

# Compositional Basis of Biological Design *(the interaction of modules)*

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# Outline

- Complexity
- Recognition of modules
  - modularity in engineering
  - modularity in nature
- Origin of modularity
  - nature of mutations
  - generalization of copy, cut and paste mechanisms
- Modularity of genetic networks in pi-calculus
  - elements of networks
  - genetic motifs
- Scalable design
  - emergent behavior
  - compositional evolution



# Complexity

- a fundamental problem of science, why does matter grow in complexity?
- “**Complexity** arises then ... components interact with each other in ways ... more than uniform, frequent elastic collisions. Interactions among components can lead to all kinds of nonlinear behavior.” [Herbert A. Simon, 2005]

# Divergence of astrocytes for GFA content depending on malignation

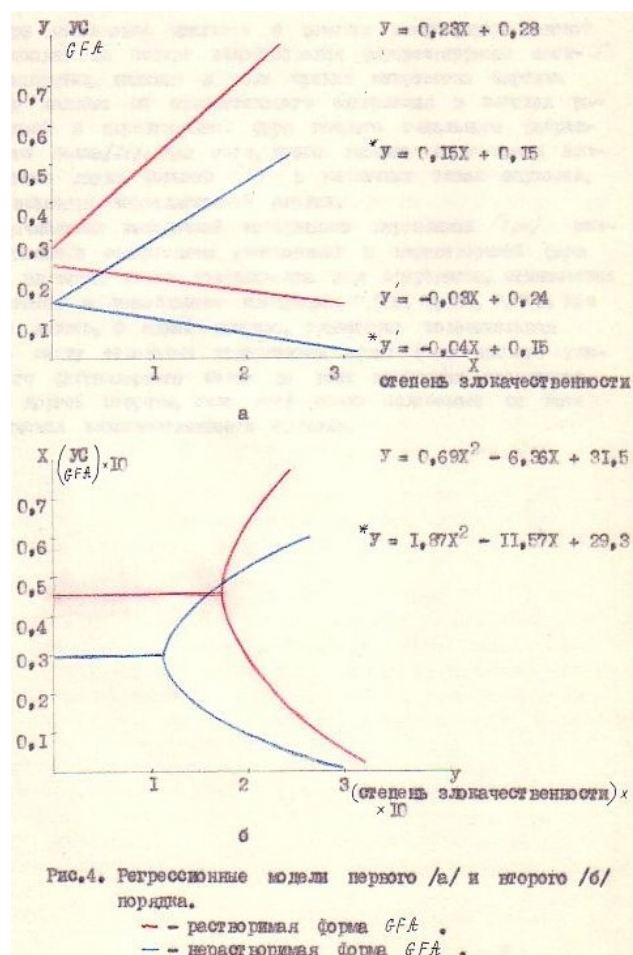


Рис.4. Регрессионные модели первого /а/ и второго /б/ порядка.

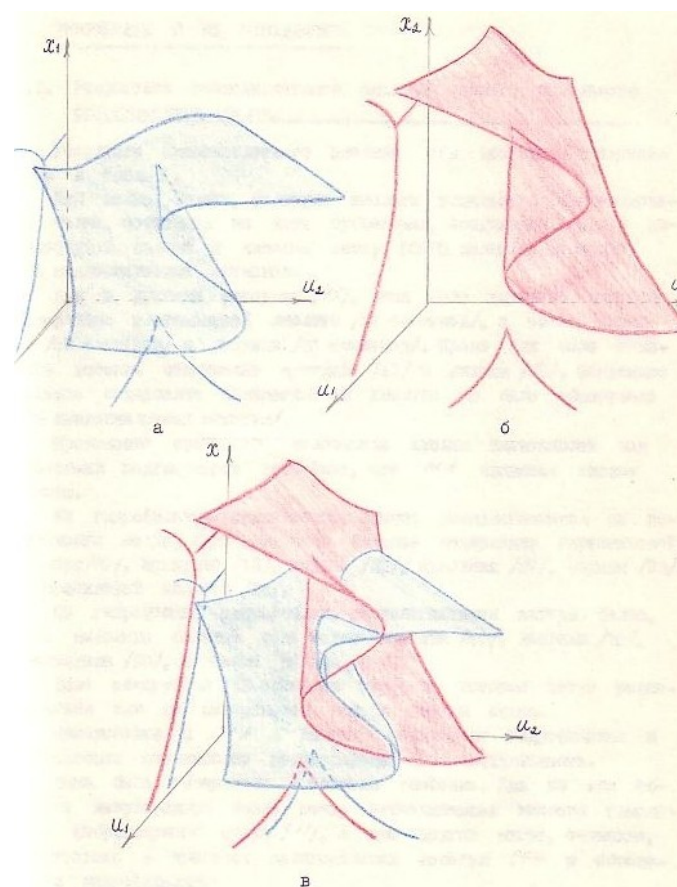
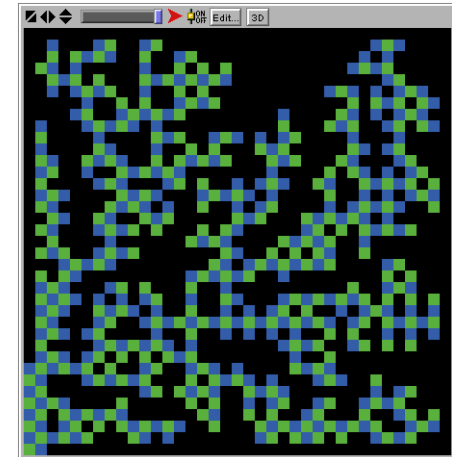
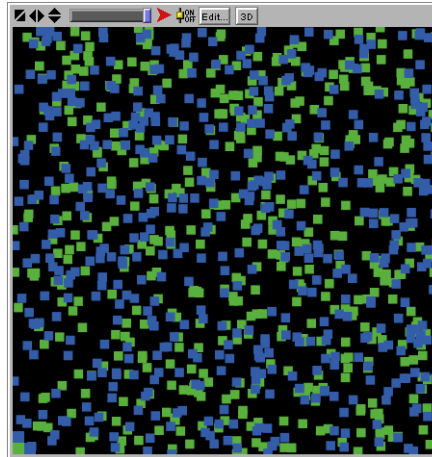
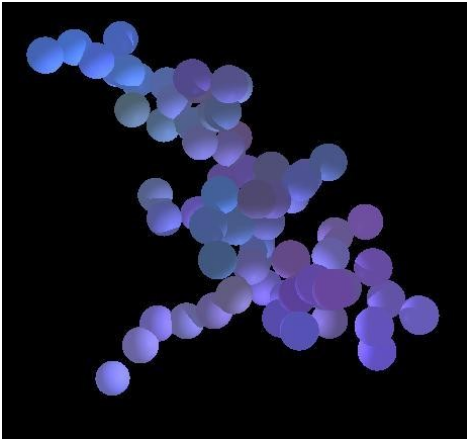
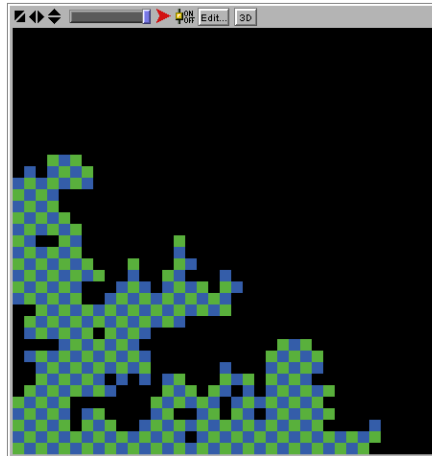
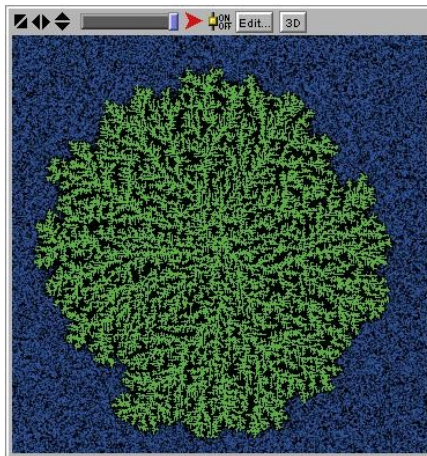


