

Taking the redpill:  
**Artificial Evolution in native x86 systems**

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October 2010

**Abstract:**

First, three successful environments for artificial evolution in computer systems are analysed briefly. The organism in these environment are in a virtual machine with special **chemistries**. Two key-features are found to be very robust under mutations: Non-direct addressing and separation of instruction and argument.

In contrast, the x86 instruction set is very brittle under mutations, thus not able to achieve evolution directly. However, by making use of a special meta-language, these two key-features can be realized in a x86 system. This meta-language and its implementation is presented in chapter 2.

First experiments show very promising behaviour of the population. A statistically analyse of these population is done in chapter 3. One key-result has been found by comparison of the robustness of x86 instruction set and the meta-language: A statistical analyse of mutation densities shows that the meta-language is much more robust under mutations than the x86 instruction set.

In the end, some Open Questions are stated which should be addressed in further researches. An detailed explanation of how to run the experiment is given in the Appendix.

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# 1. Overview

## 1.1. History

### 1.1.1. CoreWorld

Artificial evolution for self-replicating computer codes has been introduced for the first time in 1990, when Steen Rasmussen created *CoreWorld*.<sup>[1]</sup> CoreWorld is a virtual machine which can be controlled by a language called *RedCode*. This assembler-like language has a pool of ten different instructions that take two addresses as arguments. Rasmussen's idea was to introduce a random flaw of the MOV command, resulting of random mutations of the self-replicating codes within the environment. The big disadvantage of RedCode was, that nearly all flaws led to a lethal mutation, hence evolution did not occure as wished.

### 1.1.2. Tierra

In 1992, Tom Ray found out that the problem with RedCode was due to *argumented instruction set*: Independent mutations in the instruction and its arguments are unlikely to lead to a meaningful combination.<sup>[2]</sup> Instead of direct connection between the instruction and its argument, Ray developed a pattern-based addressing mechanism: He introduced two NOP-instructions (NOP0 and NOP1). These instructions do not operate themselves, but can be used as marker within the code. A pattern-matching algorithmus would find the first appearance of a complementary marker string given (after the search-command), and returns its addresse.

```
PUSH_AX    ; push ax
JMP
NOP0
NOP1
NOP0       ; jmp marker101
INC_A     ; inc ax
NOP1
NOP0
NOP1       ; marker101:
POP_CX    ; pop cx
```

There are 32 instructions available in the virtual Tierra world, roughly based on assembler (JMP, PUSH\_AX, INC\_B and so on). With these inventions, Ray was able to gain great results for artificial evolution (like parasitism, multi-cellularity<sup>[3][4]</sup>, ...).

### 1.1.3. Avida

In 1994, Christoph Adami has developed another artificial evolution simulation, called *Avida*. Beside of some different structures of the simulation, an important change has been made in the artificial chemistry: Instead of hardcoded arguments within the instructions (as in Tierra for example `PUSH AX`), instructions and arguments are completely separated. The arguments are defined by NOPs (in *avida* there are three NOPs: `nop-A`, `nop-B`, `nop-C`) following the operation (for example, a `nop-A` following a `PUSH` pushes the `AX`-register to the stack). There are 24 instructions available in *avida*, again roughly based on assembler (`call`, `return`, `add`, `sub`, `allocate` and so on).

```

push
nop-A      ; push ax
jump-f
nop-A
nop-B
nop-B      ; jmp markerBCC
inc
nop-A      ; inc ax
nop-B
nop-C
nop-C      ; markerBCC:
pop
nop-B      ; pop bx

```

With that improvements of the virtual simulation, the researchers using *avida* found out amazing results, among other things about the origin of complex features in organism[5].

## 1.2. Evolutionary Properties of different Chemistries

In 2002, an detailed analyse about different artificial chemistries has been published[6]. The authors compare several different instruction sets for evolutionary properties as Fitness and Robustness ( $R = \frac{N}{M}$  where  $N$  is the number of non-lethal mutations and  $M$  is the number of all possible mutations).

The Chemistry I consists of 28 operations and has total seperated operations and arguments (same as *Avida*). Chemistry II has 84 unique instructions and seperated operations and arguments. The last Chemistry III has 27 instructions, but within the instructions the argument is given (i.e. `push-AX`, `pop-CX`, ...). As a result, it has been found that Chemistry I is much robuster and can achieve a much higher fitness than Chemistry II, Chemistry III is the worst language for evolution.

## 1.3. Biological Information Storage

The information in natural organism is stored in the DNA. The DNA is roughly speaking a string of nucleotides. There are four nucleotides - Adenine, Cytosine, Guanine and Thymine. Three nucleotides form a codon, and are translated by tRNA to amino acids. Amino acids are the building blocks of proteins, which are main modules of cells.

