi, \psi, V^h, V^y, d) \tag{1}$$

is called *2-Band Cellular Automata (2CA)*. Further, the word $S = a_1 a_2 \dots a_s \#$ induces 2LCA (1), if $a_1 \in V^h, a_s \in V^y, \zeta\{\#\} \longrightarrow U \cup U^2, \zeta\{a_i\} \longrightarrow U \cup U^2, \forall (a_i, a_{i+1}) \in E, \psi(a_i, a_{i+1}) \longrightarrow (\Xi, \Xi \times \Xi)$. Here, CL is called *2-Band Linear Cellular Automata (2-LCA)*.

Proposition 2. 2-Band Linear Cellular Automata DNA-RNA-Automata is isomorphic to 2-Linear Cell Automata (LCA).

Proposition 3. g-LCA (2-Linear Cell Automata DNA-RNA-Automata) is logical universal.

Proposition 4. g-LCA have $N^g \geq 8, St^g \geq 30$, where N^g are rules of cell transform and St^g are cell states.

The proof's detailed is given in [3, 5, 6]

2. Mathematical Model of 2-Linear Cell Automata

In this section we give mathematical strongly extensions of our propositions 2 for 2-band Linear Cellular DNA-RNA Automata (2LD-RCA).

Without loss of generality we can be assumed that:

- a) 2-Band Linear Cellular DNA-RNA Automata make up by the two cell bands, see proposition 2;
- b) There is a finite set \mathbf{A} of symbols which we will call the *alphabet*. Let $\mathbf{A} = (\dots, \alpha_i, \dots) \neq \emptyset$ be a set, whose elements will be called *letters* or *codons*, and they will typically be denoted by $\alpha, \beta, \gamma, \dots$. DNA-RNA alphabet, for example, use the letters $\{\text{Ala, Cys, } \dots, \text{Trp, Tyr}\}$;
- c) Band of 2LCA is *z-infinite (zwei-infinite)* sequences of letters from an alphabet \mathbf{A} . Such a sequences is denoted by

$$\mathbf{b} = \dots \alpha_{-3} \alpha_{-2} \alpha_{-1} \# \alpha_0 \alpha_1 \alpha_2 \alpha_3 \dots,$$

or by $\mathbf{b} = (\alpha_i)_{i \in \mathbb{Z}}$. The letter α_i is the i -th coordinate of the band \mathbf{b} . This is conveniently done with a “diez symbol” to separate the α_i with $0 \leq i$, from those with $0 < i$.

For the following, we will give a name to the successions of 2LD-RCA. The *full band* \mathbf{B}^* is the collection of all sequences (z-infinite sequences, too!) of letters from \mathbf{A} . A *word* w over alphabet \mathbf{A} is a finite sequence of letters from \mathbf{A} . \emptyset is called the *empty word*. Let $M(\mathbf{A})$ be the free monoid generated by \mathbf{A} . If $\mathbf{A} = \{\text{Ala, Cys, } \dots, \text{Trp, Tyr}\}$, then the elements of $M(\mathbf{A})$ are called *g-words* (genetic words) and are identified with finite sequences $S = \alpha_1 \alpha_2 \dots \alpha_s \#$, here $\alpha_i \in \mathbf{A}, i = [1, s], \# = \text{end or end2}$. We recall that the *length* $l(S)$ of words (and g-words) is the numbers of letters it contains. $l(\emptyset) = 0$. The composition in $M(\mathbf{A})$ will be written multiplicatively, so that $S_1 \circ S_2 = \alpha_1 \alpha_2 \dots \alpha_s \beta_1 \beta_2 \dots \beta_r$, is the sequence obtained by juxtaposition of $S_1 = \alpha_1 \alpha_2 \dots \alpha_s$ and $S_2 = \beta_1 \beta_2 \dots \beta_r$. The 0-words $\varepsilon = \emptyset$ is the identity element of the monoid $M(\mathbf{A})$. We are given a map $w: \mathbf{A} \longrightarrow [0, 1, 2]$. $w(\alpha_i)$ is called *arity* of the codon α_i . For each non-null word $S = \alpha_1 \alpha_2 \dots \alpha_s$, we put $w(S) = \sum_{i=1}^s w(\alpha_i)$, and $w(\varepsilon) = 0, w(\alpha) = 1, w(\#) = 2$. $w(S)$ is called the *significant* of the word S . If $S_1 = S \circ S_2 \circ S$, the word S_2 is said to be a *segment* of S_1 .

