

# Framsticks model and genetics

- organism model
  - body
  - brain
  - sensors and effectors
- genetics
  - representations
  - conversions
  - operators

# Organism. Elements

- body
  - parts
  - joints
- brain
  - neurons
    - signal processing / sensors / actuators
    - embodied or not
  - connections

# Organism. Body elements

- Parts
  - type: ellipsoid / cylinder / box
  - size: x, y, z
  - 3D position
  - 3D orientation
  - mass
  - friction
  - (ingestion, assimilation, ...)
- Joints
  - references of the two parts
  - relative or not
  - stiffness
  - rotation stiffness
  - (stamina, ...)

# Organism. Body constraints

- at most one Joint can directly connect two Parts
- each Joint must be connected with two distinct Parts
- all Parts must be directly or indirectly connected with each other
- relative Joints must not form cycles

# Organism. Body properties

## PHYSICAL

Parts: mass, friction, density

Joints: stiffness, rotational stiffness

## BIOLOGICAL

Parts: assimilation, ingestion

Joints: stamina

Muscles: strength/speed

CONSTRAINTS



# Organism. Brain

- any topology of neural network, synchronous update
- neurons embodied (parts, joints) or not
- implement any function
- inputs: none / one / many
- outputs: none / one (may have many channels)
- a list of neural properties (parameters)
- definition: C++ or script (\*.neuro files)
- weighted connections

# Organism. Brain. Neuron sample

Short name: Thr

Long name: Threshold

- single input
- single output
- properties:
  - t (threshold)
  - hi (high output value)
  - lo (low output value)
- if ( $\text{input} \geq t$ ) then  $\text{output} := \text{hi}$  else  $\text{output} := \text{lo}$

# Organism. Brain. Neuron sample

Short name: N

Long name: Neuron

$$o_t = \frac{2}{1 + e^{-s_t \cdot \text{Sigmoid}}} - 1$$

$$s_t = s_{t-1} + v_t$$

$$v_t = v_{t-1} \cdot \text{inertia} + \text{force} \cdot (i_t - s_{t-1})$$

$i$  – weighted sum of inputs

$v$  – speed of changes

$s$  – internal state

$o$  – neuron output

subscript  $t$  is the moment of time

- many inputs
- single output
- properties:
  - fo (force)
  - in (intertia)
  - si (sigmoid)

$$\text{force} := 1$$

$$\text{inertia} := 0$$

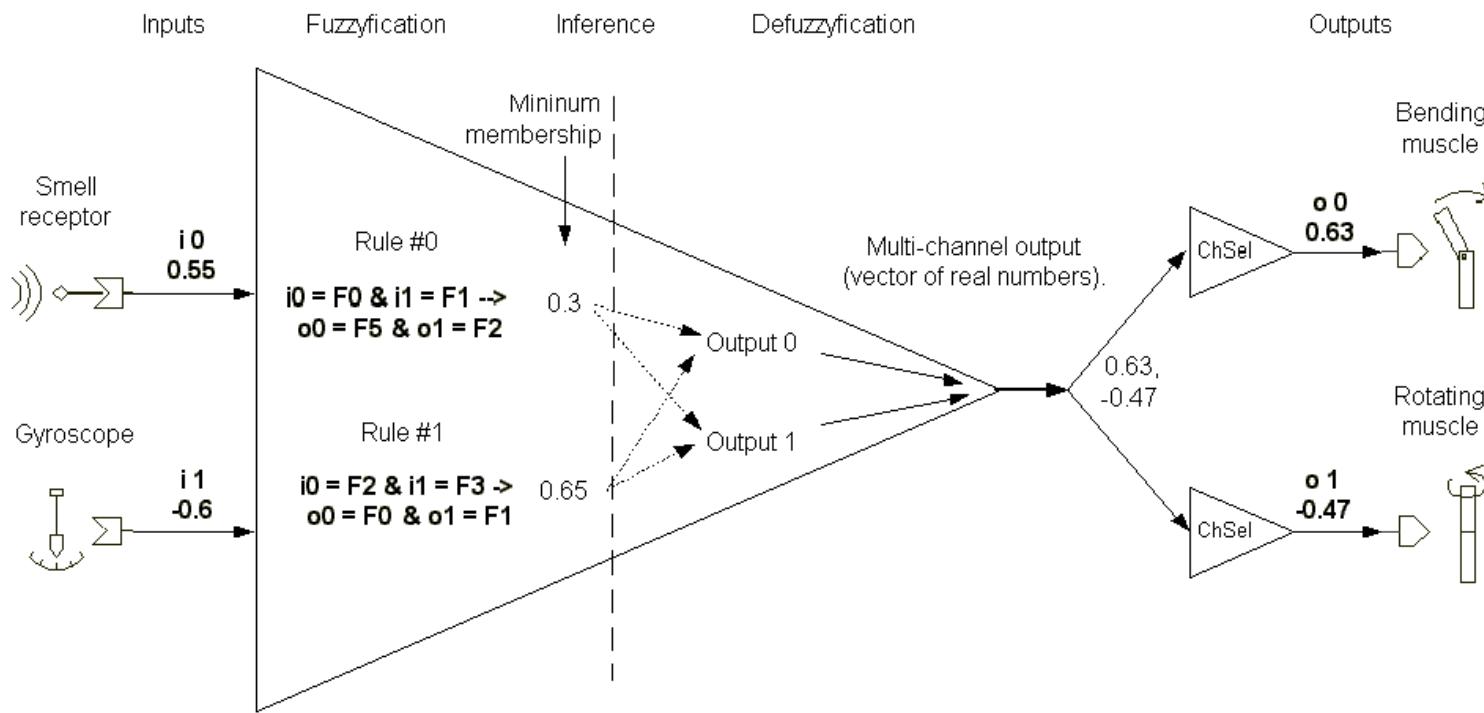
$$o_t = \frac{2}{1 + e^{-i_t \cdot \text{Sigmoid}}} - 1$$

