Chiral Asymmetry of D. Hofstadter's Typogenetics

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Abstract

Typographical genetics ("Typogenetics") introduced by Douglas Hofstadter in 1979 is an abstract recursive logic system which has been studied subsequently for insights into self-reproduction. There are immediately-observable asymmetries in the early formulations of Typogenetics, but after design of a triplet-codon Typogenetics to eliminate these, fundamental irreducible asymmetry remains. It is noted that both Typogenetics and self-reproduction of cellular automaton loop structures share the property of chiral asymmetry.

Keywords: Typogenetics, chiral asymmetry, artificial life, origin of life

Introduction

Inspired by some features of molecular biology, D Hofstadter presented *Typogenetics* (Typographical Genetics) as an example of an abstract recursive logic system, without the intention of exploring it and its implications comprehensively [2]. The opportunity to complete its logic and explore more of its meaning was taken up by HC Morris [4,5] and L Varetto [7].

Original Typogenetics as described by HC Morris [4,5] is summarized by a translation table and a tertiary structure/binding preference table (Tables 1 and 2, below). Strands are composed from the set of four *base units* {A,C,G,T}. Each strand is parsed into a sequence of *duplets* (sequential pairs of base units), analogous to codons. Each sequence of duplets corresponds to a sequence of *commands* ("typo-amino acids"). The commands-sequence (*typoenzyme*) binds to a preferred unit of its strand, determined by the sequence of *folding inclinations* {l,r,s} (Table 1) and the relative inclinations of the first (leftmost) and last (rightmost) commands/amino acids of the typoenzyme (Table 2). A sequence of *operations* corresponding to the command sequence (Table 1) is applied to the strand which generally changes it, so a recursive process of strand modification (strand → typoenzyme → modified strand(s) … *etc.*) can proceed indefinitely. This description is only a very brief introduction to Typogenetics, sufficient for the current work, and readers requiring a comprehensive description are referred to the references [2,4,5,7].

Table 1. Typogenetics translation table, reproduced from [4,5]. (Duplet AA is reserved as a no-operation punctuator between genes of a multi-gene strand).

Duplet	Command	Operation Described
AC s	cut	Cut the strand to the right of the present unit; through both levels if double strand.
AG s	del	Delete this unit, then move one unit right.
AT r	swi	Switch enzyme to unit (if any) in vertical relationship with present unit.
CA s	mvr	Enzyme moves one unit right.
CC s	mvl	Enzyme moves one unit left.

CG	r	cop	Turn on copy mode. Until turned off or detached, enzyme produces complementary units vertical to all units it touches or inserts.
CT	l	off	Turn off copy mode.
GA	s	ina	Insert A to the right of this unit.
GC	r	inc	Insert C to the right of this unit.
GG	r	ing	Insert G to the right of this unit.
GT	l	int	Insert T to the right of this unit.
TA	r	rpy	Find nearest pyrimidine (C or T) to right.
TC	l	rpu	Find nearest purine (A or G) to right.
TG	l	lpy	Find nearest pyrimidine (C or T) to left.
TT	l	lpu	Find nearest purine (A or G) to left.

Table 2. Tertiary structure/binding preference table, reproduced from [4,5].

1st Amino Acid Inclination	Last Amino Acid	Binding Preference
1. Straight	→	A
	↑	C
	↓	G
	←	T
2. Left	↓	A
	→	C
	←	G
	↑	T
3. Right	↑	A
	←	C
	→	G
	↓	T

In 1998, L Varetto introduced the application of Typogenetics to the study of *tanglecycles* which are simple generalizations of *hypercycles* [8]. Hypercycles are closed-cycles of catalysis within populations of self-replicators which sustain self-replication, introduced by M Eigen in 1971 [1], and further developed by M Eigen and P Schuster.

There is scope for modification of the original formulation of Typogenetics for consideration of a wide range of interesting questions. In original Typogenetics [2,4,5,7], each typoenzyme acts only on its corresponding strand. By relaxing this condition to allow typoenzymes to act anywhere within a population of strands, a virtual chemostat environment accommodating a simplified Typogenetics

was modelled by J Pospíchal and colleagues for the study of evolutionary emergence and persistence of hypercycles. The history of this effort is described in [3].

No-one knows what the earliest and simplest ancestral living structures were, but by studying a range of simple abstractions displaying life-relevant properties (*e.g.* Typogenetics, and self-reproducing structures in cellular automata spaces [6]), it may be possible to identify some fundamental, universal logic-of-life principles. The objective of this work is to study the symmetry properties of Typogenetics which may suggest an additional avenue for thinking about the problem of how homochirality observed in real biology came to be.