One can calculate that there are  $N = 4^3 = 64$  possibilities how you can sort the codons - one could code 64 different amino acids. But nature just provides 20 different amino acids, hence there is big redundancy in the translation process.

<b>Amino acid</b>	<b>% in human</b>	<b>Codons</b>
ALA	6.99	GCU, GCC, GCA, GCG
ARG	5.28	CGU, CGC, CGA, CGG, AGA, AGG
ASN	3.92	AAU, AAC
ASP	5.07	GAU, GAC
CYS	2.44	UGU, UGC
GLU	6.82	GAA, GAG
GLN	4.47	CAA, CAG
GLY	7.10	GGU, GGC, GGA, GGG
HIS	2.26	CAU, CAC
ILE	4.50	AUU, AUC, AUA
LEU	9.56	UUA, UUG, CUU, CUC, CUA
LYS	5.71	AAA, AAG
MET	2.23	AUG
PHE	3.84	UUU, UUC
PRO	5.67	CCU, CCC, CCA, CCG
SER	7.25	UCU, UCC, UCA, UCG, AGU, AGC
THR	5.68	ACU, ACA, ACC, ACG
TRP	1.38	UGG
TYR	3.13	UAC, UAU
VAL	6.35	GUU, GUC, GUA, GUG
STOP	0.24	UAA, UAG, UGA

There is a connection between the frequency of the amino acid in the genom and the redundancy of the translation process. This mechanism protects the organism from consequences of mutation. Imagine an Alanine (ALA) codon GCU will be mutated to GCC, this codon will still be translated to Alanine, thus there is no effect.

## 2. Artificial Evolution in x86

### 2.1. Chemistry for x86

The aim is to create an evolvable chemistry for a native x86 system. So far, all notable attempts have been done in virtual simulated platforms, where the creator can define the structure and the embedded instruction set.

On the other hand, the x86 chemistry has been defined long time ago and appears to be not very evolution-friendly. The instruction set is very big, the arguments and operations are directly connected, there is no instruction-end marker or constant instruction-size. Hence, self-replicators are very brittle in that environment, and almost all mutations are lethal.

A possibility to avoid the bad behaviour of the x86 instruction set concerning mutations is to create a (at best Turing-complete) meta-language. At execution, the meta-language has to be translated to x86 assembler instructions.

Here, a meta-language is presented with a eight bit code for each instruction, which will be translated to x86 code at execution. Obviously, this is the same procedure as in Protein biosynthesis. The eight bits coding a single instruction in the meta-language are analogs of the three codons representing one amino acid. At execution they are translated to a x86 instruction - just as tRNA transforms the codon to a amino-acid. A punch of translated x86 instructions form a specific functionality, in biology a number of amino acids form a protein (which is responsible for a certain functionality in the organism).

### 2.2. The instruction set

One intention was to create an instruction set which can be translated to x86 instructions in a very trivial way. This was a notable restriction as key instructions used in Tierra and avida (like `search-f`, `jump-b`, `dividate`, `allocate`, ...) can not be written in a simple way in x86 assembler.

The main idea of the meta-language is to have a number of buffers which are used as arguments of all operations. Registers are not used directly as arguments for instructions, but have to be copied from/to buffers, leading to a separation of operation and argument. The instructions have a very similar form as in avida; comparing `nopsA & push` vs. `push & nop-A`, or `pop & nopdA` vs. `pop & nop-A` or `nopsA & inc & nopdA` vs. `inc & nop-A` for the meta-language and avida, respectively.

It has emerged that it is enough to use three registers (`RegA`, `RegB`, `RegD`), two buffers for calculations and operations (`BC1`, `BC2`) and two buffers for addressing (`BA1`, `BA2`).

Buffer instructions (16)

nopsA	BC1=RegA	mov ebx, eax
nopsB	BC1=RegB	mov ebx, ebp
nopsD	BC1=RegD	mov ebx, edx
nopdA	RegA=BC1	mov eax, ebx
nopdB	RegB=BC1	mov ebp, ebx
nopdD	RegD=BC1	mov edx, ebx
saveWrtOff	BA1=BC1	mov edi, ebx
saveJmpOff	BA2=BC1	mov esi, ebx
writeByte	byte[BA1]=(BC1&&0xFF)	mov byte[edi], bl
writeDWord	dword[BA1]=BC1	mov dword[edi], ebx
save	BC2=BC1	mov ecx, ebx
addsaved	BC1+=BC2	add ebx, ecx
subsaved	BC1-=BC2	sub ebx, ecx
getDO	BC1=DataOffset	mov ebx, DataOffset
getdata	BC1=dword[BC1]	mov ebx, dword[ebx]
getEIP	BC1=instruction pointer	call gEIP; gEIP: pop ebx