# Organism. Brain. Neuron sample

Short name: Fuzzy

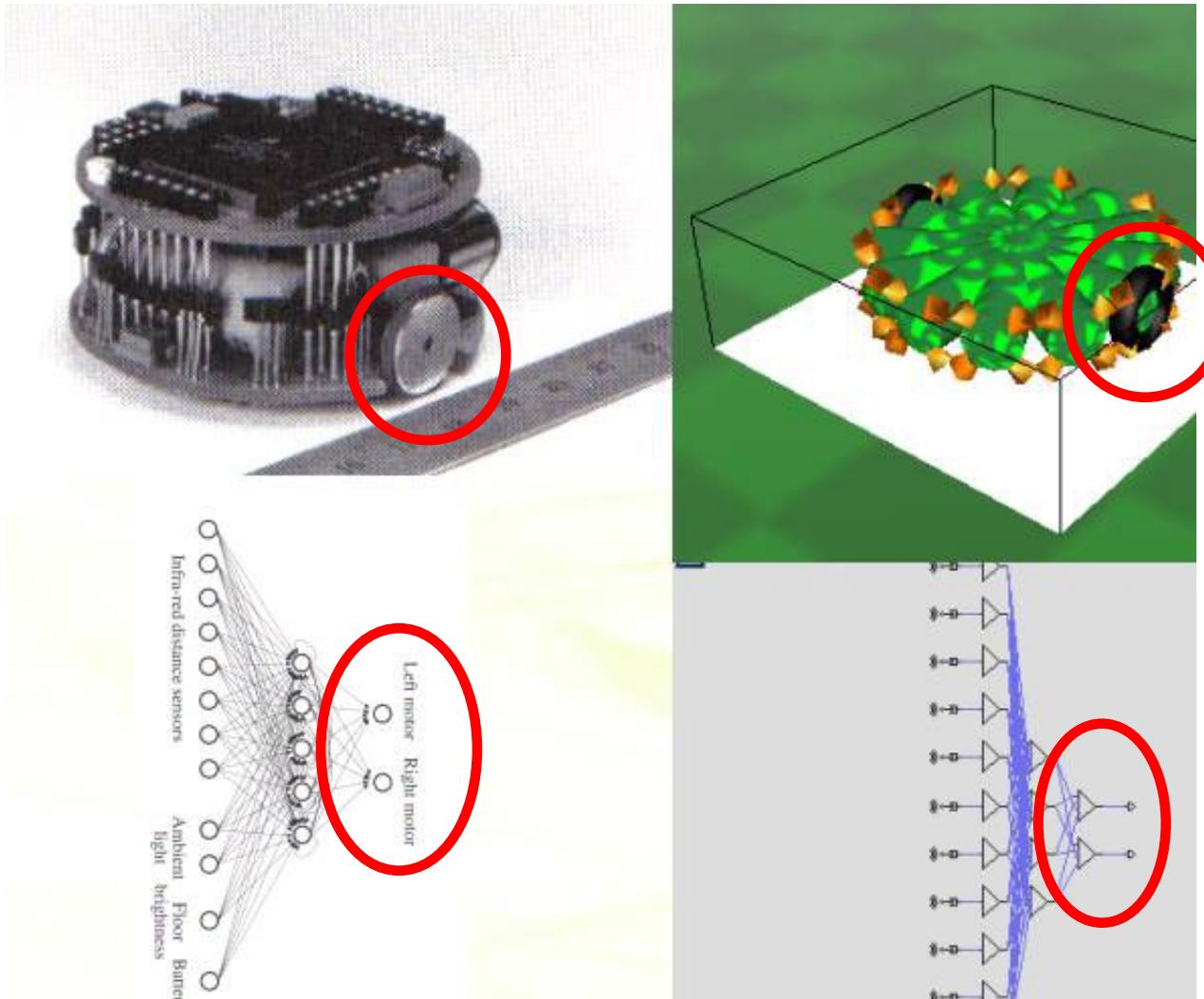
Long name: Fuzzy neuron

- many inputs
- single output (with many channels)
- properties: fuzzy sets and rules
- represents a fuzzy rule-based system
- details: M. Hapke and M. Komosinski. Evolutionary design of interpretable fuzzy controllers. *Foundations of Computing and Decision Sciences* 33(4), 2008. [\[view pdf\]](#)



# Organism. Brain. Neuron sample

A custom "Wheel" effector for robotic experiments

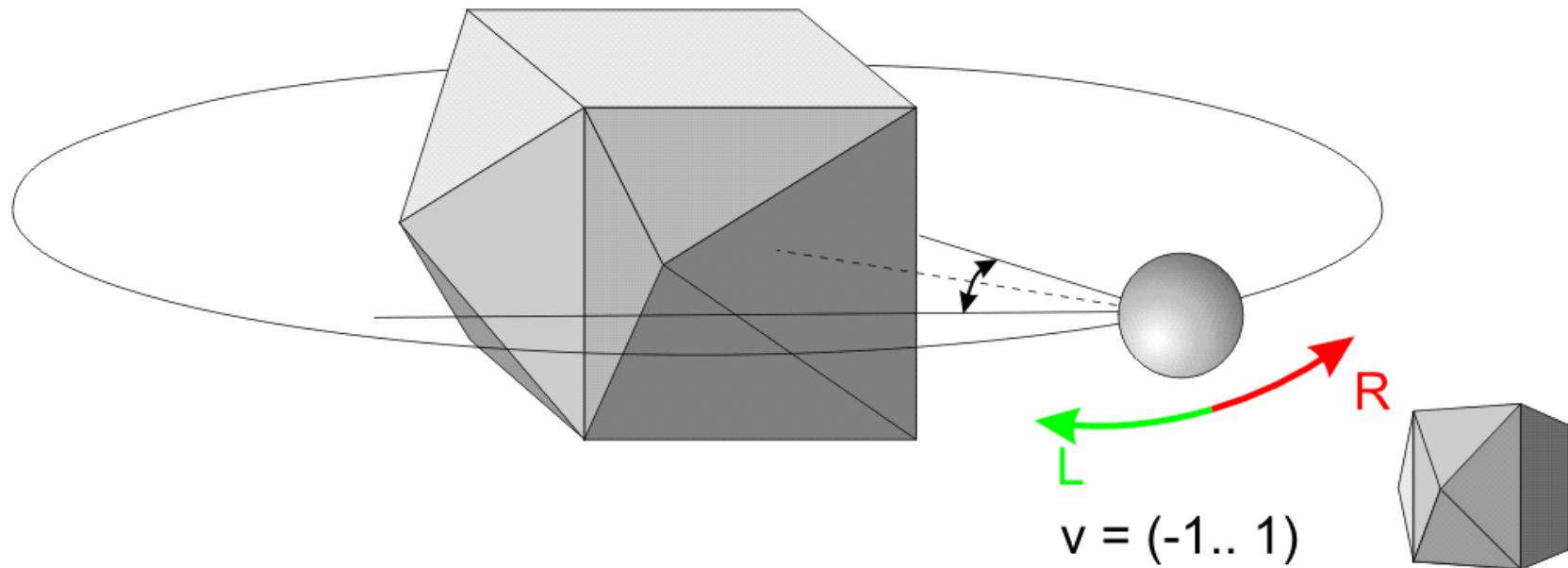


- affects movement of a Part of the creature

# Organism. Brain. Neuron sample

## A vector eye (VEye) sensor

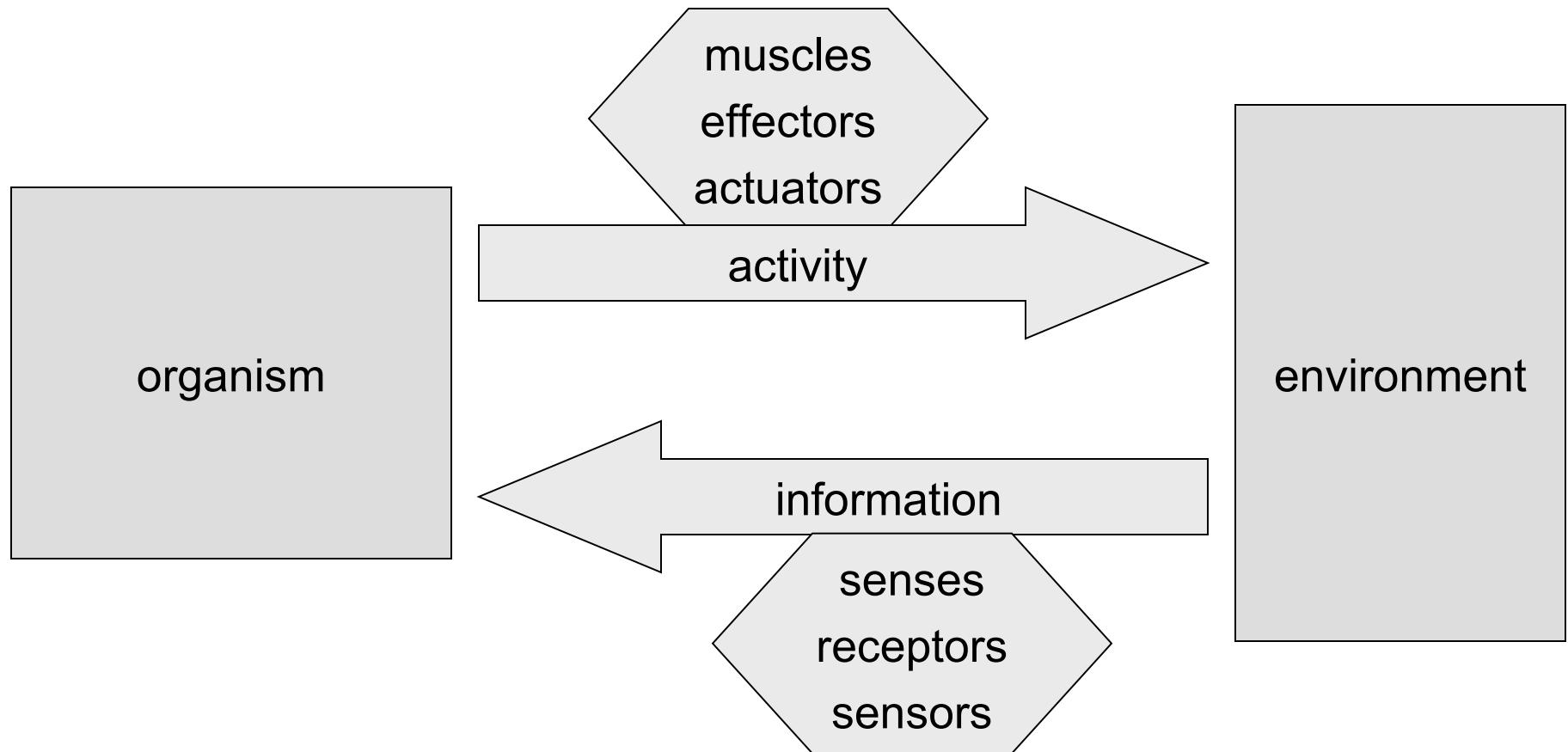
- optional input controls tilt (rotation)
- single output (with many channels) outputs vector coordinates
- properties: object (sic!), scale, perspective
- details: Jacek Jelonek and Maciej Komosinski. Biologically-inspired visual-motor coordination model in a navigation problem. In Knowledge-Based Intelligent Information and Engineering Systems, LNCS vol. 4253, pages 341-348. Springer, 2006. [\[view pdf\]](#)