Chirality in Typogenetics

Typogenetics will show chiral symmetry if the recursive development of Typogenetics strands mirrors the recursive development of the strands' corresponding mirrors (*i.e.* strands with units in reverse order). However, it can be readily observed that recursive development paths of strands and corresponding mirror-complement strands immediately diverge sharply from mirror-complementarity, *i.e.* original Typogenetics is homochiral – any history of meaningful recursive development (*e.g.* emergent self-reproduction) from an initial strand will not correspond to a mirror history complement of development from its mirror-complement strand, which will in all likelihood be meaningless. So: is heterochiral symmetry possible in any *alternative* formulations of Typogenetics?

Original typogenetics has been engineered so that the binding preference (BP) determination of typoenzymes of strands and their corresponding mirror-complement strands yields the same BP, *i.e.* BP determination is *achiral*, which is a critical requirement for a conjectured heterochiral Typogenetics. The BP determination must be achiral, otherwise the recursive sequences of operations cannot be initiated at common mirror-complement strand loci, with obvious consequential recursive divergence from symmetry. BP achirality is ensured by two features: assignment of common folding inclination to duplets and corresponding mirror-duplets, *e.g.* GC and CG are both assigned folding inclination r (Table 1), ***and*** the organization of the tertiary structure/binding preference table (Table 2). Therefore, for a prospective heterochiral Typogenetics, no alternative typoenzyme BP determination algorithm is needed.

Chiral asymmetry of original Typogenetics manifests for one immediately-obvious fundamental reason: the mirror-complement of a duplet does not correspond to a mirror-operation of the duplet, *e.g*., from Table 1: CG corresponds to "Turn on copy mode", and mirror-duplet GC corresponds to "Insert C to the right of this unit", so in the quest for a heterochiral Typogenetics, the observable asymmetries in original Typogenetics must be replaced by symmetries. A prospective heterochiral Typogenetics requires coexistence of left- and right-handed directional operations (*i.e.* a codon corresponding to a left-orientated operation must coexist with a mirror codon corresponding to the right-oriented complement operation).

Duplets of four existing bases number $4^2 = 16$, so no more than fifteen corresponding operations can be accommodated within original duplet-codon Typogenetics (duplet AA is reserved as a no-operation punctuator between multiple genes along a strand). From Table 1, we can observe that operations corresponding to the three pairs of duplets (CA,CC), (TA,TG) and (TC,TT) correspond to mirror-pairs of operations, *e.g.* in pair (CA,CC), CA corresponds to the operation "Enzyme moves one unit right" and CC corresponds to its mirror complement "Enzyme moves one unit left". While mirror-pairs of operations are accommodated by duplet pairs (CA,CC), (TA,TG) and (TC,TT), mirror-

complement operations corresponding to each of the six duplets AC, AG, GA, GC, GG and GT are absent, *e.g.* duplet GA corresponds to the operation "Insert A to the right of this unit", but there is no mirror operation "Insert A to the left of this unit". Any prospective accommodation of chiral symmetry in duplet-codon Typogenetics therefore requires an additional six operations, or 21 operations in total, which exceeds what can be accommodated with the available fifteen duplets. The solution to this problem is to accommodate a larger codon set, which can be done only by construction of a triplet-codon Typogenetics. We recognize immediately that this step brings Typogenetics one step closer to real molecular biology, with its system of $4^3 = 64$ triplet-codons. Sixty-four different codons provide freedom to include a wider range of operations (*e.g.* introduction of deterministic point mutations), and if the codon-set is still not fully-assigned to operations, a "degeneracy" condition of multiple codons corresponding to each of some operations (analogous to degeneracy of the real-biology genetic code) is required.

Table 3 shows a translation table of a provisional triple-codon Typogenetics, designed to replace the recognized asymmetries of original Typogenetics with corresponding symmetries. For operations defined in left- and right-orientation complements, note that the *folding inclination* (l, r or s) is common (*e.g*. triplet mirror-pair AAT and TAA corresponding to "Enzyme moves one unit right" and "Enzyme moves one unit left" are both assigned Folding inclination direction r (right), which serves to retain achirality of the Binding Preference determination).

Table 3. Translation table for consideration of chirality of an alternative typogenetics system.