Operations (10+8)

zer0	BC1=0	mov ebx, 0x0
push	push BC1	push ebx
pop	pop BC1	pop ebx
mul	RegA*=BC1	mul ebx
div	RegA/=BC1	div ebx
shl	BC1 << (BC2&&0xFF)	shl ebx, cl
shr	BC1 >> (BC2&&0xFF)	shr ebx, cl
and	BC1=BC1&&BC2	and ebx, ecx
xor	BC1=BC1 xor BC2	xor ebx, ecx
add0001	BC1+=0x1	add ebx, 0x0001
add0004	BC1+=0x4	add ebx, 0x0004
add0010	BC1+=0x10	add ebx, 0x0010
add0040	BC1+=0x40	add ebx, 0x0040
add0100	BC1+=0x100	add ebx, 0x0100
add0400	BC1+=0x400	add ebx, 0x0400

add1000	BC1+=0x1000	add ebx, 0x1000
add4000	BC1+=0x4000	add ebx, 0x4000
sub0001	BC1-=1	sub ebx, 0x0001

Jumps (4)

JnzUp	jz over && jmp esi && over:
JnzDown	jnz down (&& times 32: nop) && down:
JzDown	jz down (&& times 32: nop) && down:
ret	ret

API calls (11) - Windows based

CallAPIGetTickCount	stdcall [GetTickCount]
CallAPIGetCommandLine	stdcall [GetCommandLine]
CallAPICopyFile	stdcall [CopyFile]
CallAPICreateFile	stdcall [CreateFile]
CallAPIGetFileSize	stdcall [GetFileSize]
CallAPICreateFileMapping	stdcall [CreateFileMapping]
CallAPIMapViewOfFile	stdcall [MapViewOfFile]
CallAPICreateProcess	stdcall [CreateProcess]
CallAPIUnMapViewOfFile	stdcall [UnMapViewOfFile]
CallAPICloseHandle	stdcall [CloseHandle]
CallAPISleep	stdcall [Sleep]

There are 30+8 unique commands (the eight `addNNNN` and `sub0001` could be reduced to one single command, but this would make the code very big) and 11 API calls - giving 49 instructions. For translation, a command is identified by 8bits. Therefore there are  $N = 2^8 = 256$  possible combinations, thus there is a big redundancy within the translation of commands to x86 code - just as in natural organism. This gives the code a big freedom in protecting itself against harmful effects of mutations.

**2.2.1. An example: Linear congruential generator**

The following code creates a new random number (Linear congruential generator) via

$$x_{n+1} = (ax_n + c) \bmod m$$

with  $a = 1103515245$ ,  $c = 12345$  and  $m = 2^{32}$  (these are the numbers used by GCC).

```

.data
DataOffset:
    SomeData dd 0x0
    RandomNumber dd 0x0

.code
macro addnumber arg { ... }
    ; Creates the correct addNNNN combination

    getDO
    add0004
    getdata          ; mov ebx, dword[RandomNumber]
    nopdA           ; eax=dword[RandomNumber]

    zer0
    addnumber 1103515245      ; mov ebx, 1103515245
    mul          ; mul ebx

    zer0
    addnumber 12345
    save          ; mov ecx, ebx

    nopsA
    addsaved
    nopdB          ; mov ebp, (1103515245*[RandomNumber]+12345)
    ; ebp=new random number

    getDO
    add0004
    saveWrtOff     ; mov edi, RandomNumber

    nopsB
    writeDWord     ; mov dword[RandomNumber], ebp
    ; Save new random number

.end code

```

## 2.3. Translation of meta-language

As the instruction set has been created to construct a trivial translator, the translator can be written as a single loop. A meta-language instruction is one byte, the corresponding x86 instruction has 8 bytes (for 256 instructions, this gives a  $8 * 256 = 2.120$  Byte long translation table).

The Translator picks one 8bit codon, searches the corresponding x86 instruction and writes that x86 instruction to the memory. At the end of all codons, it executes the memory.

```

invoke      VirtualAlloc, 0x0, 0x10000, 0x1000, 0x4
mov         [Place4Life], eax           ; 64 KB RAM
mov         edx, 0x0                    ; EDX will be used as the
                                           ; counter of this loop

WriteMoreToMemory:
            mov     ebx, 0x0             ; EBX=0
            mov     bl, byte[edx+StAmino] ; BL=NUMBER OF AMINO ACID
            shl     ebx, 3               ; EBX*=8;
            mov     esi, StartAlphabeth ; Alphabeth offset
            add     esi, ebx             ; offset of the current amino acid
            mov     ebx, edx             ; current number of amino acid
            shl     ebx, 3               ; lenght of amino acids
            mov     edi, [Place4Life]    ; Memory address
            add     edi, ebx             ; Offset of current memory
            mov     ecx, 8               ; ECX=8
            rep     movsb                 ; Write ECX bytes from ESI to EDI
                                           ; Write 8 bytes from Alphabeth
                                           ; to Memory
            inc     edx                   ; Increase EDX

cmp         edx, (EndAmino-StAmino)
jne        WriteMoreToMemory

call       [Place4Life]                 ; Run organism!