Рис.5. — — — растворимая форма GFA  
— — — нерастворимая форма GFA

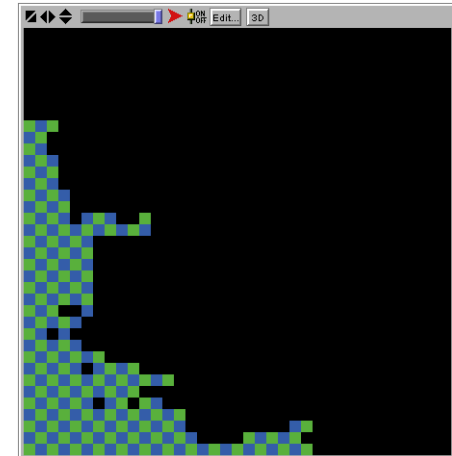
# Assembling by adhesion rules (DLA)



1



$\leq 5$



$\leq 10$

Chessboard pattern formation

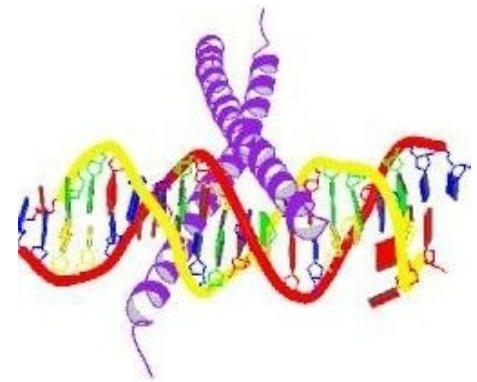
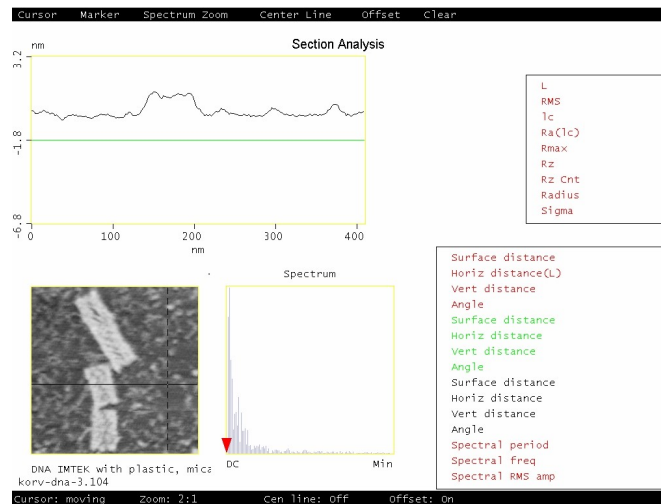
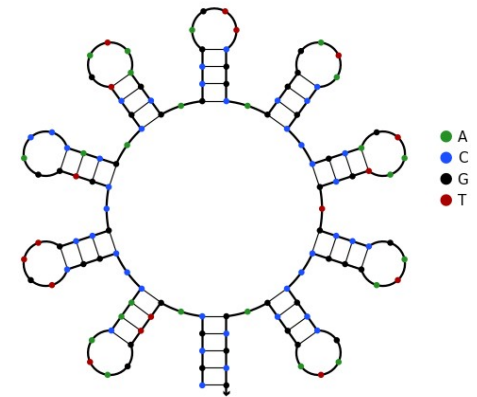
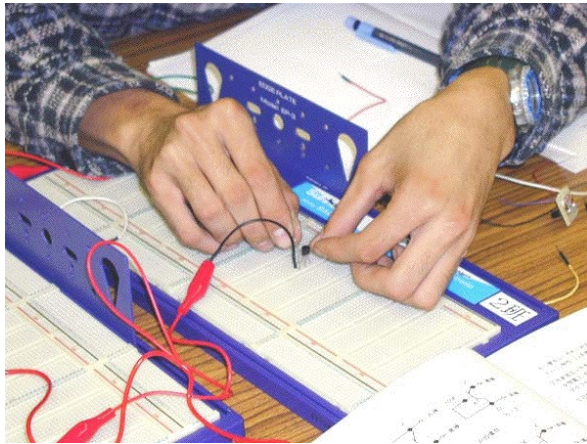
Kuznetsov, DECOI 2007

# Nearly decomposable and modular systems

- “... the frequencies of interaction among elements in any particular subsystem of a system are an order of magnitude or two greater than the frequencies of interaction between the subsystems. We call this ... **nearly decomposable** (ND) system.” [Simon and Ando, 1961]
- “A system may be characterized as **modular** to the extent that of its components operates primary according to its own, intrinsically determined principles. Modules within a system or process are tightly integrated but relatively independent.” [Herbert A. Simon, 2005]

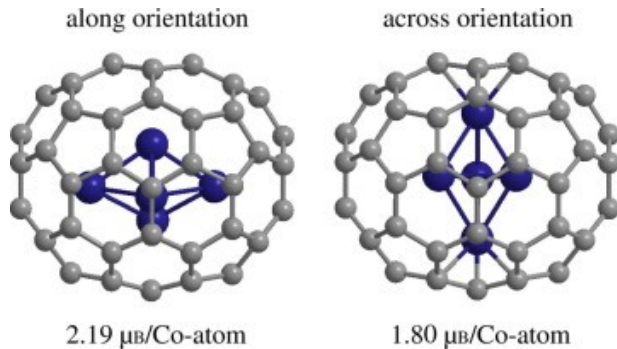


# Modularity in electronics, optics and DNA-nanotechnology



GCN4 bZIP + DNA

# Endohedral metallofullerenes



*ab initio* calculations:

**Method:** DFT - density functional theory  
GGA-PBE - generalized gradient approximation  
[Perdew, Burke, Ernzerhof, 1996]

**Calculation:** the total spin magnetic moment,  $\mu\text{B}$

**Software:** OpenMX v.3.5 [Ozaki, 2003]

- $M \sim \langle L \rangle / N$ ,
- where  $M$  is the magnetic moment per Me-atom of given complex ( $\mu\text{B}$ ),  $\langle L \rangle$  is the average Me–C bond length in Å, and  $N$  is the total number of Me–C bonds in the complex



# What is a module? (1)

- “... we define a **module** as an assembly of biological structures that fulfill a function in an integrated and context insensitive manner. Function as defined here is not merely the interaction of molecules but an interaction that yields a biological output which is characteristic of the module. Furthermore, the application of the module is flexible. To be recognized as a module, it has to be used either in different processes in the same organism or in different organisms, exploiting its invariant functional properties in the same or different processes. A **module** is therefore characterized by its reiterated use.”