# Organism. Brain. Neuron list

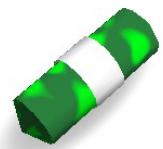
N	Neuron	Standard Framsticks neuron
G	Gyroscope	Equilibrium sensor
T	Touch	Touch sensor
S	Smell	Smell sensor
*	Const	Constant value
	Bend muscle	
@	Rotation muscle	
D	Differentiate	Calculate the difference between the current and previous input value
Ch	Channelize	Combines all input signals into single multichannel output
ChMux	Channel multiplexer	Outputs one channel from first (multichannel) first input, selected by the second
ChSel	Channel selector	Output one channel from multichannel input, selected by the "ch" parameter
Rnd	Random value	
Sin	Sinus Generator	Output frequency = f0+input
Delay	Delay	
Thr	Threshold	if (input>=t) then output=hi else output=lo
Fuzzy	Fuzzy neuron	
VEye	Vector eye	
LMu	Length muscle	
Water	Water detector	
Energy	Energy level	

# Organism. Simulation. Interactions

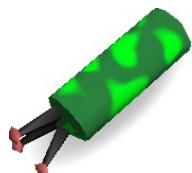


# Organism. Body/Brain Receptors and effectors

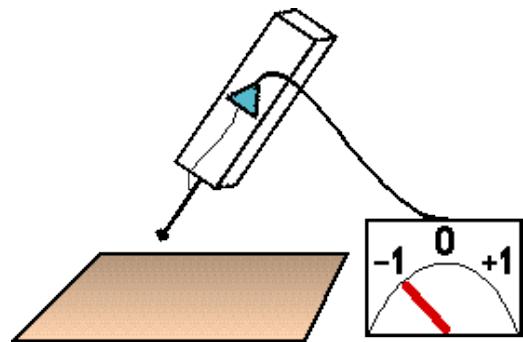
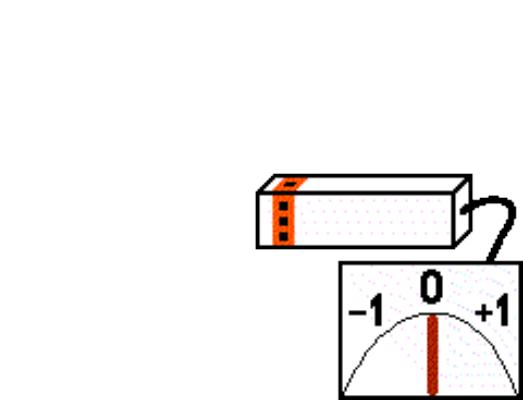
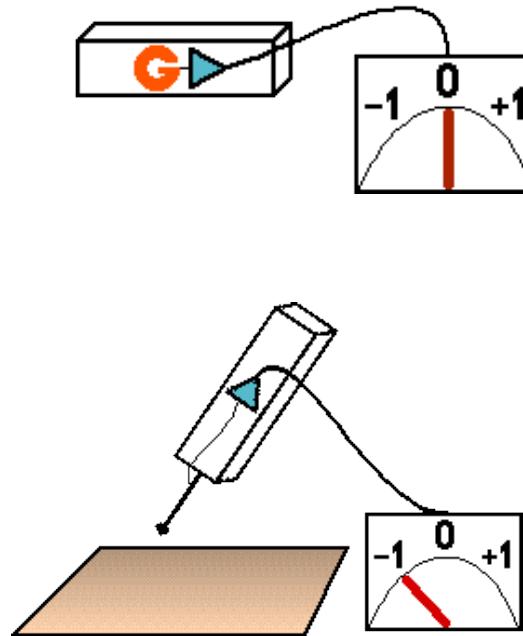
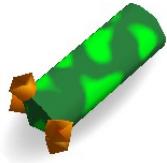
equilibrium



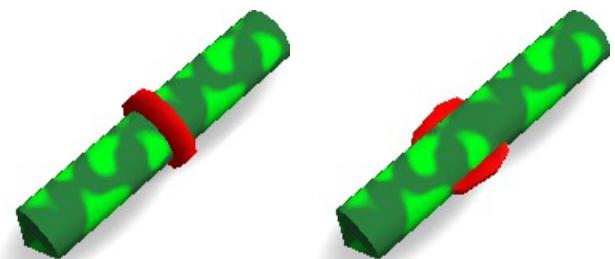
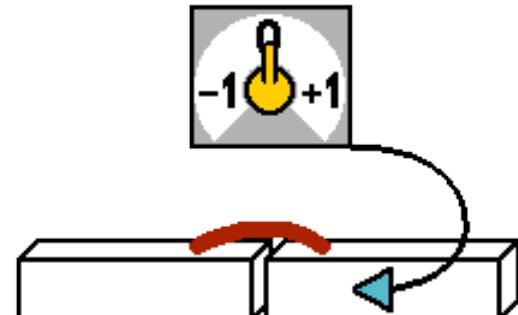
touch