```

The Translation Table/Alphabeth has the following form:

```

; 0001 1000 - 24:
_getEIP EQU 24
ACommand24:
            call  gEIP
            gEIP:
            pop  ebx

ECommand24:
times (8-ECommand24+ACommand24): nop

; 0001 1001 - 25:
_JnzUp EQU 25
ACommand25:
            jz   over
            jmp  esi
            over:

ECommand25:
times (8-ECommand25+ACommand25): nop

```

## 3. Experiments

*To achieve evolution it is necessary to have replication, mutation and selection.*

### 3.1. Overview

An ancestor organism has been written, which is able **replicate** itself. It copies itself in the current directory to a random named file and execute its offspring.

The **mutation**-algorithm is written within the code (not given by the platform as it is possible in Tierra or avida). With a certain probability a random bit within a special interval of the new file flips. Each organism can create five offspring, each with a different interval and probability of mutation.

For finding an adequate mutation probability, one can calculate the probability  $P$  that at least one bit-flip occurs giving a  $N$  byte interval and a probability  $p_{bit}$  for a single bit to flip:

$$P(N, p_{bit}) = \sum_{n=0}^{N-1} p_{bit}(1 - p_{bit})^n = 1 - (1 - p_{bit})^n$$

	<b>Interval</b>	<b>N</b>	<b>P</b>	$p_{bit}$
1	Code	2100	0.9	$\frac{1}{900}$
2	Code+Alphabeth	4200	0.9	$\frac{1}{1800}$
3	whole file	6150	0.9	$\frac{1}{2666}$
4	Code	2100	0.75	$\frac{1}{1500}$
5	Code	2100	0.68	$\frac{1}{1820}$

The second offspring has also the opportunity to change the alphabeth. This could lead to redundancy in the alphabeth to avoid negative effects of mutations (as used in nature - described in 1.3). The mutations in the third offspring can access the whole file.

Natural **selection** is not very strong in this experiment, CPU speed and harddisk space is limited. Thus, most non-lethal mutations are neutral and disribute randomly within the population. This can be used very easy to understand the relationship of the population: The smaller their *Hamming distance*, the nearer their relationship.

The Hamming distance  $\Delta(x, y)$  is defined as

$$\Delta(x, y) := \sum_{x_i \neq y_i} 1, \quad i = 1, \dots, n$$

Beside of natural selection, their could be artificial selection. Some artificial selection has been used to prevent some wired behaviour of the populations.

The experiments have been done on a native WindowsXP. For stabilization, several small C++ guard programs have been developed which searches and closes endless-loops, closes error messages and dead processes (processes that live longer than a certain time).

## 3.2. First attempts

The first attempt has shown some unexpected behaviour.

**Multiple instances of same file:** Already after a few dozen of generations, the process list started to fill with multiple instances of the same file. An analyse of the file shows that this happens due to a mutation corrupting the random name engine. The random name engine always generates the same filename (for instance `aaaaaaaa.exe`). After the mutation process (which has no effect as the file has write protection due to execution) the new/old file is executed again.

To prevent this unnatural behaviour, it has become necessary to include an artificial selection to the system. The new C++ file scans the process list for multiple file instances, and closes them.

It is interesting to see that this is a real selection, not a restriction to the system. Mutation still can create such effects, but with that additional guard file, they have negative consequences for the file (the will be deleted immediatly) and therefore will not spread within the population.

**Avoid mutations:** The first long-time experiment appeared to be very promising. The guard files closed error messages, endless loops, dead processes and multiple instances of the same file. After some hundred generations the experiment has been stopped and the files have been analysed. Surprisingly, all files had the exact same bit-code, they were all clones.

There has been a mutation in the alphabeth, changing the `xor` instruction. This instruction is responsible for changing a bit at the mutation-process. If the mutation does not work anymore, no files will change anymore.

For the organism, this is a big advantage. All offspring will survive as no more mutation happens. Other organism often create corrupt offspring, hence spread slower. After a while, the whole system is dominated by unmutable organism.

In nature, organism also created very complex systems to prevent mutation or mutational effects. DNA repairing or amino acid redundancy are just two examples.

Even this discoverment is very interesting and has a great analogon in nature, it prevents from further discoverments in this artificial system. Therefore another guard file has been developed, which scans the running files for clones and deletes them.

It's not natural to prohibit clones at all, thus a adequate probability should be found. If there are 42 clones in the process list, they should be detected by a probability of 51% in one guard file cycle. This gives a probability of  $P = \frac{1}{59}$  that a running file will be checked whether it has clones. A controlled file will be compared to all other running files, all clones will be deleted.