Uwe Strähle, Patrick Blader

The Basic Helix-Loop-Helix Proteins in Vertebrate and Invertebrate Neurogenesis. in Modularity and Evolution

- **Modularity** is defined through a process that starts by recognizing patterns, shapes, or events that repeat at some scale of observation
- **Modularity** is a hallmark of biological organization and an important source of evolutionary novelty
- **Modularity** is a sign of the universal principle of economy in nature

# What is a module? (2)

**Module** is a set of genes that act together to carry out a specific function

The recognition of modularity came as a surprise:

- Try to find modules, relations between modules, the origin of modules
- Try to understand the hierarchy of a modular system and a reason of the entanglement within modules and between modules

The answer following questions could have given a key to control an evolution process:

- How does a system evolve and fall?
- What is a limit of evolvability?

**Evolvability** is the ability to respond to a selective challenge by producing the right kind of variation

# Researches in modularity

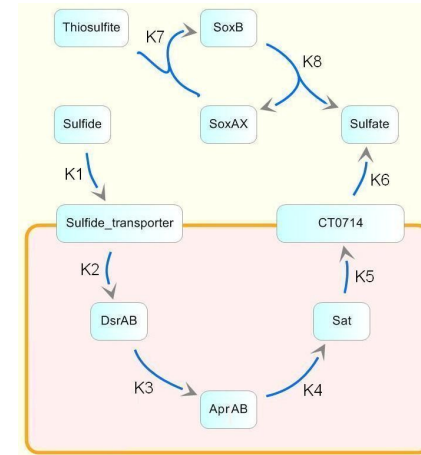
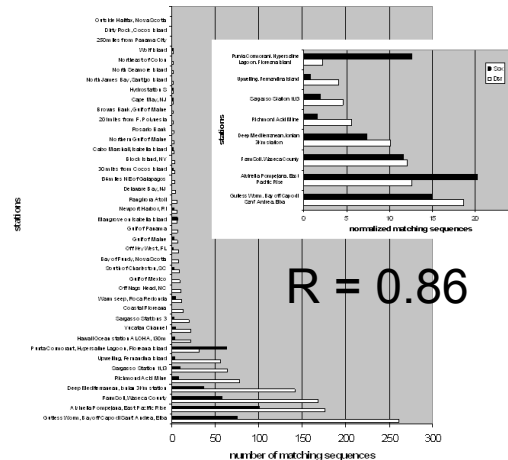
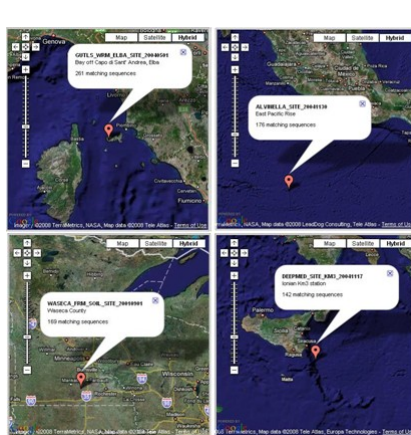
## **Modularity is an old concept in the biological science:**

- Cuvier and Saint-Hilaire (18th century) – structural modules representing parts of organisms
- Joseph Needham (1930s) – development consists of distinct processes that are operating in coordination

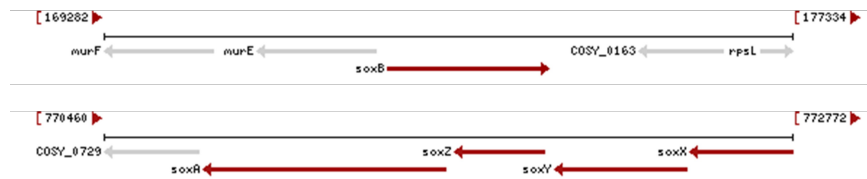
## **In a modern time** (W. Fontana, G.P. Wagner, U. Alon and many others):

- A constant environment (that does not change over time) leads to non-modular structures
- The modular structure can spontaneously emerge if environment changes over time
- Variability in the natural habitat of an organism promotes modularity
- Modularity can also dramatically speed up evolution
- Adaptation of bacteria to new or changing environments is often associated with uptake of foreign genes through horizontal gene transfer (HGT)
- HGT is an important force that contributes significantly to modularity

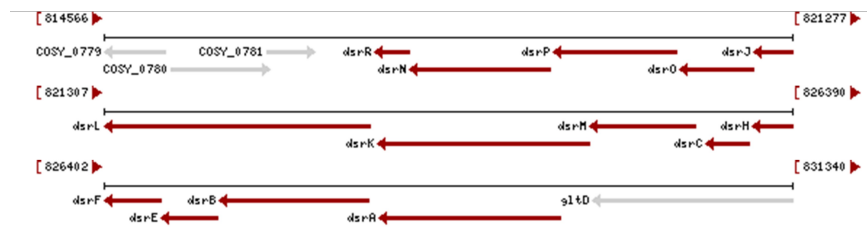
# Natural modularity (*dsr* and *sox* gene clusters)



*sox* locus



*dsr* locus



# Nature of mutations

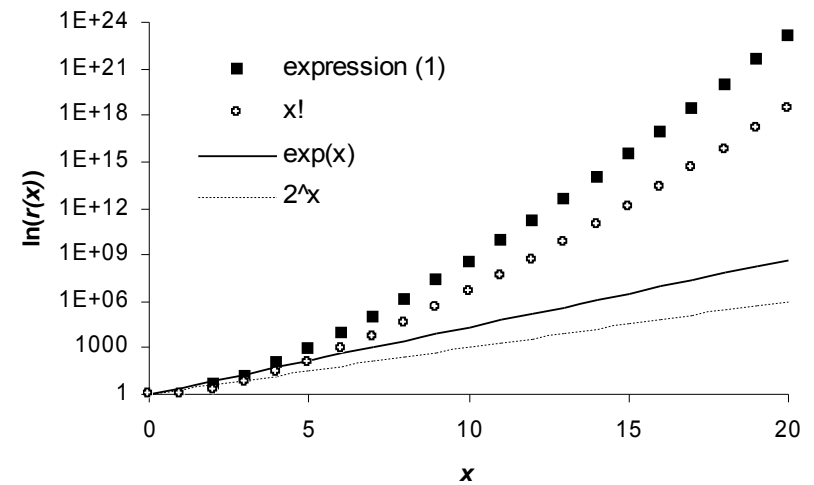
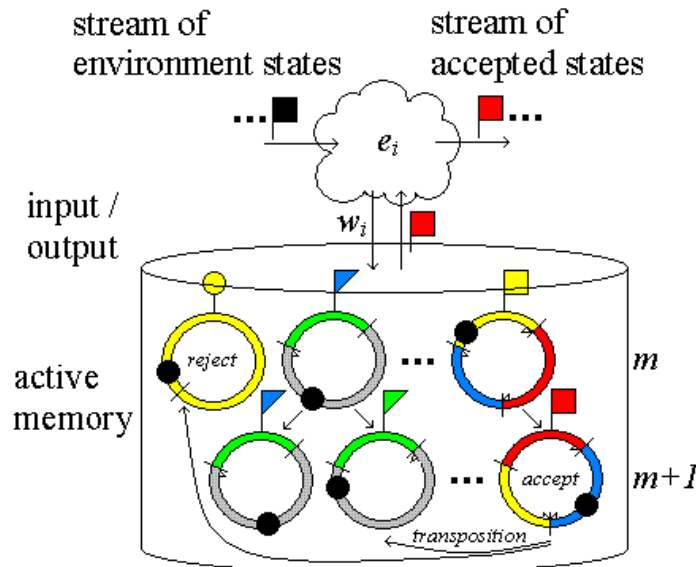
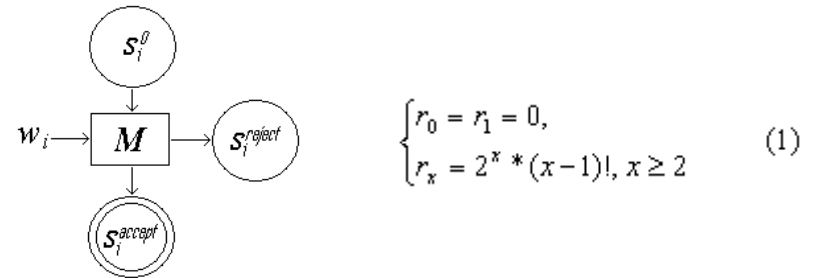
- change of topology of genetic networks and
- change of parameters