Triplet	Folding inclination	Command	Operation Described
AAC	r	cutl	Cut the strand to the left of the present unit; through both levels if double strand.
CAA	r	cutr	Cut the strand to the right of the present unit; through both levels if double strand.
AAG	r	delr	Delete this unit, then move one unit right.
GAA	r	dell	Delete this unit, then move one unit left.
GGG, TTT ACA	s	swi	Switch enzyme to unit (if any) in vertical relationship with present unit.
AAT	r	movr	Enzyme moves one unit right.
TAA	r	movl	Enzyme moves one unit left.
ACC, CCA CGC, CTC	s	cop	copy on
AGA, ATA CAC	s	off	copy off

ACG	l	inar	Insert A to the right of this unit.
GCA	l	inal	Insert A to the left of this unit.
ACT	r	incr	Insert C to the right of this unit.
TCA	r	incl	Insert C to the left of this unit.
AGC	l	ingr	Insert G to the right of this unit.
CGA	l	ingl	Insert G to the left of this unit.
AGG	r	intr	Insert T to the right of this unit.
GGA	r	intl	Insert T to the left of this unit.
AGT, ATC	l	rpy	Find nearest pyrimidine (C or T) to right.
TGA, CTA	l	lpy	Find nearest pyrimidine (C or T) to left.
ATG, ATT	r	rpu	Find nearest purine (A or G) to right.
GTA, TTA	r	lpu	Find nearest purine (A or G) to left.
CAG, CAT CCG, GAC TAC, GCC	l	tac	Toggle A <-> C. If present unit is “A” change to “C”. If present unit is “C” change to “A”. If present unit is neither, no operation. Change unit in vertical relationship accordingly.
CCT, CGG CGT, TCC GGC, TGC	r	tat	Toggle A <-> T. If present unit is “A” change to “T”. If present unit is “T” change to “A”. If present unit is neither, no operation. Change unit in vertical relationship accordingly.
CTG, CTT GAT, GTC TTC, TAG	l	tgc	Toggle G <-> C. If present unit is “G” change to “C”. If present unit is “C” change to “G”. If present unit is neither, no operation. Change unit in vertical relationship accordingly.
GCT, GGT GTT, TCG TGG, TTG	s	tgt	Toggle G <-> T. If present unit is “G” change to “T”. If present unit is “T” change to “G”. If present unit is neither, no operation. Change unit in vertical relationship accordingly.
AAA, CCC			Punctuators separating genes on a single strand.
GAG, GCG GTG	s	tga	Purine to other purine: If present unit is “G” change to “A”. If present unit is “A” change to “G”. If present unit is neither, no operation. Change unit in vertical relationship accordingly.

TAT TCT TGT	s	tct	Pyrimidine to other pyrimidine: If present unit is “C” change to “T”. If present unit is “T” change to “C”. If present unit is neither, no operation. Change unit in vertical relationship accordingly.

Does an alternative Typogenetics based on Table 3, with Table 2 inherited from original Typogenetics satisfy heterochirality?

The Appendix shows a BASIC program listing for identifying one or more genes in triplet-codon strands, and determining the binding preference(s) of the corresponding typoenzyme(s). The script is adapted directly from the code for duplet-Typogenetics provided by HC Morris [4,5], and so can be directly compared with his listing. For reasons previously discussed, the binding preference of each of the typoenzymes of the mirror-pair of typoenzymes is common, *e.g.* :

The strands GCTGAAAGTTCAGCT and TCGACTTGAAAGTCG are a mirror-pair of single-gene triplet-codon strands, with common typoenzyme BP “G”. Noting more than one G unit in each strand and applying the convention adopted in [7] that the first BP unit encountered along the strand is the typoenzyme initial-attachment locus, the loci of attachment are identified in lower-case below:

gCTGAAAGTTCAGCT

TCgACTTGAAAGTCG (*not* TCGACTTGAAAGTCg)

We see immediately that mirror-symmetry breaks at typoenzyme attachment. In the Discussion section below, further fundamental asymmetries of Typogenetics are explored.

Discussion

A strand comprising a multiple-of-three number of units comprises only complete codons. The typoenzymes of these strands, and of the corresponding mirror-strands are complementary mirror-pairs themselves, differing only in the sequence-direction of the commands. However, a strand need not comprise only complete codons, and indeed the nett result of unit-deletion and unit-insertion operations on only-complete-codons strands will very often be strands comprising complete codons plus one or two more units.