### 3.3. Statistical analyse of experiment

Afer installing the new guard file, a further experiment has been run. This first "long-term" experiment can be analysed statistically by comparing the density and type of mutation from the ancestor file and the latest population. Unfortunatley it is very hard to determinate the number of generations in the population; by comparing mutations in the oldest population with the primary ancestor and using the mutation probability, one could speculate that there have been 400-600 generations.

**Number of mutations - ancestor vs. successor:** A number of 100 successor have been randomly picked and compared with the ancestor. One can calacate the average number of mutation during the lifetime of the experiment, and its standard deviation:

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i = 192.02 \text{ Mutations}$$

$$\sigma = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (X_i - \bar{X})^2} = 4.59$$

The standard deviation gives an unexpected small value, which means that the number of mutations is quite constant over the lifetime of the population.

**Relations between individua:** One can analyse the relation between the individua by calculating their Hamming distance (the number of differences in their bytecode). A number of six files have been selected randomly and analysed.

```

ancestor.exe - a.exe: 195
ancestor.exe - b.exe: 195
ancestor.exe - c.exe: 184
ancestor.exe - d.exe: 192
ancestor.exe - e.exe: 194
ancestor.exe - f.exe: 200

```

```

a.exe - b.exe: 2          c.exe - a.exe: 75          e.exe - a.exe: 9
a.exe - c.exe: 75        c.exe - b.exe: 75          e.exe - b.exe: 9
a.exe - d.exe: 20        c.exe - d.exe: 73          e.exe - c.exe: 74
a.exe - e.exe: 9         c.exe - e.exe: 74          e.exe - d.exe: 19
a.exe - f.exe: 28        c.exe - f.exe: 81          e.exe - f.exe: 27

b.exe - a.exe: 2          d.exe - a.exe: 20          f.exe - a.exe: 28
b.exe - c.exe: 75        d.exe - b.exe: 20          f.exe - b.exe: 28
b.exe - d.exe: 20        d.exe - c.exe: 73          f.exe - c.exe: 81
b.exe - e.exe: 9         d.exe - e.exe: 19          f.exe - d.exe: 16
b.exe - f.exe: 28        d.exe - f.exe: 16          f.exe - e.exe: 27

```

While `a.exe`, `b.exe` and `e.exe` are near related, `c.exe` is far away from all other files. `d.exe` and `f.exe` are medium related. Interestingly, while `c.exe` has the biggest distance to all other successors, it has the smallest distance to the ancestor.

**Distribution of mutations:** It is interesting to see which mutations are rare and which are widely spread within the population. There are 153 mutations which appear in every single file, 32 mutations appearing in 84 files and so on. Many mutations are located in unused areas of the file, for instance in the Win32 .EXE padding bytes or in the unused part of the alphabeth. A list of mutations of the active-code (whether the used part of the alphabeth or the meta-language code) and its appearance in the population is given here.

527:	100	e52:	100	12af:	100	147f:	100	e13:	32
551:	100	e9a:	100	12b1:	100	1498:	100	1298:	23
56c:	100	eac:	100	12d9:	100	14a5:	100	f0a:	17
5af:	100	f04:	100	130e:	100	14b3:	100	4c3:	16
5ed:	100	f34:	100	131f:	100	14b9:	100	558:	16
61a:	100	fbf:	100	1327:	100	14c3:	100	58a:	16
625:	100	fed:	100	1328:	100	5b9:	84	60d:	16
c74:	100	1090:	100	1333:	100	d86:	84	ca9:	16
c7b:	100	10b8:	100	1343:	100	e43:	84	cac:	16
c98:	100	10c4:	100	135c:	100	1037:	84	d83:	16
c9b:	100	1119:	100	1373:	100	106b:	84	df4:	16
ca1:	100	1121:	100	138d:	100	109c:	84	f5a:	16
ca4:	100	1126:	100	139c:	100	1148:	84	105c:	16
d02:	100	118f:	100	13b3:	100	127d:	84	1085:	16
d4f:	100	1194:	100	13d5:	100	12a8:	84	10ef:	16
d5d:	100	11a2:	100	13eb:	100	130f:	84	12d1:	16
d7a:	100	11a9:	100	13fd:	100	1388:	84	12ee:	16
d7d:	100	11b1:	100	1430:	100	1392:	84	1323:	16
e3b:	100	124d:	100	144c:	100	13e4:	84	1353:	16
e49:	100	1265:	100	1459:	100	c9d:	32	139a:	16

A full analyse of these mutations would be worthwhile, but has not be done in this primary analyse due to its great effort. However, to understand this system and its prospects better, detailed code analyse will be unavoidable.

Nevertheless, examples of two mutations can be given.

First one is **Byte 0x527**: This is within the alphabeth, defining the behaviour for the `JnzUp` instruction. A bit-flip caused following variation:

```

jz over          jz over
jmp esi          → jmp esi
over:           nop
                over:

```

This has no effect in the behaviour, but effects just the byte-code - a neutral mutation.