We also need to infinite symbolic. Let z -word $\mathbf{b} = \dots \alpha_{-3} \alpha_{-2} \alpha_{-1} \# \alpha_0 \alpha_1 \alpha_2 \alpha_3 \dots$ and $i \leq j$, then we will denote the *word of coordinates* in \mathbf{b} from coordinate i to coordinate j by $\mathbf{b}_{[i, j]} = \alpha_i \dots \alpha_j$. $M^z(\mathbf{A})$ is the free monoid of word and word of coordinates D generated by \mathbf{A} . The *linked map* ω on the full

bond \mathcal{B}^* maps a z-word $\mathbf{b}_1 = \dots \alpha_{-3}\alpha_{-2} \alpha_{-1}\#\alpha_0\alpha_1\alpha_2\alpha_3 \dots$ to the point $\mathbf{b}_2 = \omega(\mathbf{b}_1) = \dots \beta_{-3}\beta_{-2}\beta_{-1}\#\beta_0\beta_1\beta_2\beta_3 \dots$ ($\omega : \mathbf{b}_1 \mapsto \omega(\mathbf{b}_1)$) whose i-th coordinate is $\beta_i = \alpha_{i+1}$, see fig.1.

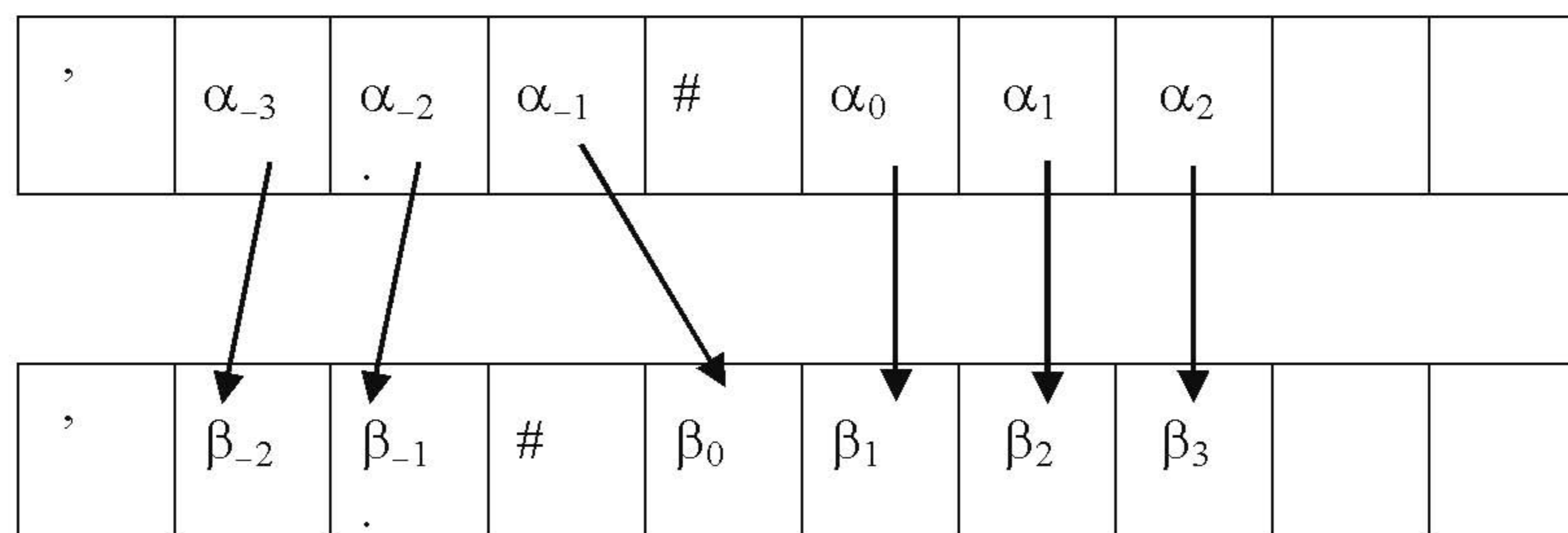


Fig. 1

The *linked transformation* τ on the full bond \mathcal{B}^* is called the linked map onto itself. A z-word \mathbf{b} is *periodic* for the linked transformation τ if $\tau^n(\mathbf{b}) = \mathbf{b}$ for some $\mathbb{N} \ni n \geq 1$. If \mathbf{b} is periodic, the smallest n for which $\tau^n(\mathbf{b}) = \mathbf{b}$ is the *period* of \mathbf{b} . If $\tau(\mathbf{b}) = \mathbf{b}$ then \mathbf{b} is called a fixed z-word for τ . Let S is a word over the alphabet \mathbf{A} . We will say that *locale* in a z-word \mathbf{b} if there are coordinate i and j so that $\mathbf{b}_{[i,j]} = S$. Further, L be a set of words over the alphabet \mathbf{A} . For any such L , define \mathcal{L}_L to be the subset the full bond \mathcal{B}^* which do not contain any locale is equal to words in L . A *bond fund* (or *b-fund*) is a subset $\mathcal{B}^*(L)$ of the full bond \mathcal{B}^* such that $\mathcal{B}^*(L) = \mathcal{L}_L$. A *bond space* \mathfrak{R} is called a triple $\mathfrak{R} = (\mathbf{A}, \mathcal{B}^*, L)$. Finally, let subbond $D \subseteq \mathcal{B}^*$, and let $U^n(D)$ denote the set of all locale S of D , $l(S) = n$, the *language* $\Theta(D)$ of subbond D is $\Theta(D) = \bigcup_{i=0}^{\infty} \Theta^i(D)$.