Asymmetry by frameshift occurs for strands comprising an integer-number of codons plus one or two more units. These strands will generally be structurally and functionally unrelated to their mirror-complements, as shown by the example below:

Strand GCTGAAAGTTCAGCTC parses to codon-sequence GCT GAA AGT TCA GCT C

but its mirror-strand CTCGACTTGAAAGTCG parses to CTC GAC TTG AAA GTC G which is a completely different codon-sequence and corresponding typoenzyme-operations sequence.

Operations do not commute

In strands of only complete codons, for which typoenzymes and complement mirror typoenzymes differ only in the sequence-direction of the commands, asymmetry is a consequence of non-commutability of operations, as shown by the two-codon strand example below:

TATgAA and AAgTAT are mirror-complementary two-codon strands. The operation corresponding to codon TAT is the toggle between C and T units, so the first operation at g on TATgAA has no effect. The operation corresponding to GAA is to delete current unit and move left, so this second and last operation delivers TATAA and the typoenzyme detaches.

The operation corresponding to codon AAG is to delete current unit and move right, which transforms AAgTAT to AAtAT. The toggle between C and T operation corresponding to TAT then transforms AAtAT to AACAT and the typoenzyme detaches. After one typoenzyme recursion for each initial strand of the mirror-pair the result is TATAA and AACAT - these are not a mirror-pair.

So is symmetry complete for single-codon strands?

The strands AGc, cGA are a mirror-pair of single codon/single operation strands. After four successive typoenzyme attachment-operations-detachment recursion cycles, AGc develops to AGcGGGG by repeated insertion of "G" units. After just two recursions, complement mirror-strand cGA develops to GCGG which is a "dud" (BP is "A") with no further development. Mirror-complementarity of the initial single-codon strands does not correspond to mirror-complementarity of subsequent recursive development, so the hypothesis of chiral-symmetry limited to the sub-universe of single-codon parent strands fails.

After some experience with Typogenetics, it will perhaps be intuitive that Typogenetics (*any* formulation) must be asymmetric. Asymmetry of original duplet-codons Typogenetics is immediately observed. Mirror-pairs of operations (left- and right-handed forms of an operation) do not (and cannot) correspond to mirror pairs of duplets. An arbitrary triplet-codon typogenetics was defined in which the triplets/operations are symmetric, and the binding-preference determination is achiral (Table 3). However, chiral asymmetry persists due to the left-to-right unidirectional interpretation of strands, and BP typoenzyme attachment. We must accept irreducible asymmetries inherent in Typogenetics. To alternatively allow interpretation of all mirror-complementary pairs of strands in opposite directions requires a contrived "God's eye view" of the Typogenetics universe, and above all, is trivial - merely supporting only mirror-of-mirror duplication, and so not contributing to a sought-for non-trivial heterochiral solution. This state of affairs is analogous to absence of information about loop-handedness within the chirality-critical CA transition-function rules contributing to driving self-reproduction in cellular-automaton (CA) space [6].

The self-reproducing loop-structures embedded in CA spaces are distinct from the state-transition rule sets which facilitate reproduction of the structures. Chiral asymmetry in CA self-reproduction exists because of contradictions between state-transition rule sets and complement mirror-rule sets [6]. In Typogenetics, by contrast, a strand decodes directly to a corresponding typoenzyme which acts on it, *i.e.* strand structure and function are not distinct. Chiral asymmetry in Typogenetics occurs as a consequence of consistent left-to-right interpretation of strands. These two different recursive logic families are chirally-asymmetric for different reasons, which suggests the hypothesis that chiral-asymmetry is a fundamental property in the logic-of-life.