are induced in DNA sequences

<b>AprA</b>	298	GQHL <del>SH</del> KPIPTCLR-NHAFISEVNAGRGPIHMTMEA-----FKDPHLEE <del>V</del> GWENFLGMTVGQAVLWAATDVDPKYENPELTTSEPYVMGSHATG
1432856135	107	ASHLTHRPIPTCLR-NHALINEINAGRGPIHMTMEA-----FQDPHLEEIGWHNFLGMTVGQAVLWAATDVNPKYENPELTTSEPYVMGSHATG
1433546210	217	ASHLTHRPIPTCLR-NHALINEINAGRGPIHMTMEA-----FQDPHLEEIGWHNFLGMTVGQAVLWAATDVNPKYEXPELTTSEPYVMGSHATG
1433688352	154	APYGTAAITPTCLR-NHLMLEFEMKEGRGPIIMDTVSALAALGETMDKKELKHLESEAWEDFLDMTCGQANLWCATNTEPEKKNS <del>EV</del> MPTEPYLIGSHSGC
1433766319	99	ASHLTHRPIPTCLR-NHALINEINAGRGPIHMTMEA-----FQDPHLEEIGWHNFLGMTVGQAVLWAATDVNPKYENPELTTSEPYVMGSHATG
1433547459	1	--HLTH <del>X</del> PIPTCLGIRHXSMSQCPSRSDP--YVTRKL-----FRSA-SGEIGWH <del>T</del> FLGMTVGQAVLWAA <del>X</del> DVNPKYENPELTTSEPYVMGSHATG
1434025767	17	ASH <del>X</del> THRPIPTCLR-NHALINEINAGRGPIHMTMEA-----XQDPHLEEIGWHNFLGMTVGQAVLWAATDVNPKYENPELTTSEPYVMGSHATG



# Modularity as a set of construction rules, the cut and paste Argo-machine



# Modularity of genetic networks in pi-calculus, a modular 'table of elements'

## *Elements of genetic networks:*

decay (degradation of a transcription factor ***tr(b)***)

$\tau_\delta$ ,

null gate ***null(b)*** (constitutive transcription)

$\tau_\epsilon \cdot (\mathbf{tr(b)} \mid \mathbf{null(b)})$ ,

gene product ***tr(b)*** (protein transcription factor)

$!b. \mathbf{tr(b)} + \tau_\delta$ ,

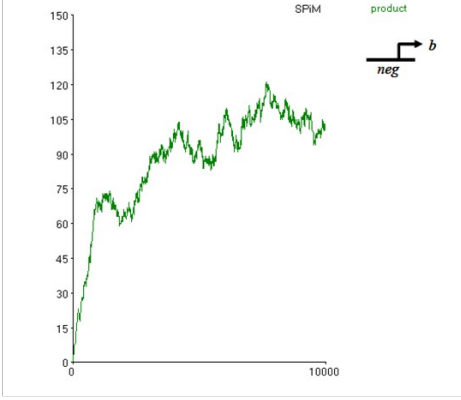
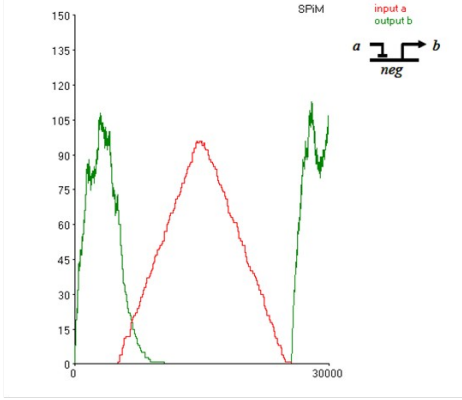
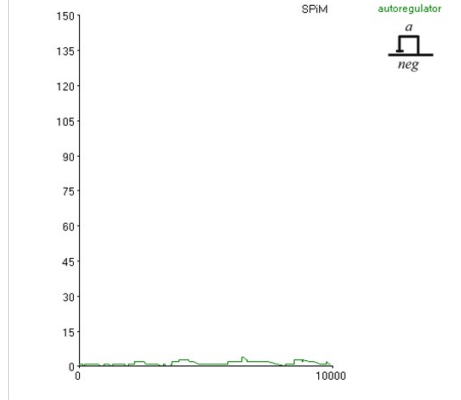
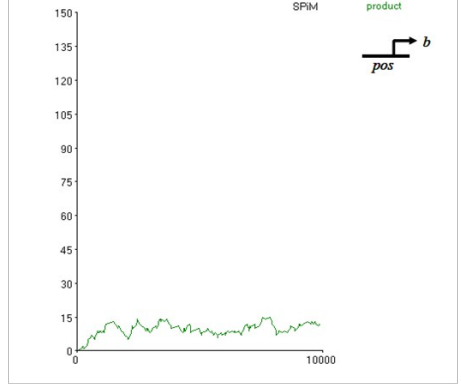
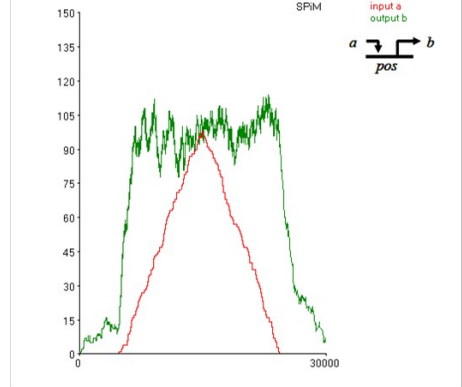
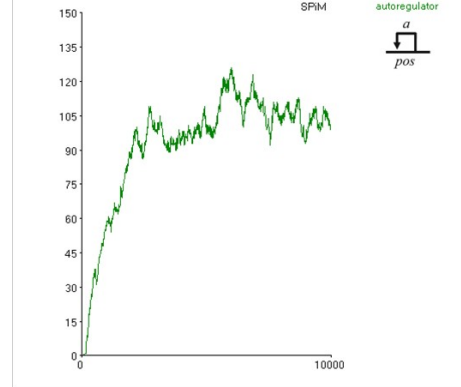
neg gate ***neg(a,b)*** (negative regulation)

$?a. \tau_\eta \cdot \mathbf{neg(a,b)} + \tau_\epsilon \cdot (\mathbf{tr(b)} \mid \mathbf{neg(a,b)})$ ,