The second example is the mutation in **Byte 0xC7B**, which is within the meta-language code. The unmutated version is the instruction `add0001`, the mutated one represents `add0004`. This is part of the `addnumber 26` instruction, which is used as modulo number for the random name generator.

Due to this mutation, the genom not just picks letters from  $a-z$  for its offspring's filename, but also the next three in the ASCII list, {, | and }. Thus, filenames can also contain these three characters. This mutation has an effect of the behaviour, but still seems to be a neutral mutation.

### 3.4. Comparing Robustness with x86 instruction set

In 2005 a program called `Gloeobacter violaceus` has been developed, that uses artificial mutations in the x86 instruction set, without making use of a meta-language.[7] That program also replicates in the current directory, and is subjected by point mutations, and rarely by inseration, deletion and dublication. Due to the brittleness of the x86 instruction set, that attempt was not very fruitful. Still it gives a good possibility of comparison.

Both systems have changed to the same initial situation: Point mutations occure in the whole file with same probability. After several hundreds of generations, all non-minor mutations (occure in more than 50 different files) of 2.500 files have been analysed. The mutations have been classified by their position: x86-code mutations, mutation in some padding region or in the meta-language code.

*Through this classification we find out whether the new meta-language concept is more robust than the x86 instruction set.*

We define the mutation density of a specific region in the code by

$$\rho_{mut}(\text{Region}) = \frac{\text{mutations in region}}{\text{size of region}}$$

**Meta-Language concept:**

$$\rho_{mut}(\text{whole code}) = \frac{291}{6144} = 0.047$$

$$\rho_{mut}(\text{padding}) = \frac{151}{2427} = 0.062$$

$$\rho_{mut}(\text{meta-code}) = \frac{81}{2084} = 0.039$$

$$\rho_{mut}^*(\text{x86}) = \frac{14}{576} = 0.024$$

The  $\rho_{mut}(\text{x86})$  combines the very small translator code and the alphabeth, but as the alphabeth is no real x86 code, comparing this advisable. If that problem would be neglected,

one would see that the meta-language is more robust under mutations as the x86 code. For a fair comparison *Gloeobacter violaceus* can be used.

**Gloeobacter violaceus:**

$$\begin{aligned}\rho_{mut}(\text{whole code}) &= \frac{351}{3584} = 0.098 \\ \rho_{mut}(\text{padding}) &= \frac{284}{2229} = 0.127 \\ \rho_{mut}(\text{x86}) &= \frac{10}{683} = 0.015\end{aligned}$$

Mutations in the padding bytes do not corrupt the organism, thus it is the initial mutation density. A comparison between  $\rho_{mut}(\text{padding})$  and  $\rho_{mut}(\text{Region})$  gives the percentage of non-lethal mutations in that region, therefore gives the robustness R of that region.

$$\text{Robustness}(\text{Region}) := \frac{\rho_{mut}(\text{Region})}{\rho_{mut}(\text{padding})}$$

The interesting comparison is between the x86 region and the meta-language region.

$$\text{Robustness}(\text{x86}) = \frac{\rho_{mut}(\text{x86})}{\rho_{mut}(\text{padding})} = \frac{0.015}{0.127} = 0.115$$

$$\text{Robustness}(\text{meta-code}) = \frac{\rho_{mut}(\text{meta-code})}{\rho_{mut}(\text{padding})} = \frac{0.039}{0.092} = 0.424$$

Even this analysis is based on low statistics, it already indicates a great result:

**This new meta-language concept for x86 systems is much more robust than the original x86 instruction set.**

# 4. Outlook

## 4.1. Open questions

**Development of new functionality:** The most important question is whether an artificial organism with this meta-language in a x86 system can develop new functionalities.

In a long-term evolution experiment by Richard Lenski, they discovered that simple E.coli was able to make a major evolutionary step and suddenly acquired the ability to metabolise citrate.[8] This happened after 31.500 generations, approximatively after 20 years.

The generation time of artificial organism are of many orders of magnitude smaller, therefore beneficial mutation such as development of new functionality may occur within days or a few weeks. The question that remains is whether this meta-language concept is the right environment or not.

**Other types of mutations:** Point mutation is one important type of mutation, but not the only one. In DNA, there is also Deletion, Duplication, Insertion, Translocation, Inversion. Especially insertion of code and deletion of code is proved to be important in artificial evolution too.[9] The question is how one can create such a type of mutation without file structure errors occurring after every single mutation.

One possibility would be to move the n last byte of the meta-language code forwards (deletion) or backwards (insertion), filling the gap with `NOPs`. However, how could you find out where the end of the meta-language code is without some complex (and thus brittle) functions?