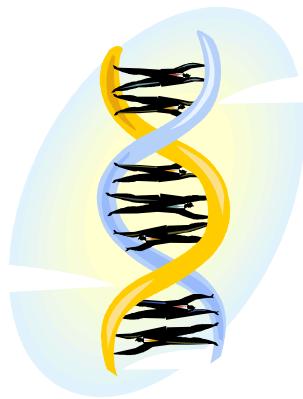
smell



bending and  
rotating muscles



# Genetics. Transformations.



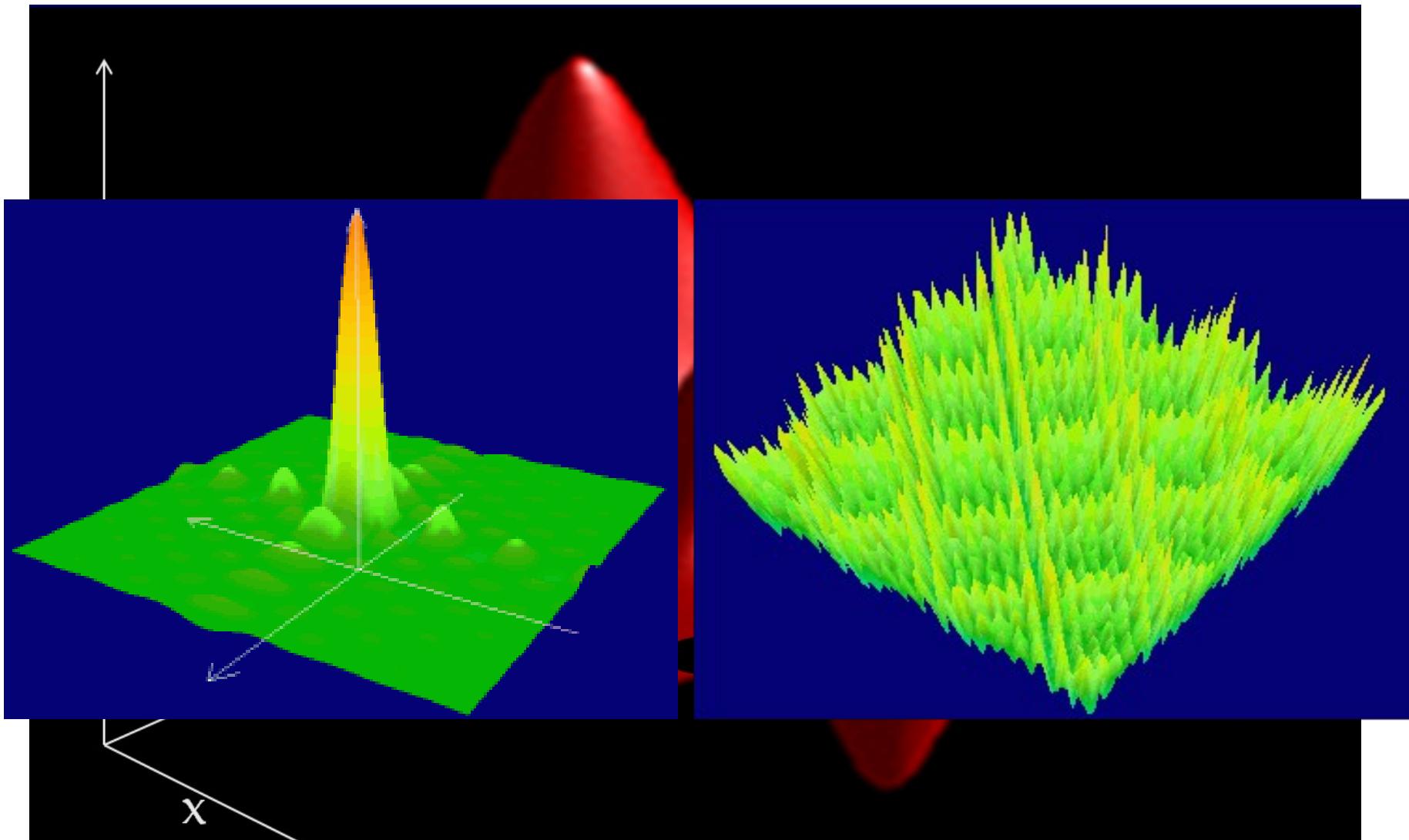
DNA → organism



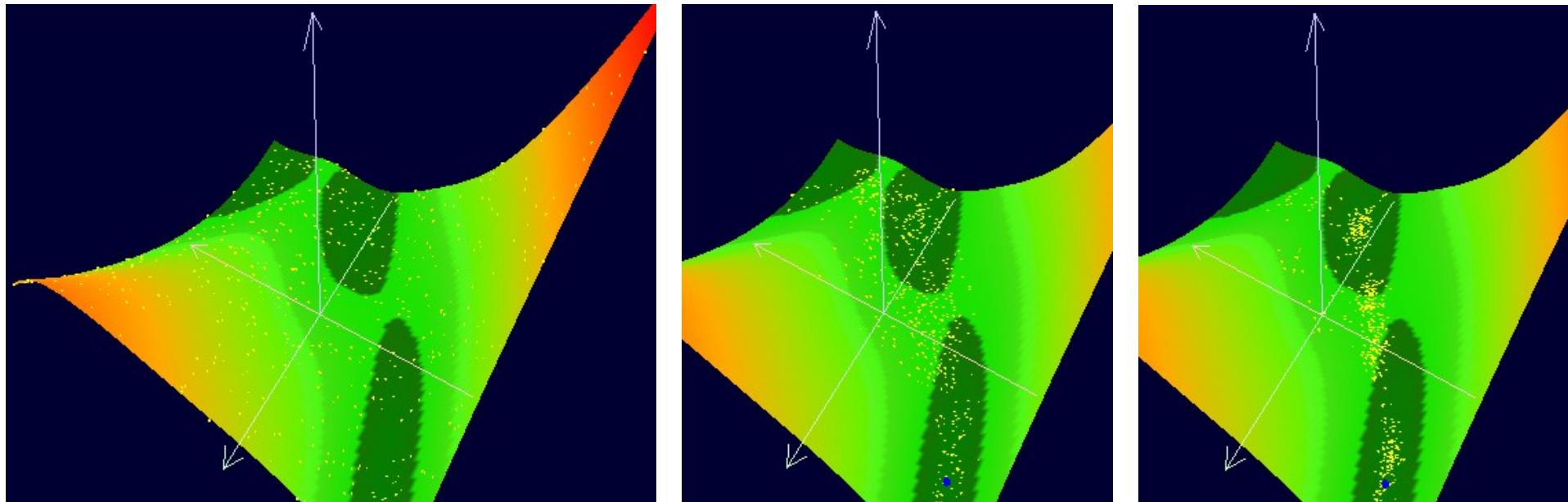
genotype → model

# Why so important?

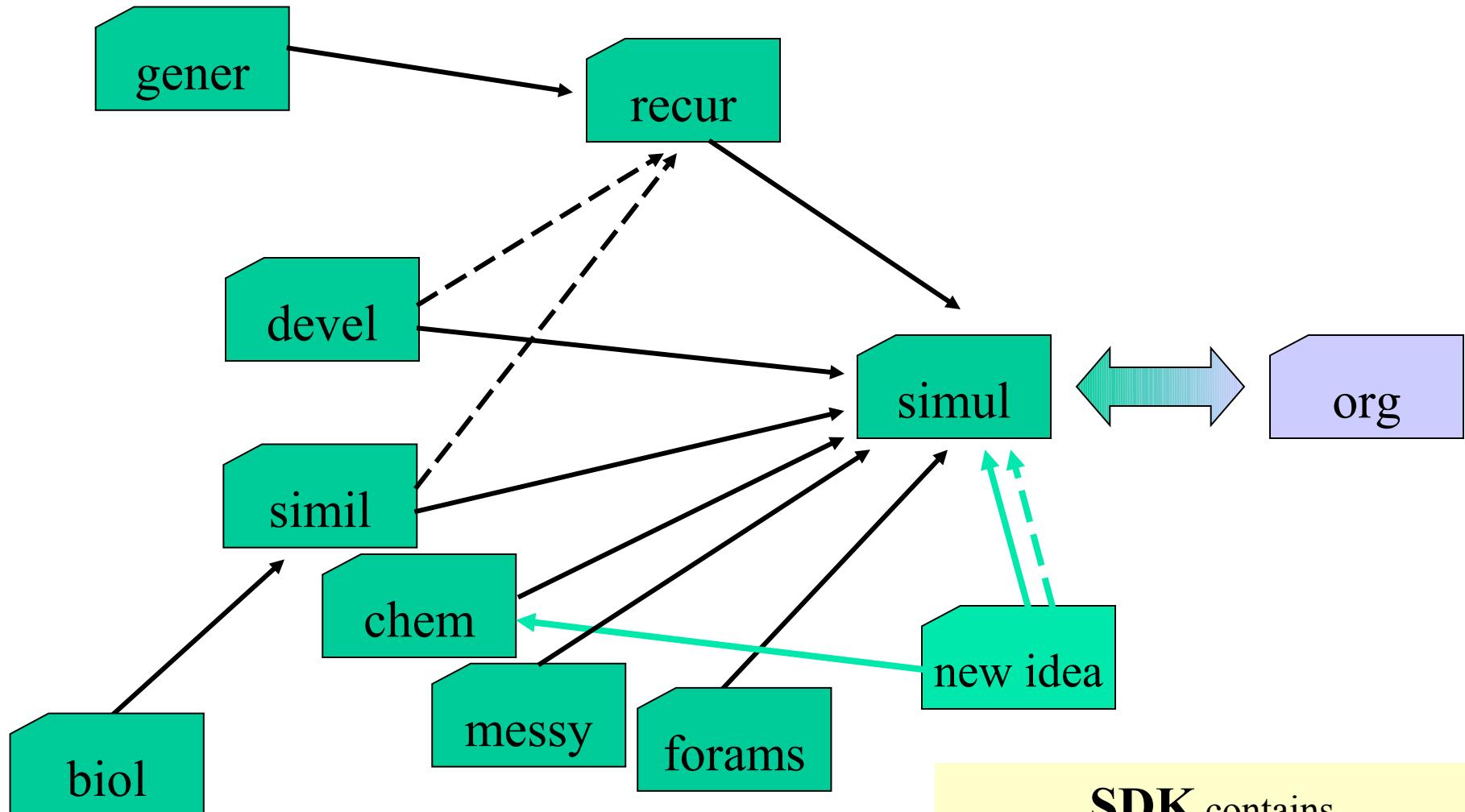
Fitness landscapes!



# Evolutionary algorithms



# Representation conversion graph



**SDK** contains  
“Genotype Developer Kit”

# Genetics. Mapping.

gene ↔ gene ↔ ... ↔ phene

output

i

n

p

u

t

g

2

X

E

3

#

#

#

#

#

#

#

#

#

#

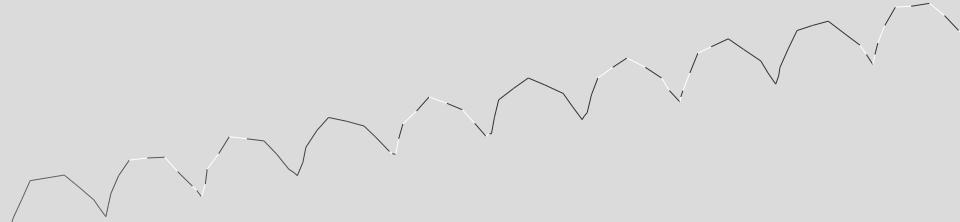
Points	Neurons
0	0
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
0	1
1	2
2	3
3	4
4	5
5	6
6	7
7	8
8	9
9	0

```

/*4*/mSiSlla#4a#2ELLLL#<
L<LLL<SL<X>i,CfL>RfIXrXX>
<SXm>L<LXi>LSLEL<L>>
ReCSaLe<X>LX>m,CfLM
RaR<LM>XL>LEL<X>cEeC
SLe<X>X>N>>509744,-1
n (LFMA(LLX[| 1 :3.4550,0.1459]>| -509744,-1
p * 44 A@Wx@G:93.351,1.72
u 1.6201 X@G:1.151
t >>#3#2E>>T>RA#3W#4#
g 0.9701 X@G:1.151
2R>#2ML#2>F>#2>R
X#3#R>c>X#R#2RL>
EcCM>aF#4SML#2>>>L
<#3#2R>#4ML#2R>F>>
3#2E>>X><X><#3R>RA
X#3#2RL>c#2M>>E><IE
cCMX>X#4ML>
/*4*/L<X#2MC#LFme>>>LLLLLFLeSLe#3s#4F#6w,fLWIS<Xf>LLeLSLem<FaIX#2
#AM>>s>#6LaL>r>F#6w,fLWIS<X#21>LeLSLem<FaIX#2#AM>>s>#5LaL>r>MC
asllL#2<0:-2.54369>N@,X[-1:4.64293]>