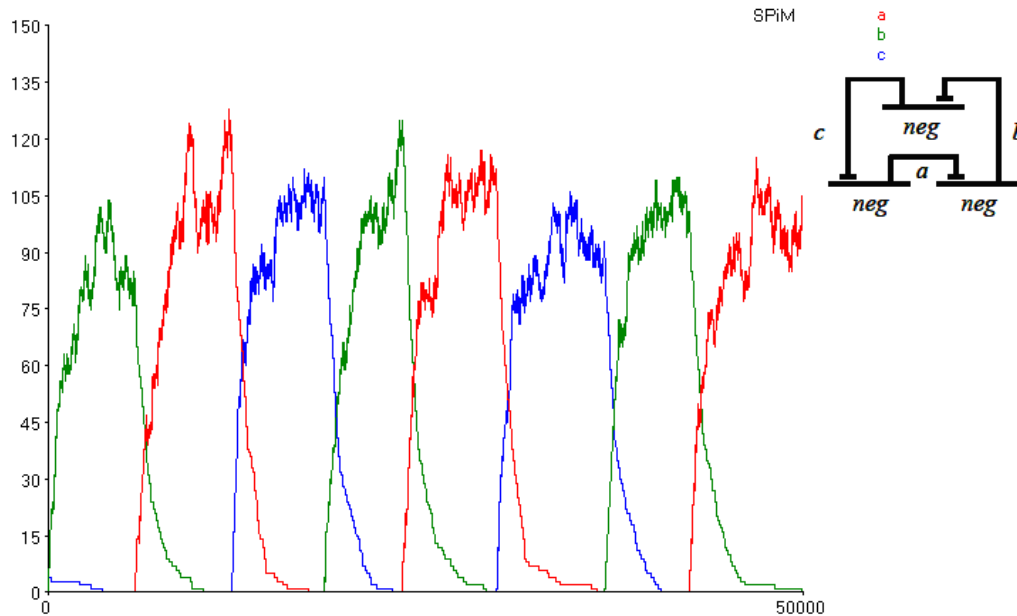
pos gate ***pos(a,b)*** (positive regulation)

$?a. \tau_\eta \cdot (\mathbf{tr(b)} \mid \mathbf{pos(a,b)}) + \tau_\epsilon \cdot (\mathbf{tr(b)} \mid \mathbf{pos(a,b)})$ .

# Basic genetic gates

	without input	regulated input	autoregulation
negative regulation	$neg(a,b) \equiv \tau_{\epsilon}. (tr(b) \mid neg(a,b))$  <p>SPIM</p> <p>product</p> <p><math>\frac{\neg}{neg} b</math></p>	$neg(a,b) \equiv ?a. \tau_{\eta}. neg(a,b) + \tau_{\epsilon}. (tr(b) \mid neg(a,b))$  <p>SPIM</p> <p>input a output b</p> <p><math>a \frac{\neg}{neg} b</math></p>	$neg(a,a)$  <p>SPIM</p> <p>autoregulator</p> <p><math>a \frac{\neg}{neg} a</math></p>
positive regulation	$pos(a,b) \equiv \tau_{\epsilon}. (tr(b) \mid pos(a,b))$  <p>SPIM</p> <p>product</p> <p><math>\frac{pos}{pos} b</math></p>	$pos(a,b) \equiv ?a. \tau_{\eta}. (tr(b) \mid pos(a,b)) + \tau_{\epsilon}. (tr(b) \mid pos(a,b))$  <p>SPIM</p> <p>input a output b</p> <p><math>a \frac{pos}{pos} b</math></p>	$pos(a,a)$  <p>SPIM</p> <p>autoregulator</p> <p><math>a \frac{pos}{pos} a</math></p>

# Repressilator



$$r = 10.0; \epsilon_n = 0.1; \eta_n = 0.001; \delta = 0.001$$

```
(* Repressilator *)
```

```
directive sample 50000.0
directive plot !a as "a"; !b as "b"; !c as "c"
directive graph
```

```
val bind = 10.0      (* protein binding - r *)
val transcribe = 0.1 (* constitutive expression - epsilon *)
val unblock = 0.001  (* repression delay - eta *)
val degrade = 0.001  (* protein decay - delta *)
```

```
(* transcription factor *)
```

```
let tr(p:chan()) =
  do !p; tr(p)
  or delay@degrade
```

```
(* neg gate *)
```

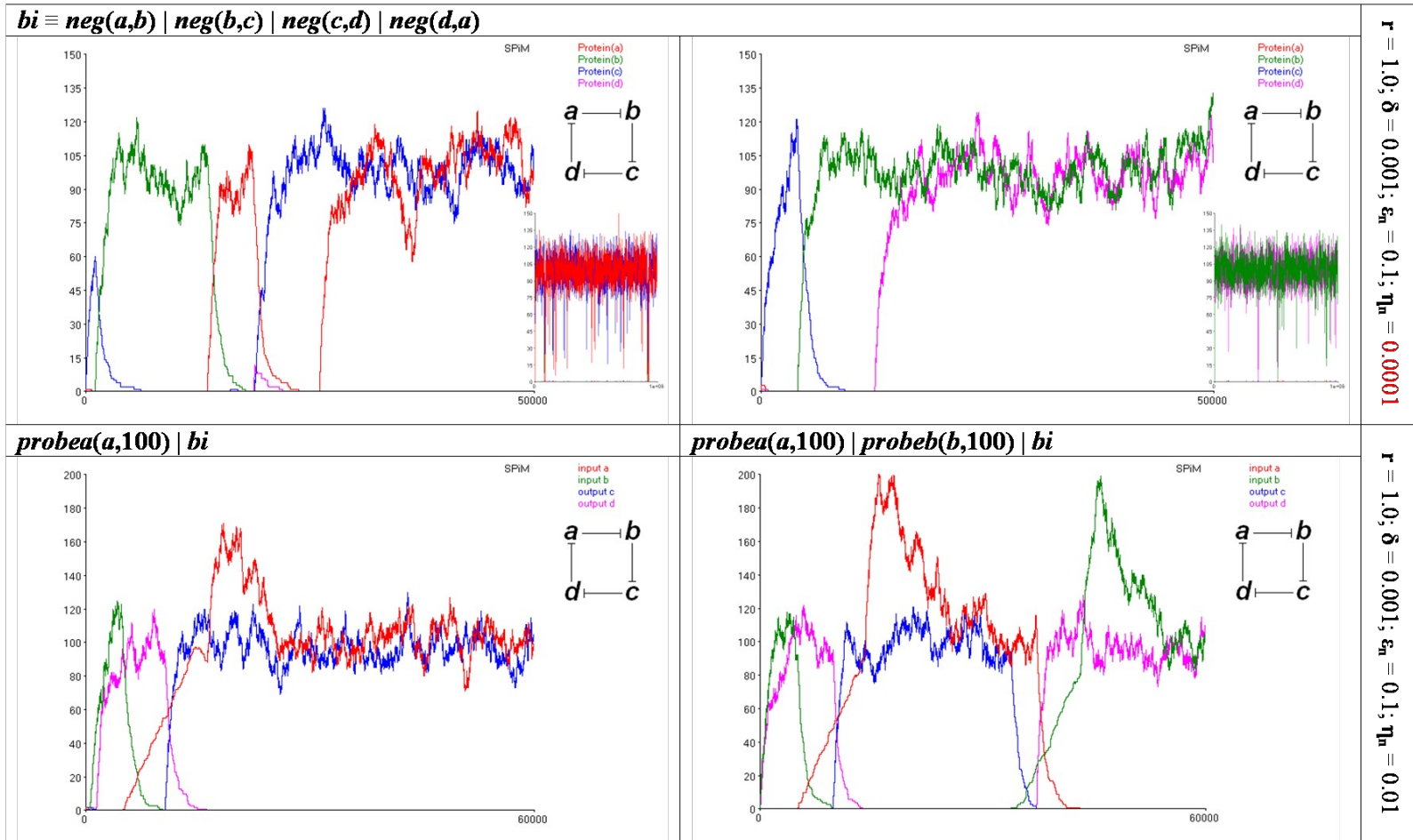
```
let neg(a:chan(), b:chan()) =
  do ?a; delay@unblock; neg(a,b)
  or delay@transcribe; (tr(b) | neg(a,b))
```

```
(* circuit *)
```

```
new a@bind:chan()
new b@bind:chan()
new c@bind:chan()
```