**Behaviour of Hamming distance:** How is the time evolution of the average Hamming distance between a population and the primary ancestor? Does it have a constant slope or is it rather like a logarithm? How is the behaviour of the Hamming distance when taking into account other types of mutations (as described above)? Large-scale experiments are needed to answer that questions properly.

**APIs:** This is an operation system specific problem, and can not be solved for any OS at once. For Windows, the current system of calling APIs is not very natural. It is a call to a specific address of a library, needing the right numbers of arguments on the stack and the API and library defined in the file structure. Hence, API calls are not (very) evolvable in this meta-language, restricting the ability to use new APIs by mutations.

One possible improvement could be the usage of `LoadLibraryA` and `GetProcAddress`, which loads the APIs from the kernel autonomously. This technique would not need the APIs and libraries saved within the file structure, and could make it possible to discover new functionalities. Unfortunately, this requires complex functions, which may be very brittle and inflexible.

Still it needs more thoughts to find an adequate solution to this problem.

## 4.2. Computer malware

This technique could be used in autonomous spreading computer programs as computer viruses or worms. This has been discussed in a very interesting paper by Iliopoulos, Adami and Ször in 2008.[10]

Their main results are: The x86 instruction set does not allow enough neural mutations, thus it is impossible to develop new functionalities; a 'evolvable' language or a meta-language would be needed. Further, together with smaller generation times, the selective pressure and the mutation rate would be higher, speeding up evolution. Conclusion is, that it is currently unclear what would be a defence against such viruses.

In contrast to the experiment explained in chapter 3 - where natural selection was nearly absent, computer malware are continuously under selective pressure due to antivirus scanners. This is the same situation as in biological organism, where parasites are always attacked by the immune system and antibiotics.

Theoretically, computer malware could also find new ways to exploit software or different OS APIs for spreading. This is not as unlikely as it seems in the first moment. Experiments with artificial and natural evolution have shown that complex features could evolve in acceptable time.[5][9]

## 4.3. Conclusion

An artificial 'evolvable' meta-language for x86 Systems has been created using the main ideas of *Tierra* and *avida*: Separation of operations and arguments, and not using direct addressing. The experiments have been very promising, showing that the robustness of the new meta-language is approximately four times higher as for usual x86 instructions. Several open questions are given in the end, which should motivate for further research.

Howsoever, the most important step has been done:

**The artificial organism are not trapped in virtual systems anymore, they can finally move freely - they took the redpill...**

# Bibliography

- [1] Christoph Adami, *Introduction to Artificial Life*, Springer, 1998.
- [2] Tom S. Ray, *An approach to the synthesis of life*, Physica D, 1992.
- [3] Kurt Thearling and Tom S. Ray, *Evolving Parallel Computation*, Complex Systems, 1997.
- [4] Tom S. Ray and Joseph Hart, *Evolution of Differentiated Multi-threaded Digital Organisms*, Artificial Life VI proceedings, 1998.
- [5] Richard E. Lenski, Charles Ofria, Robert T. Rennock and Christoph Adami, *The evolutionary origin of complex features*, Nature, 2003.
- [6] Charles Ofria, Christoph Adami and Travis C. Collier, *Design of Evolvable Computer Languages*, IEEE Transition on Evolutionary Computation, 2002.
- [7] SPTH, *Code Evolution: Follow nature's example*, 2005.
- [8] Zachary D. Blount, Christina Z. Borland, and Richard E. Lenski *Historical contingency and the evolution of a key innovation in an experimental population of Escherichia coli*, National Academy of Sciences, 2008.
- [9] Richard E. Lenski, Charles Ofria, Robert T. Rennock and Christoph Adami, *Phenotypic and genomic evolution along the line of descent in the case-study population through the origin of the EQU function at step 111*, 2003.
- [10] Dimitris Iliopoulos, Christoph Adami and Peter Ször, *Darwin inside the machines: malware evolution and the consequences for computer security*, Virus Bulletin Conference, 2008.

# A. Appendix

This artificial evolution system can be started on every common Windows Operation System. Even it is a chaotic process, due to the guard files the process can run for hours without a breakdown of the system.

## A.1. The package

### The package:

binary\run0ndgens.bat: This script starts all guard files, then starts the 0th generation. Adjust the hardcoded path in the file to the directory of the guard files. This file has to be at H:, you can use `subst` for that.

binary\NewArt.exe: This is the 0th generation. It has to be started with the shell (or a .bat file) - not via double-click. It is highly recommended to not run the file without the guard files. This file has to be as H: aswell.

ProcessWatcher\\*.\*: This directory contains the binary and source of all guard files.

ProcessWatcher\CopyPopulation.cpp: This file copies every 3 minutes 10% of the population to a specific path given in the source. This path has to be adjusted before usage.