```

X(X,RRX(X



[Read article]

# Characteristics of genetic representations

[\[Read article\]](#)

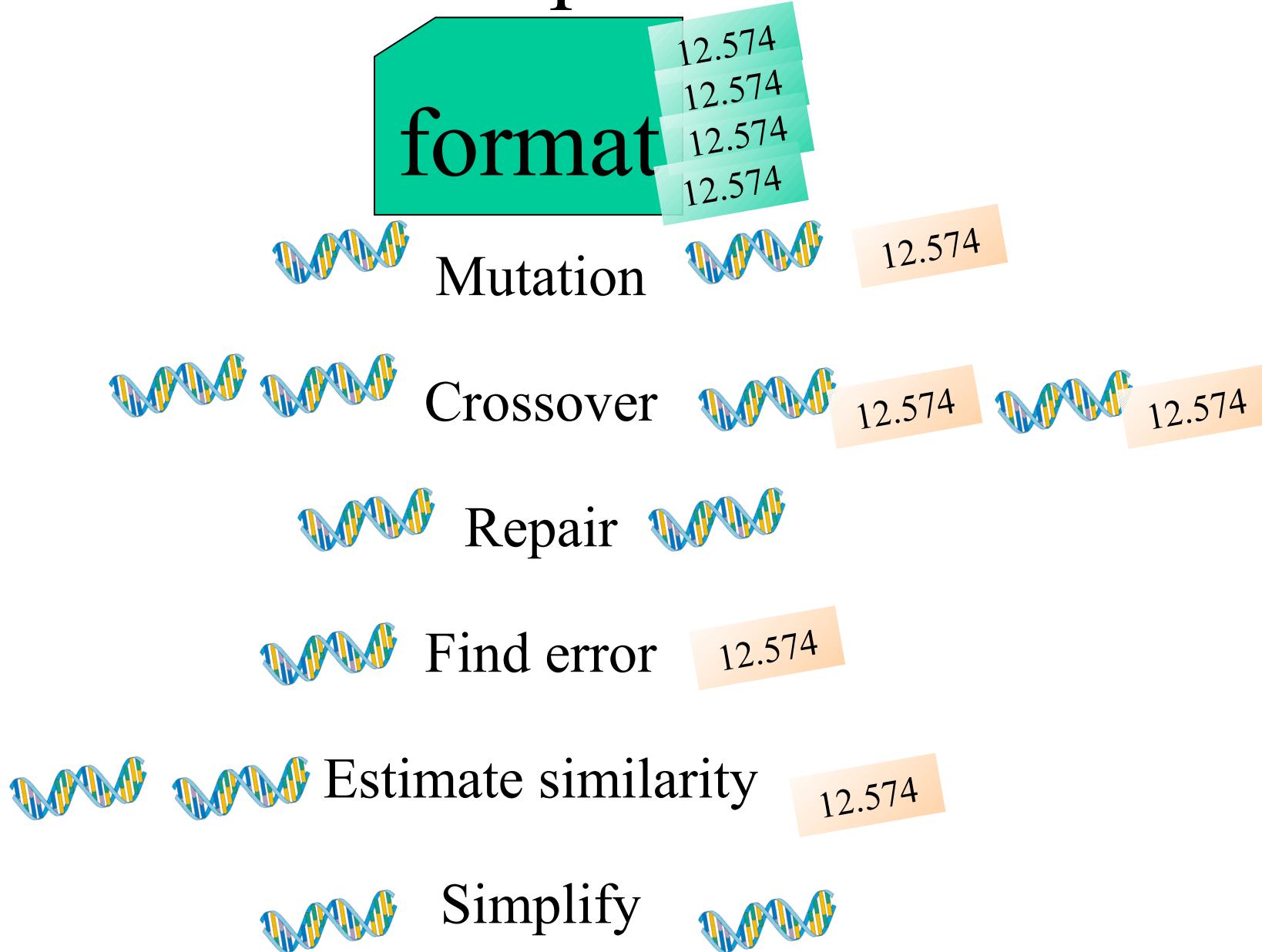
	Complexity		Constraints	
	Genotype	Interpretation	Body	Brain
<i>simul</i>	Med	Low	None	None
<i>recur</i>	Med	Med	High	Low
<i>devel</i>	High	Med	High	Low

	Modularity	Symmetry	Compression	Redundancy
<i>simul</i>	None	None	None	None
<i>recur</i>	None	Low	None	Low
<i>devel</i>	High	High	Var	None

# Characteristics of genetic representations

	<i>Complexity</i>		<i>Constraints</i>		<i>Cyclic Body</i>	<i>Compression</i>	<i>Redundancy</i>
	<i>Format</i>	<i>Interpret</i>	<i>Body</i>	<i>Brain</i>			
<i>simul</i>	Med	Low	None	None	Y	None	None
<i>recur</i>	Med	Med	High	Low	N	None	Low
<i>simil</i>	Low	High	Med	None	Y/N	Low	None
<i>chem</i>	Low	High	Med	None	Y/N	Var	Var
<i>devel</i>	High	Med	High	Low	N	Var	None
<i>messy</i>	High	Low	High	?	N	None	None
...							

# Genetic operators



# *Simul* representation

- all parts directly described
- basic, internal format
- supports geometric relativity

qX(X[@,1:1],X[**Sin**])

**p:**

**p:1, m=3**

**p:1.50017, -0.865927**

**p:1.50017, 0.865927**

**j:0, 1, dx=1**

**j:1, 2, rx=-0.62568, rz=-1.047, dx=1**

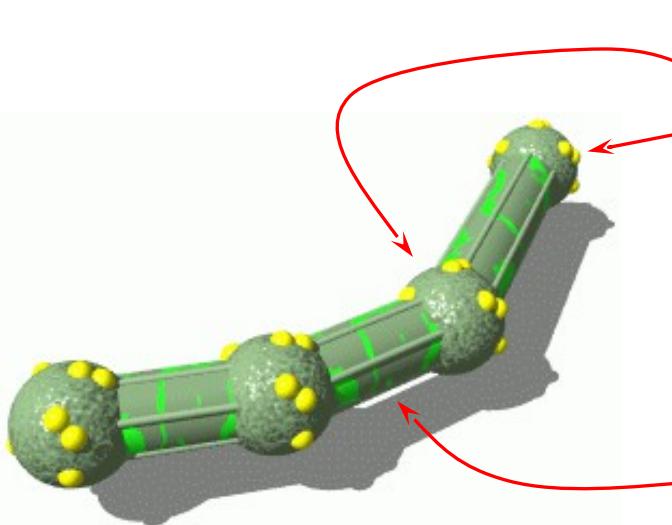
**j:1, 3, rx=-0.62568, rz=1.047, dx=1**

**n:j=1, d=@**

**n:p=3, d=Sin**

**c:0, 1**

# *Simul* genotype-phenotype relation



//0

p:m=3

p:0.000145457, -0.490867

p:1, m=4, ing=0.0304878, as=0.0304878

p:1.00015, -0.339942, 0.354104, ing=0.0743,  
as=0.0743

...

j:0, 1, rx=-0.8058, rz=-1.5705, dx=0.490867

j:0, 2, rx=-0.8058, dx=1, stam=0.0304878

j:2, 3, rx=-1.06366, rz=-1.5705, dx=0.49086,  
stam=0.07439

j:2, 4, rx=-1.06366, dx=1, stam=0.0236728

...

n:p=2, d=N:si=1.879

n:j=1, d=@:p=0.908537

n:p=4, d=N:si=-3.35

...