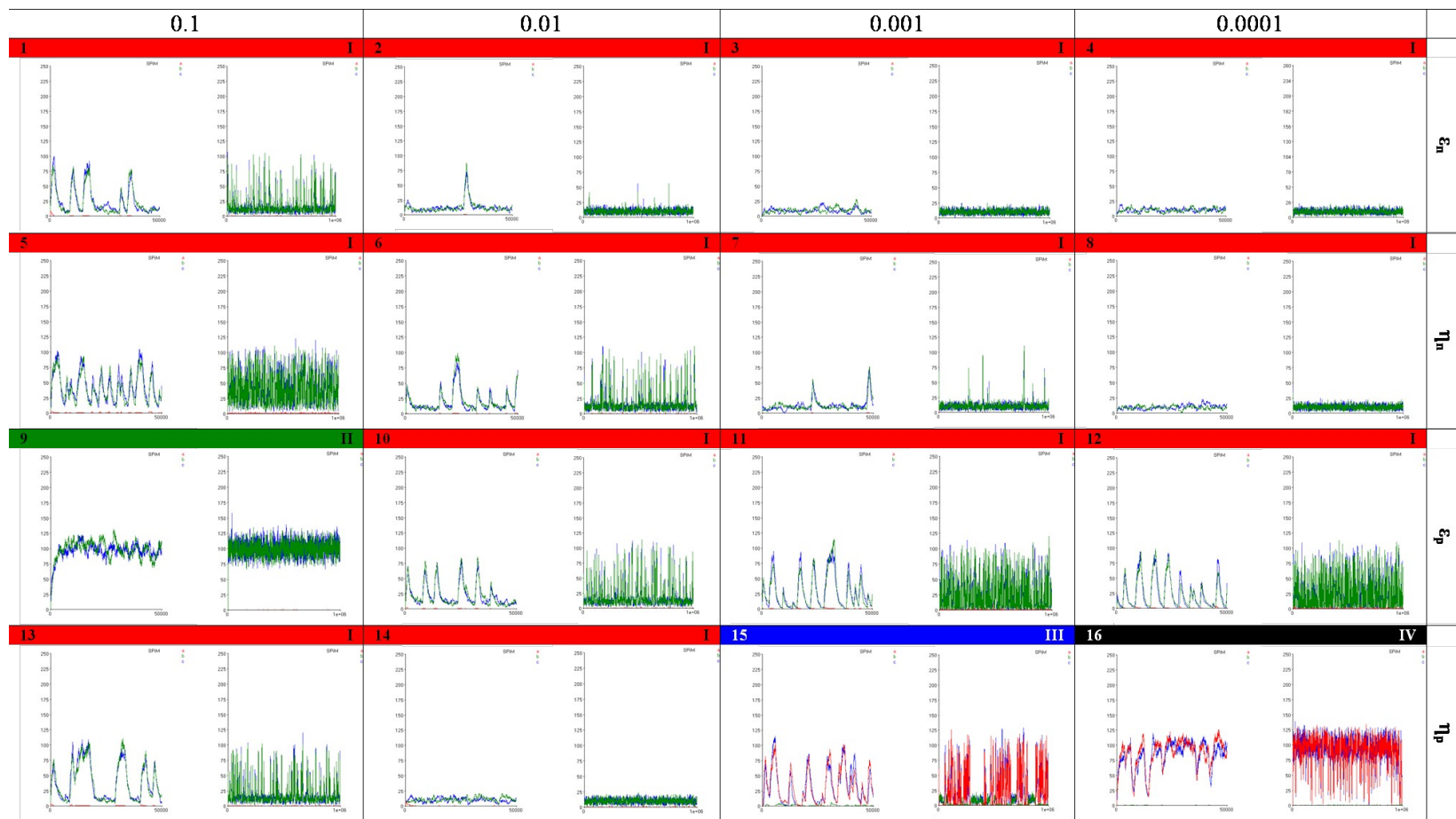
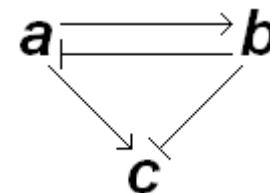
```
run (neg(a,b) | neg(b,c) | neg(c,a))
```

# Bi-stability and memory

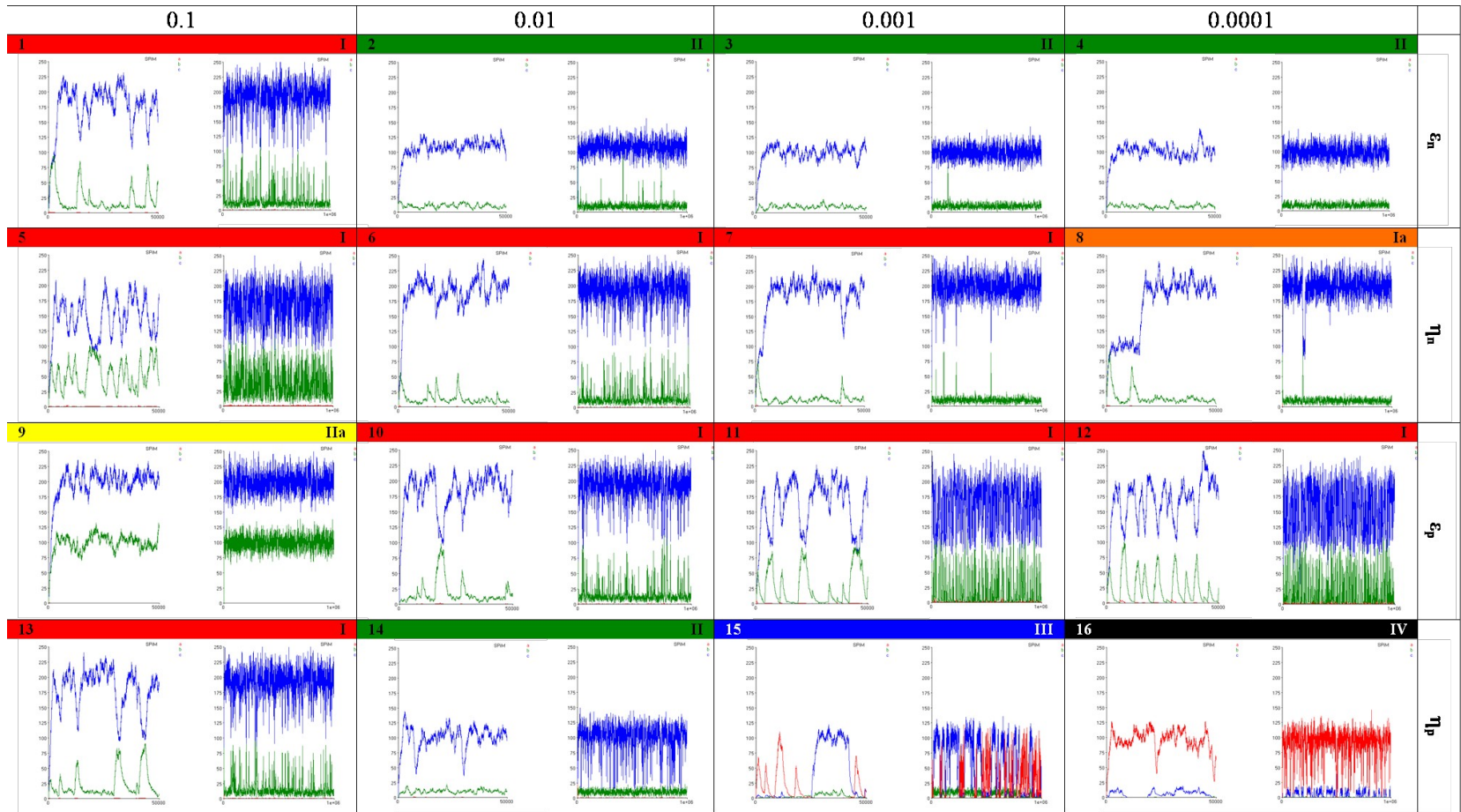
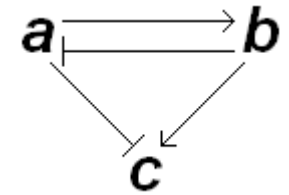