Appendix

```
    ' Adapted from HC Morris binding preference function [4,5].
    ' Alternative version for chirality study
    ' - with triplet-codons (not duplets).

        DECLARE SUB Bind (T, BX$, A$, G$, C$, T$)
        DECLARE SUB Morris (SS$, G$(), BP$(), G)
        DIM S$(4), G$(64), BP$(64), TT$(64)

        CLS
        OPEN "TYPOOUT.TXT" FOR OUTPUT AS #1

' Eight mirror-pairs of strands
    DATA "GATTATTCA"
    DATA "ACTTATTAG"
    DATA "GTCCGT"
    DATA "TGCCTG"
    DATA "ACTCCG"
    DATA "GCCTCA"
    DATA "CGCGCGCGTAAT"
    DATA "TAATGCGCGCGC"
    DATA "ATCGCGCGTATT"
    DATA "TTATGCGCGCTA"
    DATA "TACGCGCGATCGAAATTATATTACGCGCGC"
    DATA "CGCGCGCATTATATTAAAGCTAGCGCGCAT"
    DATA "GCTGAAAGTTCAGCT"
    DATA "TCGACTTGAAAGTCG"
    DATA "CGACAC"
    DATA "CACAGC"

        G = 1

        FOR A% = 1 TO 16
        BP$(1) = ""
        READ S$(1)

        CALL Morris(S$(1), G$(), BP$(), G)

        PRINT #1,
        PRINT
        NEXT A%

        CLOSE #1
        END
```

```
'  Identify the Binding Preference from the Tertiary Structure table:
          SUB Bind (T, BX$, A$, G$, C$, T$)
          IF (T = 0) THEN BX$ = A$: GOTO 10
          IF (T = 1) THEN BX$ = G$: GOTO 10
          IF (T = -3) THEN BX$ = G$: GOTO 10
          IF (T = 3) THEN BX$ = C$: GOTO 10
          IF (T = -1) THEN BX$ = C$: GOTO 10
          IF (T = 2) THEN BX$ = T$: GOTO 10
          IF (T = -2) THEN BX$ = T$
10      END SUB

SUB Morris (SS$, G$(), BP$(), G)
          G = 0
          LS = LEN(SS$)
          LT = INT(LS / 3) * 3
          T$ = LEFT$(SS$, LT)

          FOR P2 = 1 TO LT STEP 3

          C$ = LEFT$(T$, 3)
          LT = LEN(T$)

' Triplets corresponding to inter-gene punctuators
          IF (C$ = "AAA") THEN T$ = MID$(T$, 4, (LT - 3)): GOTO 145
          IF (C$ = "CCC") THEN T$ = MID$(T$, 4, (LT - 3)): GOTO 145
          GOTO 150

145     NEXT P2

150     FOR P = 1 TO LT STEP 3

          IF (MID$(T$, P, 3) = "AAA") THEN 240
          IF (MID$(T$, P, 3) = "CCC") THEN 240

          NEXT P

          IF (LT > 2) THEN G$ = T$

          FOR K = 1 TO LT
          K$ = MID$(T$, K, 1)
          IF (K$ <> "A") THEN 290
          NEXT K
          GOTO 31

240     AA = AA + 1
          G$ = LEFT$(T$, P - 1)
          W1 = LT
          W2 = LEN(G$)
```

```
        W3 = W1 - W2 - 3

290     G = G + 1: G$(G) = G$

        PRINT #1, G$(G); "  ";
        PRINT G$(G); "  ";

        FOR I = 1 TO LEN(G$) STEP 3

        D$ = MID$(G$, I, 3)
        IF (LEN(D$) = 3) THEN GOSUB 530
        IF (LEN(D$) < 3) THEN 380
        IF (I < 3) THEN 480

        T = T + X
        IF (T = 4) THEN T = 0
        IF (T = -4) THEN T = 0
380     NEXT I

' Tertiary Structure table:
        IF (TB = 1) THEN CALL Bind(T, BX$, "A", "G", "C", "T")
        IF (TB = 2) THEN CALL Bind(T, BX$, "C", "A", "T", "G")
        IF (TB = 3) THEN CALL Bind(T, BX$, "G", "T", "A", "C")

        IF (LEN(G$(G)) = 0) THEN IF (G > 1) THEN G = G - 1: GOTO 450
        BP$(G) = BX$

        PRINT #1, BP$(G)
        PRINT BP$(G)

        IF (AA = 0) THEN 31

450     IF (AA > 0) THEN AA = 0: X = 0: T = 0
        T$ = RIGHT$(T$, W3)
        LT = LEN(T$)  ' This statement added as correction to Morris script.
        GOTO 150

' Select Tertiary Structure sub-table 1,2 or 3
480     IF (X = 0) THEN TB = 1
        IF (X = -1) THEN TB = 2
        IF (X = 1) THEN TB = 3
        X = 0
        GOTO 380

' TRANSLATION TABLE FOR TRIPLET CODONS:
'  Folding inclinations: Right(r, = 1), Left(l, = -1), straight(s, = 0) lookup

530     IF (D$ = "AAC") THEN X = 1
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```
IF (D$ = "CAA") THEN X = 1
IF (D$ = "AAG") THEN X = 1
IF (D$ = "GAA") THEN X = 1
IF (D$ = "AAT") THEN X = 1
IF (D$ = "TAA") THEN X = 1
IF (D$ = "ACC") THEN X = 0
IF (D$ = "CCA") THEN X = 0
IF (D$ = "ACG") THEN X = -1
IF (D$ = "GCA") THEN X = -1
IF (D$ = "ACT") THEN X = 1
IF (D$ = "TCA") THEN X = 1
IF (D$ = "AGC") THEN X = -1
IF (D$ = "CGA") THEN X = -1
IF (D$ = "AGG") THEN X = 1
IF (D$ = "GGA") THEN X = 1
IF (D$ = "AGT") THEN X = -1
IF (D$ = "ATC") THEN X = -1
IF (D$ = "TGA") THEN X = -1
IF (D$ = "CTA") THEN X = -1
IF (D$ = "ATG") THEN X = 1
IF (D$ = "ATT") THEN X = 1
IF (D$ = "GTA") THEN X = 1
IF (D$ = "TTA") THEN X = 1
IF (D$ = "CAG") THEN X = -1
IF (D$ = "CAT") THEN X = -1
IF (D$ = "CCG") THEN X = -1
IF (D$ = "GAC") THEN X = -1
IF (D$ = "TAC") THEN X = -1
IF (D$ = "GCC") THEN X = -1
IF (D$ = "CCT") THEN X = 1
IF (D$ = "CGG") THEN X = 1
IF (D$ = "CGT") THEN X = 1
IF (D$ = "TCC") THEN X = 1
IF (D$ = "GGC") THEN X = 1
IF (D$ = "TGC") THEN X = 1
IF (D$ = "CTG") THEN X = -1
IF (D$ = "CTT") THEN X = -1
IF (D$ = "GAT") THEN X = -1
IF (D$ = "GTC") THEN X = -1
IF (D$ = "TTC") THEN X = -1
IF (D$ = "TAG") THEN X = -1
IF (D$ = "GCT") THEN X = 0
IF (D$ = "GGT") THEN X = 0
IF (D$ = "GTT") THEN X = 0
IF (D$ = "TCG") THEN X = 0
IF (D$ = "TGG") THEN X = 0
IF (D$ = "TTG") THEN X = 0
```

```
' Palindrome (achiral) triplets

        IF (D$ = "AAA") THEN X = 0  'punctuator
        IF (D$ = "CCC") THEN X = 0  'punctuator
        IF (D$ = "GGG") THEN X = 0
        IF (D$ = "TTT") THEN X = 0
        IF (D$ = "ACA") THEN X = 0
        IF (D$ = "AGA") THEN X = 0
        IF (D$ = "ATA") THEN X = 0
        IF (D$ = "CAC") THEN X = 0
        IF (D$ = "CGC") THEN X = 0
        IF (D$ = "CTC") THEN X = 0
        IF (D$ = "GAG") THEN X = 0
        IF (D$ = "GCG") THEN X = 0
        IF (D$ = "GTG") THEN X = 0
        IF (D$ = "TAT") THEN X = 0
        IF (D$ = "TCT") THEN X = 0
        IF (D$ = "TGT") THEN X = 0

        RETURN
31    END SUB
```