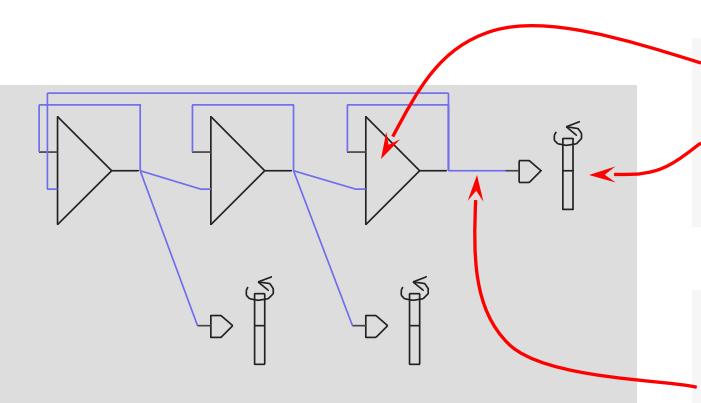
c:0, 0, 2.408

c:0, 2, -0.812

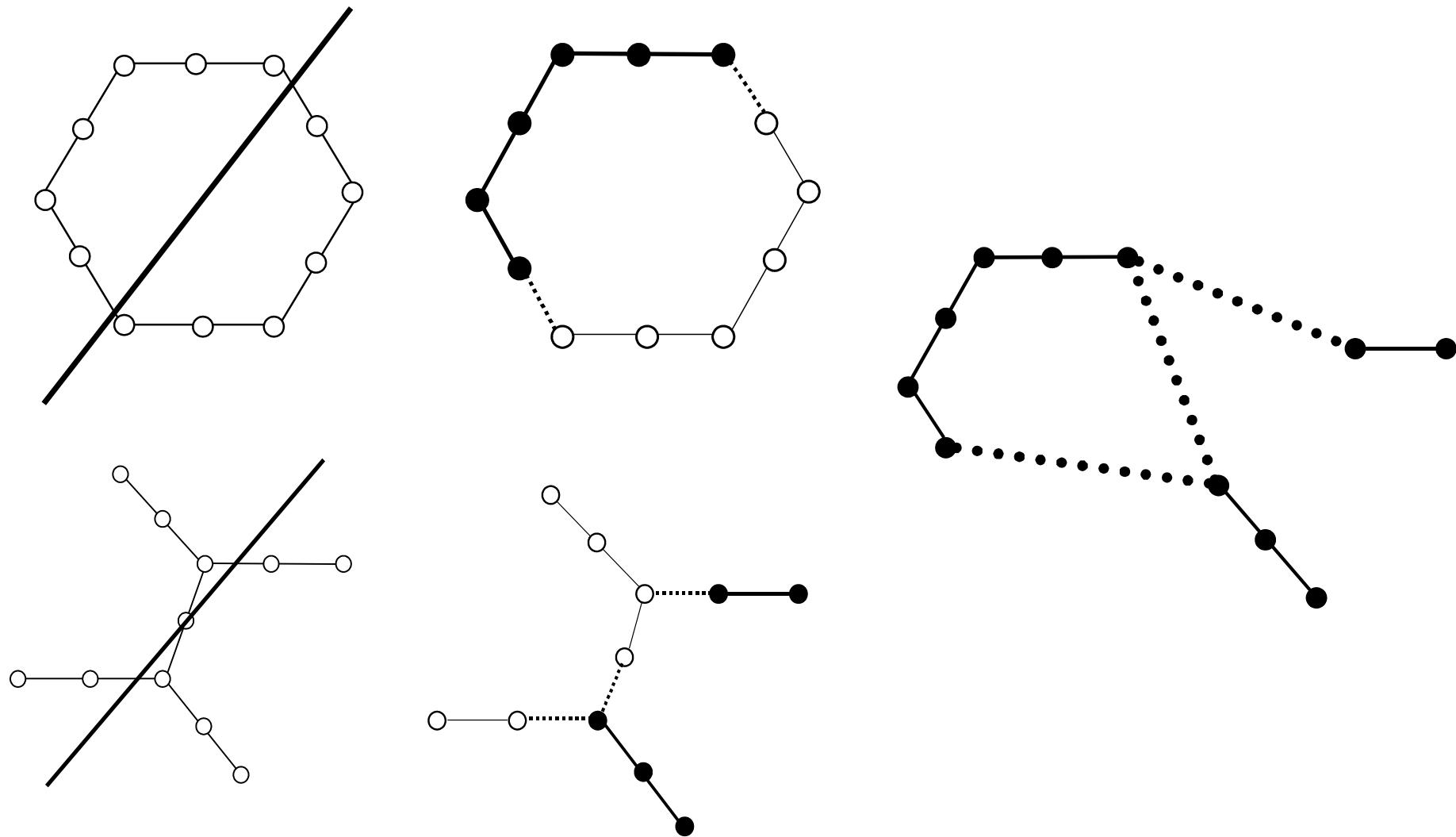
c:1, 0

neurons

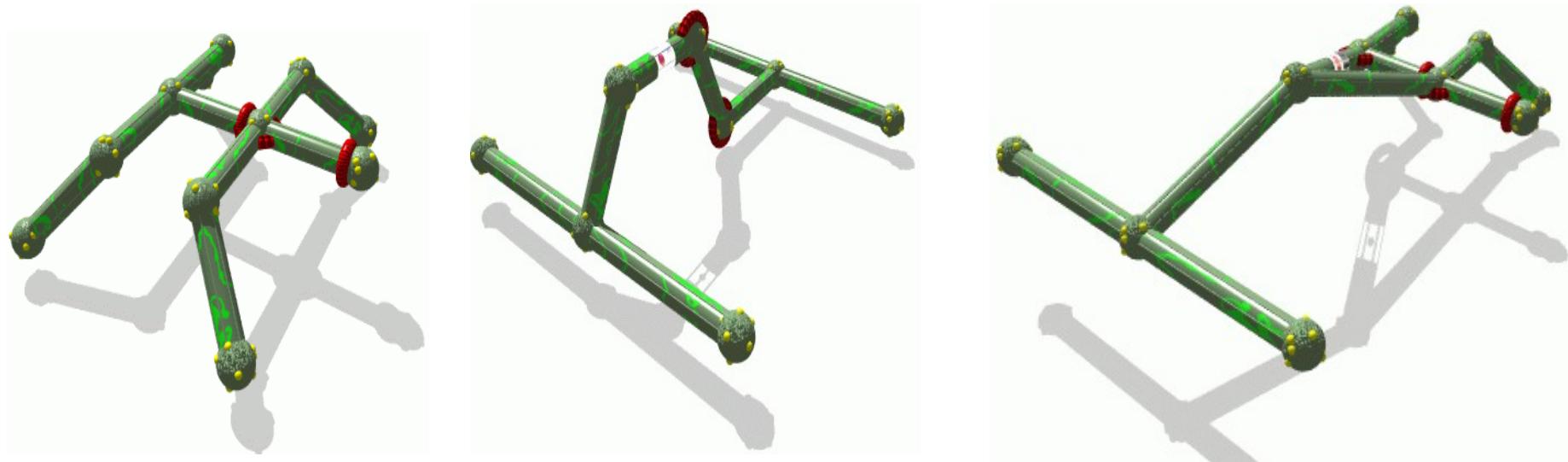
conn's



# *Simul* crossing-over

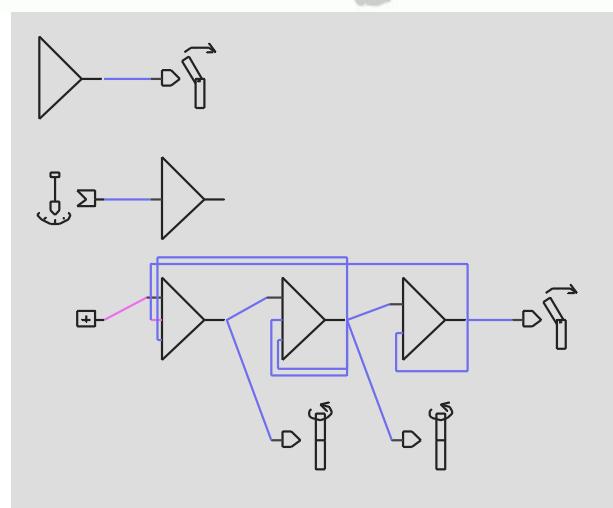
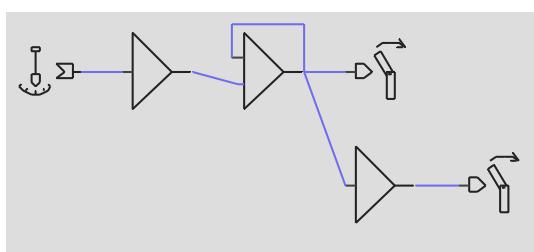
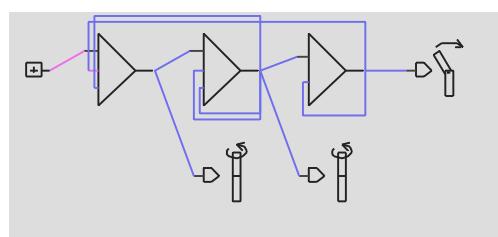