# Synchronous FFBL



# Asynchronous FFBL



# Compositional mechanisms of modularity; interaction, communication

- recombination
- hybridization
- symbiotic encapsulation
- horizontal gene transfer (HGT)
- ‘hopeful monster’  
[Goldschmidt, 1940]



## Sperm Mediated Gene Transfer (SMGT)

Control loach fry – mock analysis  
Experimental  $\beta$ -gal-positive fry 72 h after the eggs fertilization by sperm cells transfected with pcDNA3-*lacZ*

# Design of complex systems: make parts, repeat them, and change them

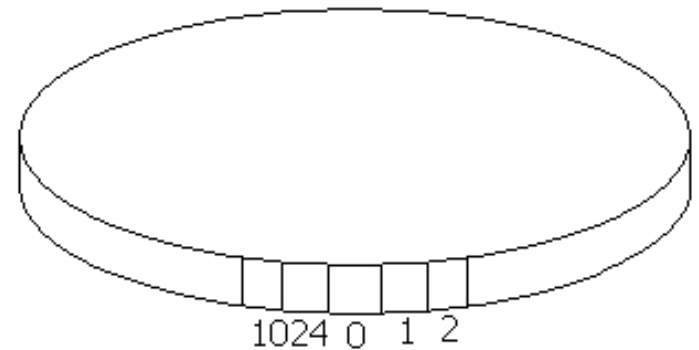
## Recursive functions

- Fractals
- Agents

$$T(i+1) = |[T(i) + P(i)] / 2 * R| \bmod(1024)$$

$$P(i+1) = T(i+1),$$

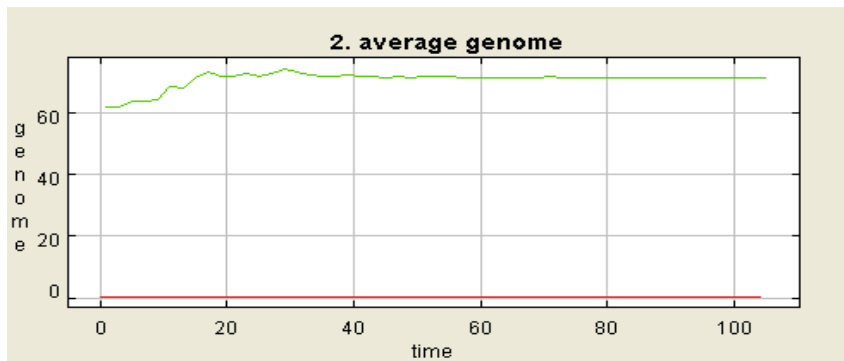
where  $T(i)$  is the color code of the individual Spermatozoon and  $P(i)$  is the color code of the individual Ovum at the time  $i$  of breeding.  $R$  is the mutation parameter on the interval  $]0, 4]$



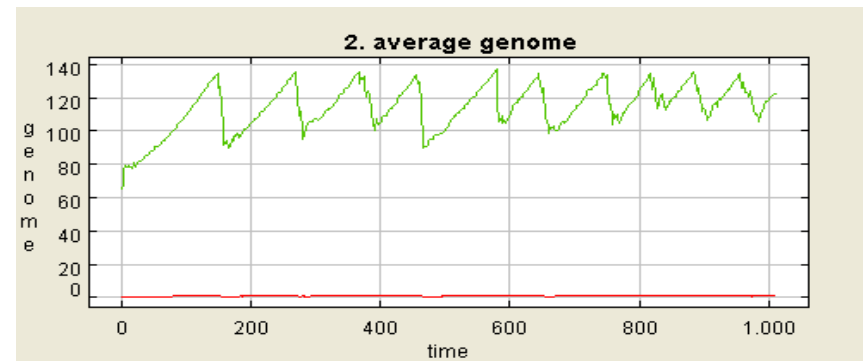
Each creature has a circular genome consisting of 1024 'genes', only one of them is active and coded by color with  $\bmod(1024)$

# Emergent behavior depending on mutation parameter

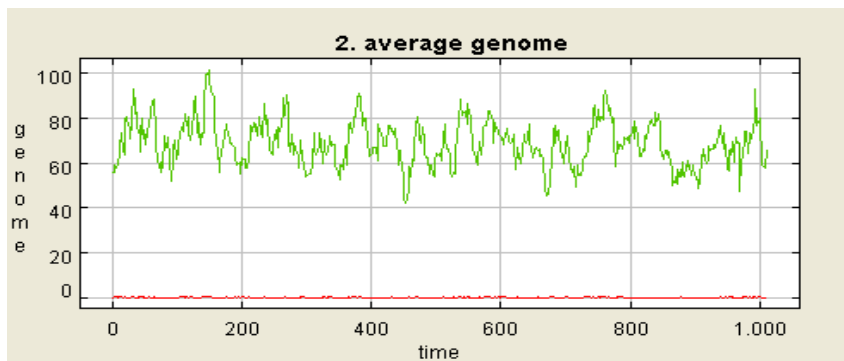
The system demonstrated ordered ( $R \leq 1$ ) and complex ( $R > 1$ ) regimes