References

[1] M Eigen, Selforganization of Matter and the Evolution of Biological Macromolecules. *Die Naturwissenschaften* **58** (1971) 465–523.

[2] D Hofstadter; *Gödel, Escher, Bach: An Eternal Golden Braid*, 20th anniversary Edition. (Penguin Books, Australia, Ltd., Ringwood, 2000).

[3] V Kvasnička and J Pospíchal, A Study of Replicators and Hypercycles by Hofstadter's Typogenetics. *International Journal of Signs and Semiotic Systems* **3** (2014) 10-26.

[4] HC Morris, Typogenetics: A Logic for Artificial Life. In: CG Langton (ed.), *Artificial Life. The Proceedings of an Interdisciplinary Workshop on the Synthesis and Simulation of Living Systems.* (Addison-Wesley, Redwood City, 1989).

[5] HC Morris, *Typogenetics: A Logic of Artificial, Propagating Entities.* (Doctoral dissertation, University of British Columbia, 1989).

[6] PW Swanborough, Chiral Asymmetry of Self-Reproduction in Cellular Automata Spaces. *viXra: 1904.0225* (2019).

[7] L Varetto, Typogenetics: An Artificial Genetic System. *Journal of Theoretical Biology* **160** (1993) 185-205.

[8] L Varetto, Studying Artificial Life with a Molecular Automaton. *Journal of Theoretical Biology* **193** (1998) 257-285.