ProcessWatcher\Dead.cpp: This program can be used to manually stop all organism. You can enter a probability of how many organism should be survive. For instance, if you enter 10, 90% of the population will be terminated - 10% survive.

ProcessWatcher\DoubleProcess.cpp: This program searches and destroys multiple instances of the same file. See Chapter 3.2 for more information.

ProcessWatcher\EndLessLoops.cpp: This guard file searches for endless loops in the memory and terminates them.

ProcessWatcher\JustMutation.cpp: Also described in chapter 3.2, this program searches and terminates clones in the process.

ProcessWatcher\Kill2MuchProcess.cpp: This guard is very important for stability of the operation system while running the experiment. If there are more than 350 processes running, it terminates 75% of them.

ProcessWatcher\RemoveCorpus.cpp: As space is restricted, this guard deletes files that are older than a 30sec.

ProcessWatcher\SearchAndDestroy.cpp: This program removes error messages (by clicking at "OK"), terminates error-processes (as `dwwin.exe` or `drwtsn32.exe`), and it terminates dead processes (processes that are older than 100sec).

ProcessWatcher\malformed\_PEn.exe: These are two malformed .EXE files, which will be

called by `SearchAndDestroy.exe` at the start to find the "OK"-Button. They have to be in the directory of the guard files.

`Analyse\SingleFileAnalyse`: This directory contains an analyse file, that compares the bytecode of two genotypes. Copy the file to the directory, change the name in the source and execute it.

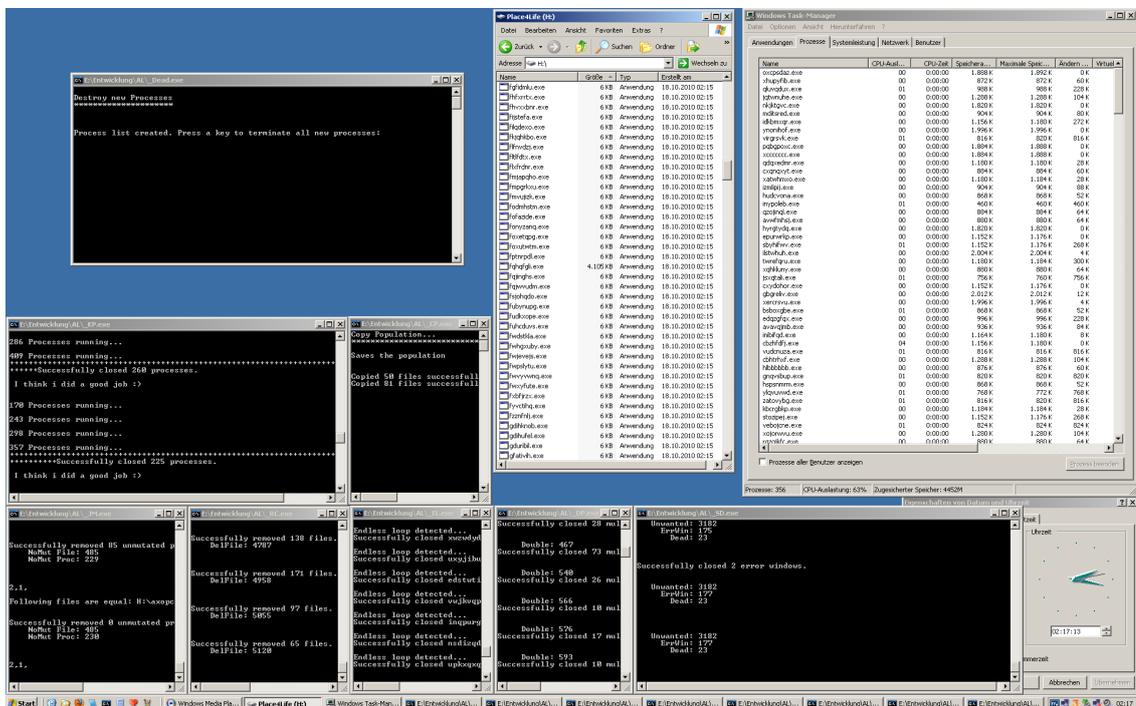
`Analyse\Relation`: This file compares gives you the Hamming distance of all .exe files.

`Analyse\MutationDistribution`: With this file you can get a distribution of all mutations compared with `NewArt.exe`.

## A.2. Running the experiment

Copy the `run0ndgens.bat` and `NewArt.exe` to `H:\`. Adjust the path in `CopyPopulation.cpp` to the backup directory (and compile it) and in `run0ndgens.bat` to the directory of the guard files.

Now you can start `run0ndgens.bat`, move over the two error-messages (dont click them, this will be done by `SearchAndDestroy.exe`). Then you are ready and can press a key in the `run0ndgens.bat`, which will start 10 instances of `NewArt.exe`.



Running Experiment: This is how the experiment should look like