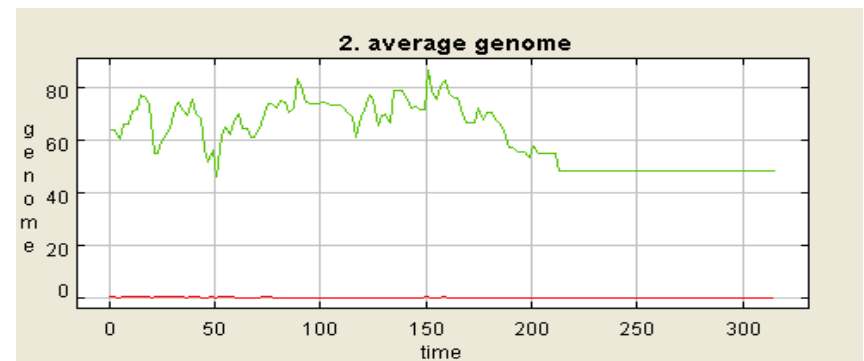
stable focus,  $R=1$



periodic,  $R=1.01$



chaotic,  $R=3$


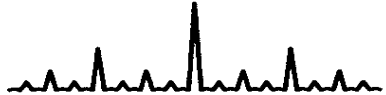



strange attractor,  $R=4$



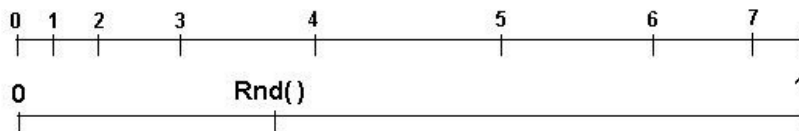
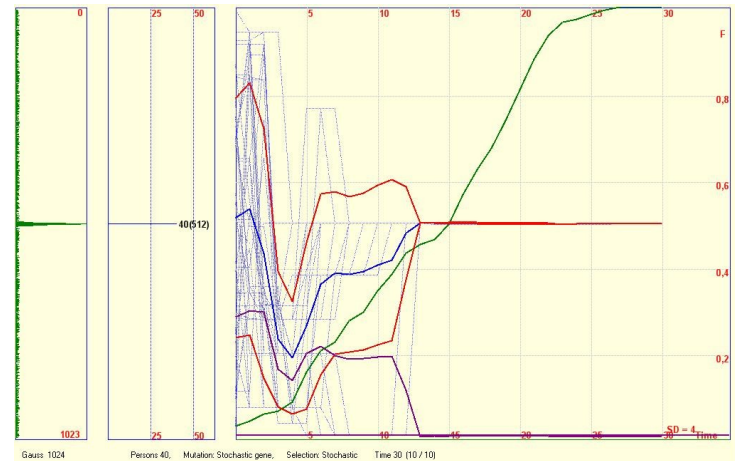
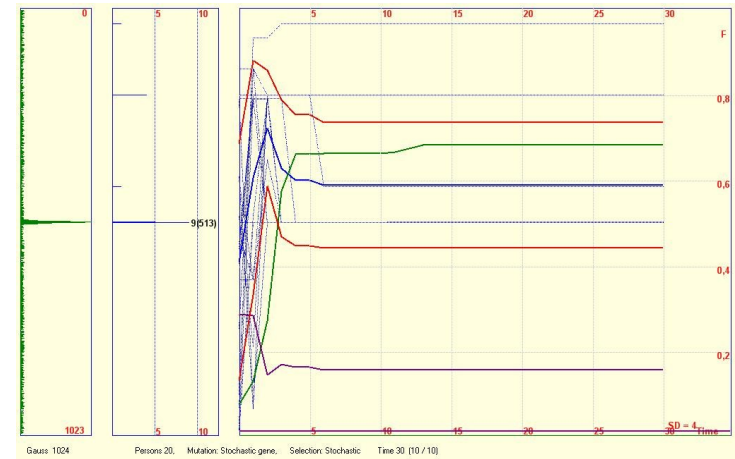
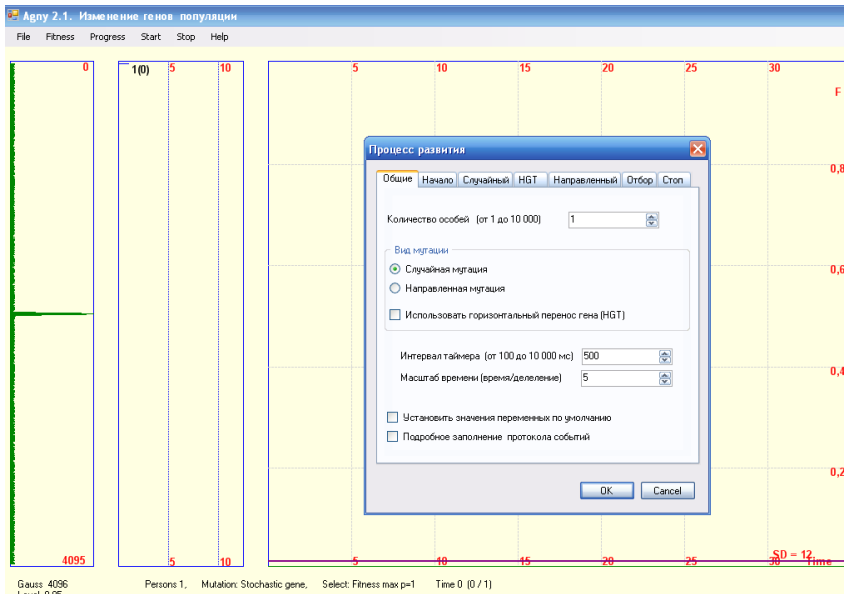
# Compositional evolution

by Richard Watson, 2006

Dependency of variables	Few / weak interdependencies	Modular interdependencies	Arbitrary interdependencies
Landscape			
Algorithmic paradigm	hill-climbing – accumulation of small variations	divide-and-conquer problem decomposition	exhaustive search, random search
Complexity	$KN$	$N^K$	$K^N$
Evolutionary analogy	gradual evolution	compositional evolution	“impossible” / “intelligent design”

N – # of variables, K – # of values for each variable

# Agny simulator, S. Golutvin



# Conclusion

- A module is the component which operates independent of other components of the system
- A functional modularity is the independence in space and time
- Modularity is driven by interaction and communication of components
- A set of modules can be combined in different ways when the environment changes (HGT)
- Origin of modularity is in the compositional evolution
- Modularity expands parallel development and enhances evolvability
- Specific interaction between modules is a subject of compositional design of complex systems
- Modularity is the relationships between the whole and the parts

# Literature

- Kuznetsov A. **From carbides to Co<sub>5</sub> and Co<sub>13</sub> metallofullerenes: first-principles study and design** // American Journal of Biomedical Engineering. 2012. V. 2(1). P. 32-38.
- Kuznetsov A. **Magnetic properties of endohedral complexes Co<sub>5</sub>@C<sub>n</sub> depending upon the size and symmetry of fullerenes as well as orientation of cobalt cluster** // Computational Materials Science. 2012. V. 54. P. 204–207.
- Kuznetsov A. **Modularity and distribution of sulfur metabolism genes in bacterial populations: search and design** // Journal of Computer Science & Systems Biology. 2010. V. 3(5). P. 091-106.
- Kuznetsov A. **Genetic networks described in stochastic Pi Machine (SPiM) programming language: compositional design** // Journal of Computer Science & Systems Biology. 2009. V. 2(5). P. 272-282.
- Kuznetsov A. **Synthetic Biology as a proof of Systems Biology** // in Handbook of Research on Systems Biology Applications in Medicine. Ed. Andriani Daskalaki. IGI Global. P. 97-115, 2009
- Kuznetsov A. **Barbie nanoatelier** // IET Synthetic Biology. V. 1(1–2), P. 7–12, 2007
- Kuznetsov A. **Assembling by adhesion rules on the nanoscale** // DECOI 2007: Design of Collective Intelligence, International School on Collective Intelligence and Evolution. Amsterdam, Holland, 20-24 August 2007
- Kuznetsov A, Schmitz M, Mueller K. **On Bio-Design of Argo-Machine** // GWAL-7: 7th German Workshop on Artificial Life. Jena, Germany, P. 125-133, 26-28 July 2006
- Kouznetsov A.V. **Toy SMGT** // Alife Mutants Hacking session on Systems and Organisms (AMHSO), Rule 110 Winter Workshop. Bielefeld, Germany, 6-13 March 2004
- Andreeva L.E., Sleptsova L.A., Grigorenko A.P., Gavriushkin A.V., Kuznetsov A.V. **Loach spermatozoa transfer foreign DNA, which expression is discovered in the early development stages** // Russian Journal of Genetics. V. 39(6), P. 758-761, 2003
- Березин В.А., Шевченко Г.М., Жмарева Е.Н., Кузнецов А.В., Кузнецова И.В. **Кислый глиальный фибриллярный белок в опухолях головного мозга различной гистоструктуры и степени злокачественности** // Нейрохимия. Т.3(3), С. 327-328, 1984

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- Steven Benner
- ...