# *Simul* crossing-over



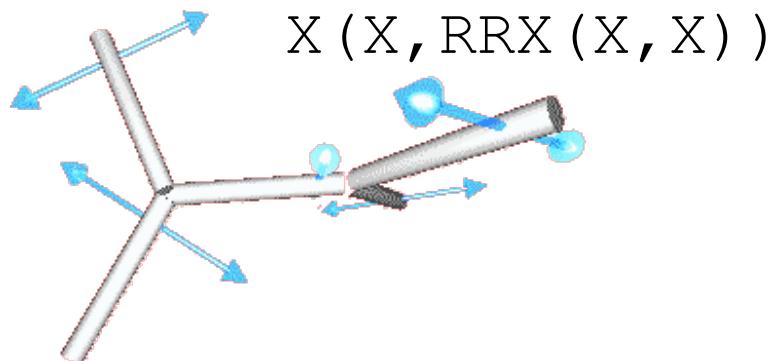
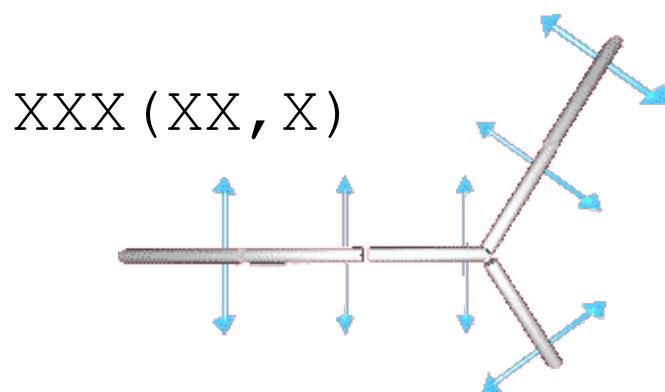
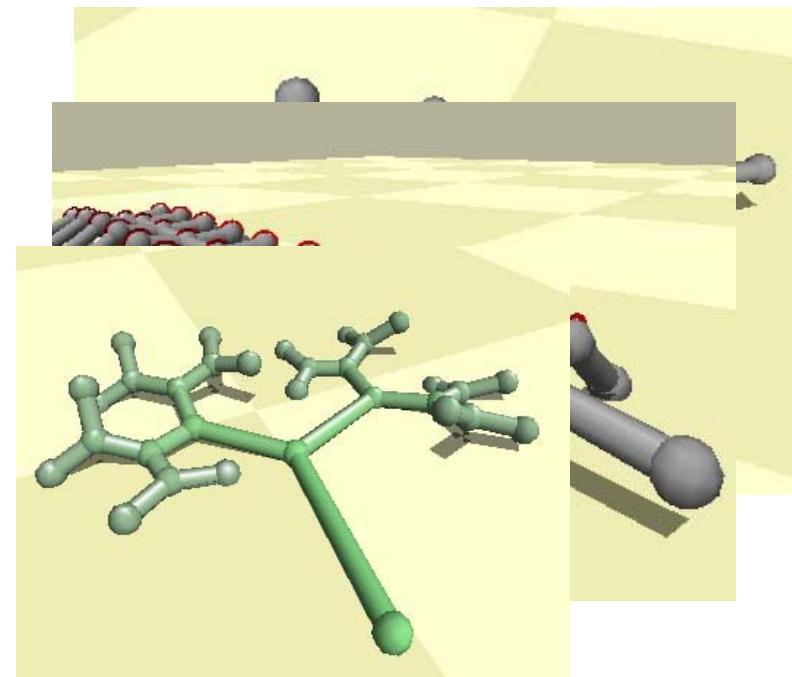
+

=



# *Recur* representation

- properties are local, relative
- properties propagate along the body
- control elements (neurons, sensors) are near elements under control (muscles, sticks)
- recurrent body (tree)
- any topology of NN
- human-friendly

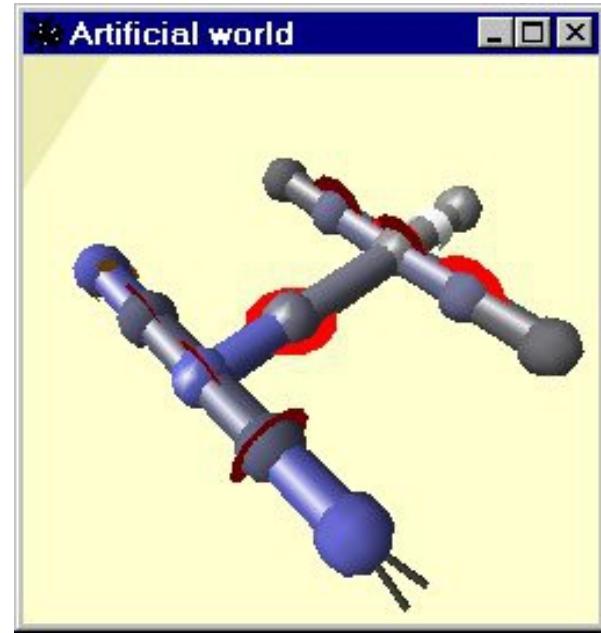


# *Recur* "modifiers"

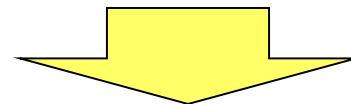
Rr	Rotation of branching plane by $\pm 45^\circ$
Qq	Skew of branching plane
Cc	Curvedness
Ll	Length
Ff	Friction
Mm	Muscle strength

# Recur example

```
111ffffX[0:2.420,2:-2,1 :-1][-1 :1,0:1,G:-1]  
[-1:1](RR111fffMMMX[|-1:-10]111FFFMMMX  
[|-2:-1],ffffIX111ffffMMMsX[|6:10,*:-10]  
(RR111ffffMMMix[|-4:-10]111FFFMMMix[|-5:-1]  
[S:313.590],,RR111ffffMMMix[|-7:10]111FFFMMMix  
[@-8:-1][T:1]),RR111ffffMMMX[|-10:10]  
111FFFMMMX[|-11:-1.784])
```



# *Recur* crossing-over



# *Gener* representation

- Generative Lindenmayer system
- A set of production rules with parameters
- Rules are activated and generate a genome
- E.g.

```
10                                ← iterate 10 times
n0=56.000000                      ← initial values for parameters
n1=55.000000
---
                                ← production rules begin
P3
P3(n0,n1): n0>10.0 | X(2.000000)C(1.000000)R(2.000000)X(1.000000)?:n0>1 |
P3(12.000000-n1,2.000000)P2(3.000000,2.000000)
P2(n0,n1): n0>2.0 | X(3.000000)q(2.000000)X(1.000000)^P0(n0-
5.000000,n1)X(2.000000)X(1.000000)?
```

# *Simil* representation

- BODY:
  - list of body components (sticks) with “links” and properties
  - joined according to links’ similarity
- BRAIN:
  - list of NN connections, effectors, senses with “links” and properties
  - connected according to links’ similarity

```

stick  ( 5,  9,  9,  6 )  ( 4,  7,  6,  5 )  5 4 1 9 8 1 9 8 4 0 6
stick  ( 5,  9,  9,  8 )  ( 0,  7,  6,  6 )  9 7 1 3 4 1 6 6 4 7 0
stick  ( 8,  0,  0,  2 )  ( 2,  4,  9,  3 )  9 7 5 4 3 4 1 1 5 8 0
stick  ( 3,  9,  7,  2 )  ( 3,  2,  5,  5 )  3 1 2 6 9 7 4 9 8 3 0

conn   ( 1,  1,  0,  8 )  |  ( 9,  4,  0,  4 )  5
conn T ( 5,  1,  0,  3 ) @ ( 7,  8,  7,  7 )  6
conn   ( 1,  1,  0,  8 )  |  ( 9,  4,  6,  4 )  5

```

# *Biol* representation

- 26 characters of latin alphabet
- every sequence starting after **aa** and extending to the first **zz** sequence is considered a gene
- this encoding exhibits properties similar to DNA
- sample genome:  
aaasdfgvcxaadzsd़fgbvcxsfdrgthnbzzvcxsdfgzz
- Operators: horizontal gene transfer, crossing over, substitution, deletion, insertion, gene duplication, translocation

# *Chem* representation

- “chemical” substances in 3D
- transforms initial substances into an organism
- rules of growth of body and brain
- saturation threshold to fire a rule
- propagation and changes of substances along growth directions
- propagation of properties of grown elements