Theorem 1. Let $\mathfrak{R}_1 = (\mathbf{A}, \mathcal{B}^*, L_1)$, $\mathfrak{R}_2 = (\mathbf{A}, \mathcal{B}^*, L_2)$, $D_1 \subseteq \mathcal{B}^*$, $D_2 \subseteq \mathcal{B}^*$, and $\Theta(D_1) = \bigcup_{i=0}^{\infty} \Theta^i(D_1)$, $\Theta(D_2) = \bigcup_{i=0}^{\infty} \Theta^i(D_2)$ its languages. Two bond spaces $\mathfrak{R}_1, \mathfrak{R}_2$ are equal \Leftrightarrow they have $\Theta(D_1) = \Theta(D_2)$.

Theorem 2. Let $\mathfrak{R} = (\mathbf{A}, \mathcal{B}^*, L)$ be a bond space, and $\Theta(\mathcal{B}^*)$ be its language, N is a subset of bond over the alphabet \mathbf{A} , then $N = \Theta(\mathcal{B}^*)$ for the bond space $\mathfrak{R} \Leftrightarrow$ if N satisfies condition

- (1) if a word $S \in N$, then every sublocale of S belongs N
- (2) there are nonempty $S_1, S_2 \in \Theta(D)$, so that $S_1 \circ S \circ S_2 \in \Theta(D)$.

3. Elements Molecular of Biocomputing

Let us take note of the fact that the basic elements of the experimental biological molecular computing structure S are a microscopically biochemistry ensemble E under research and a macroscopically device D interacting with the ensemble which brings about certain detectable changes in it. Conclusions on the behaviour and parameters of the ensemble are then drawn from the changes detected in the device states. As almost everywhere in S are multivariate, numerous copies of a molecular biocomputers (kerns of biocell, devices of molecular computers etc) must be available.

Let S is a biological computing structure (bmcs) and $\mathfrak{T} = (\mathbf{A}, T)$ is a topological space and S is a point of \mathfrak{T} ($S \in \mathbf{A}$). \mathbf{R} is a measuring instrument. Suppose S_1 is a biochemistry ensemble after our

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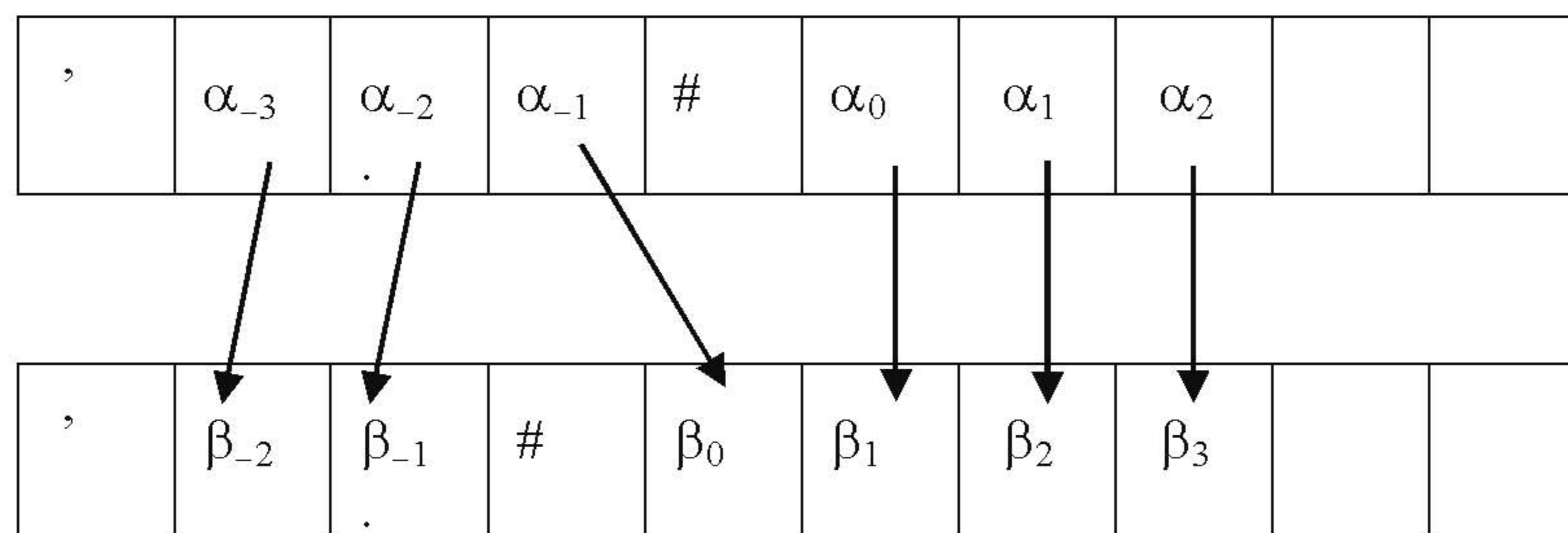


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