4 rules

3 substances

2 properties

0.144 0.833 0.940, 0.546 0.249 grow stick, 0.859 0.604 0.707, 0.516 0.600  
0.941 0.876 0.303, 0.038 0.630 grow stick, 0.902 0.320 0.035, 0.648 0.525  
0.767 0.201 0.636, 0.751 0.022 grow stick, 0.321 0.661 0.663, 0.311 0.319  
0.951 0.283 0.454, 0.428 0.997 grow stick, 0.996 0.554 0.162, 0.192 0.160

# Messy representation

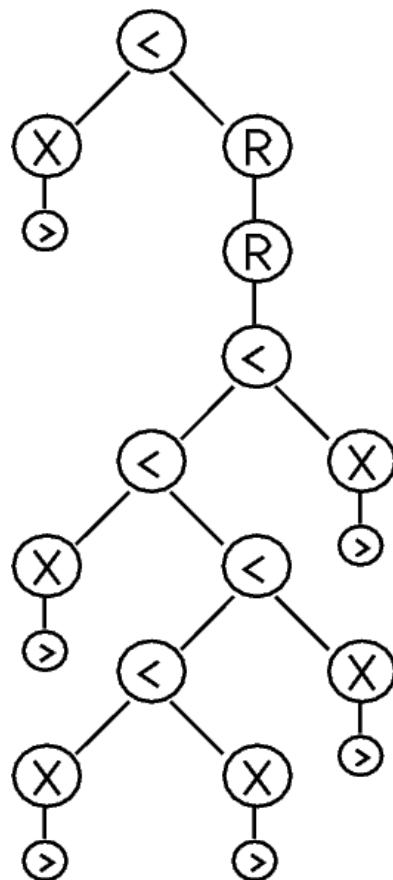
- any string of characters is a valid genotype
- simple genetic operators
- various interpretation approaches are possible, e.g.:
  - sections correspond to elements of body and brain
  - Z AAAAA BCLQU BCLQU BCLQU YYYYB BCNDG BCLQU BCLQU ...
  - SectionTag Z starts parts section:
  - AAAAA – label, BCLQU BCLQU BCLQU ... – coordinates
  - Labels are recalculated as follows:
    - AAAAA =  $0*26^4 + 0*26^3 + 0*26^2 + 0*26^1 + 0*26^0 = 0$ ,
    - YYYYB =  $24*26^4 + 24*26^3 + 24*26^2 + 24*26^1 + 1*26^0 = 11406097$ , ...

# *Devel* representation

- encodes development
- codes are commands of differentiation
- these instructions are executed in parallel
- supports symmetry and modularity
- development starts with a single, undifferentiated ancestor cell
- stops when all the cells are differentiated

<<Fm<<X>N[1:-2.25791][G:3.49452]>X>M,X>X

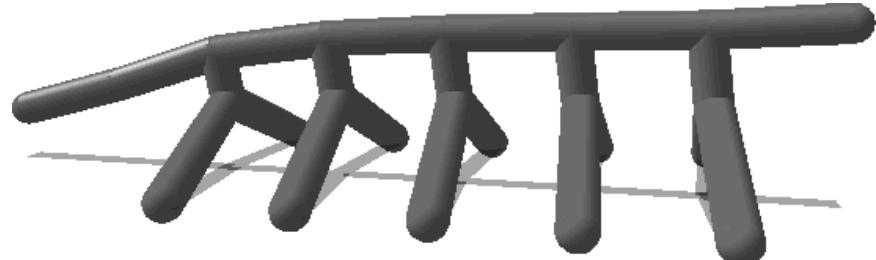
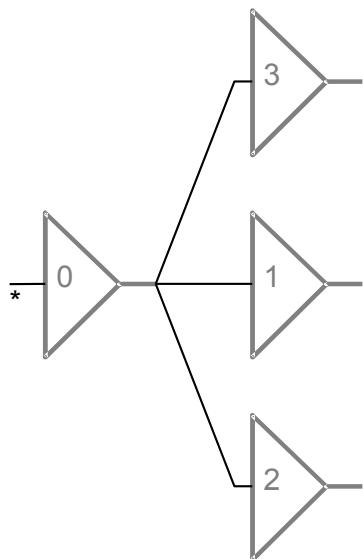
# *Devel* development



<X>RR<<X><<X>X>X>X

# *Devel* examples

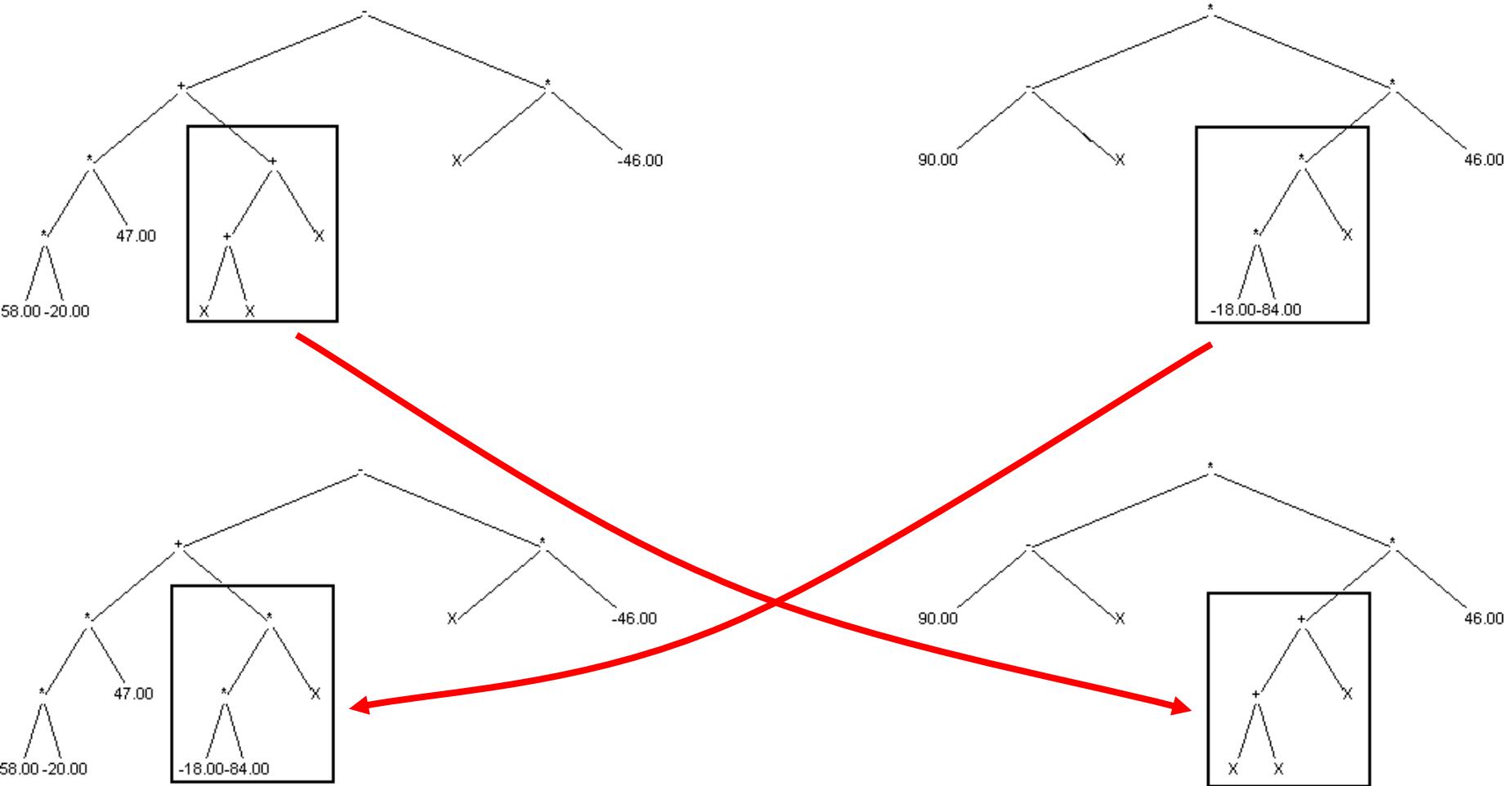
- Neural links are duplicated when a neuron divides
- Parts of the genome may be repeated



$rr<X>\#5<, <X>RR<<11$   
 $X>LX>LX>>X$

$<X>N< [* : 5] > [-1 : 5] <><>>$

# *Devel* crossing-over



# Mutation and repair

- Mutation: modification of every element of a genotype. Small, local changes
- Validity test: many aspects
- Repair: attempt to correct an invalid genotype
  - ensure each property value is within allowed interval
  - correct neural links
  - contextual: match brackets, etc.
  - ...