Morphogenesis and evolution of Foraminifera in Framsticks

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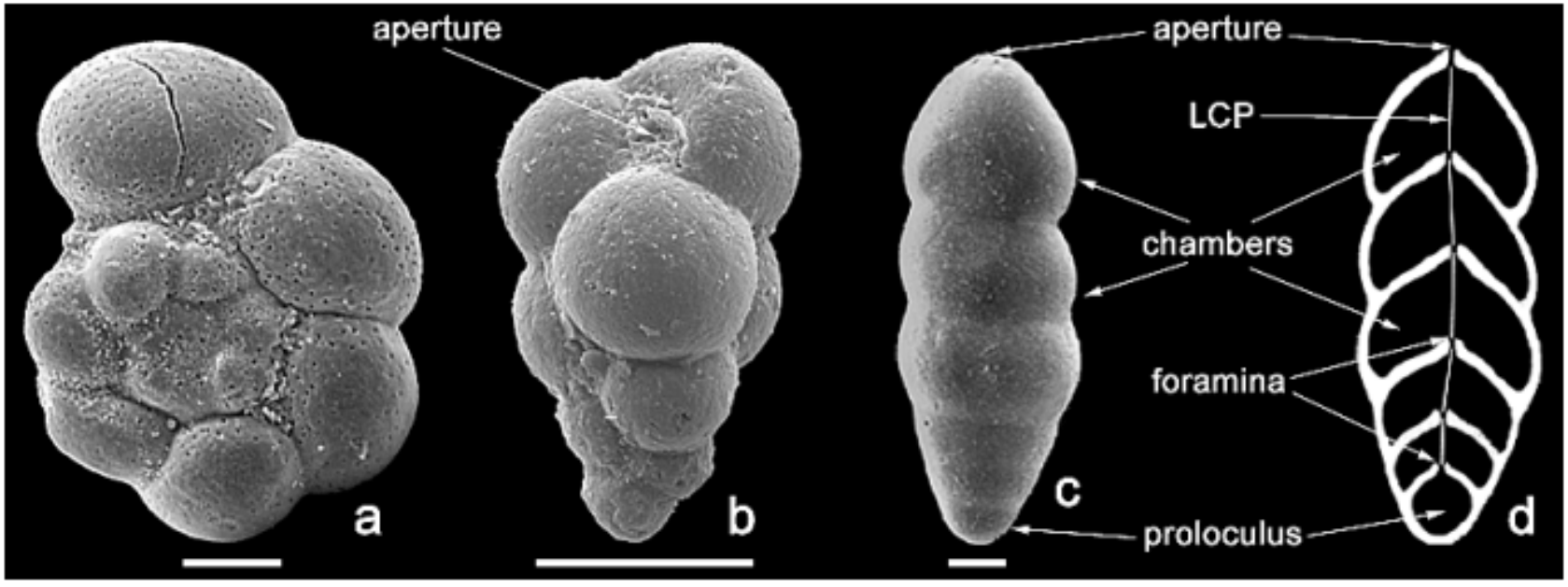
www.framsticks.com/foraminifera



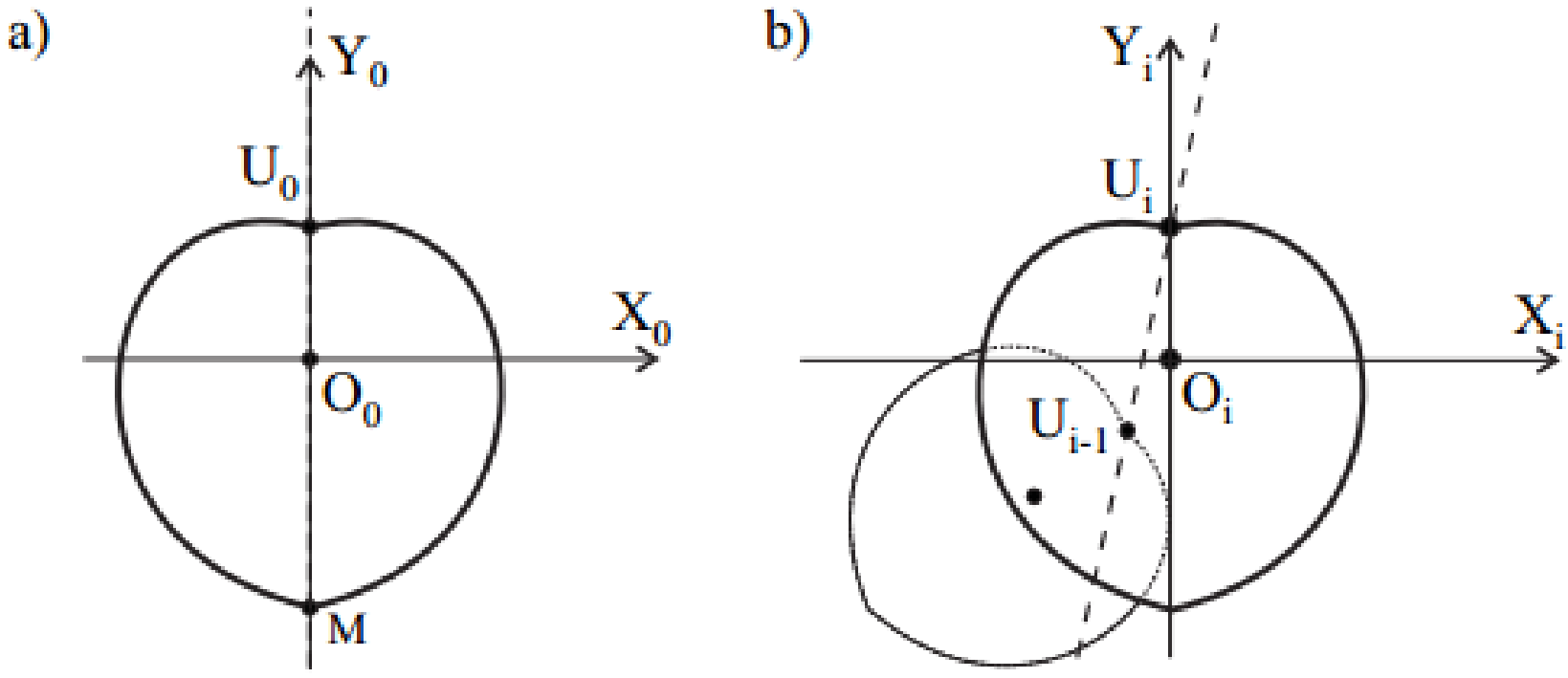
Examples of foraminiferal morphotypes. Scale bar = 50 μm.

Some diagrams shown here come from, and the algorithm is based on: Łabaj, P., Topa, P., Tyszka, J., & Alda, W. (2003). 2D and 3D numerical models of the growth of foraminiferal shells. In LNCS 2657 (ICCS 2003), Springer.

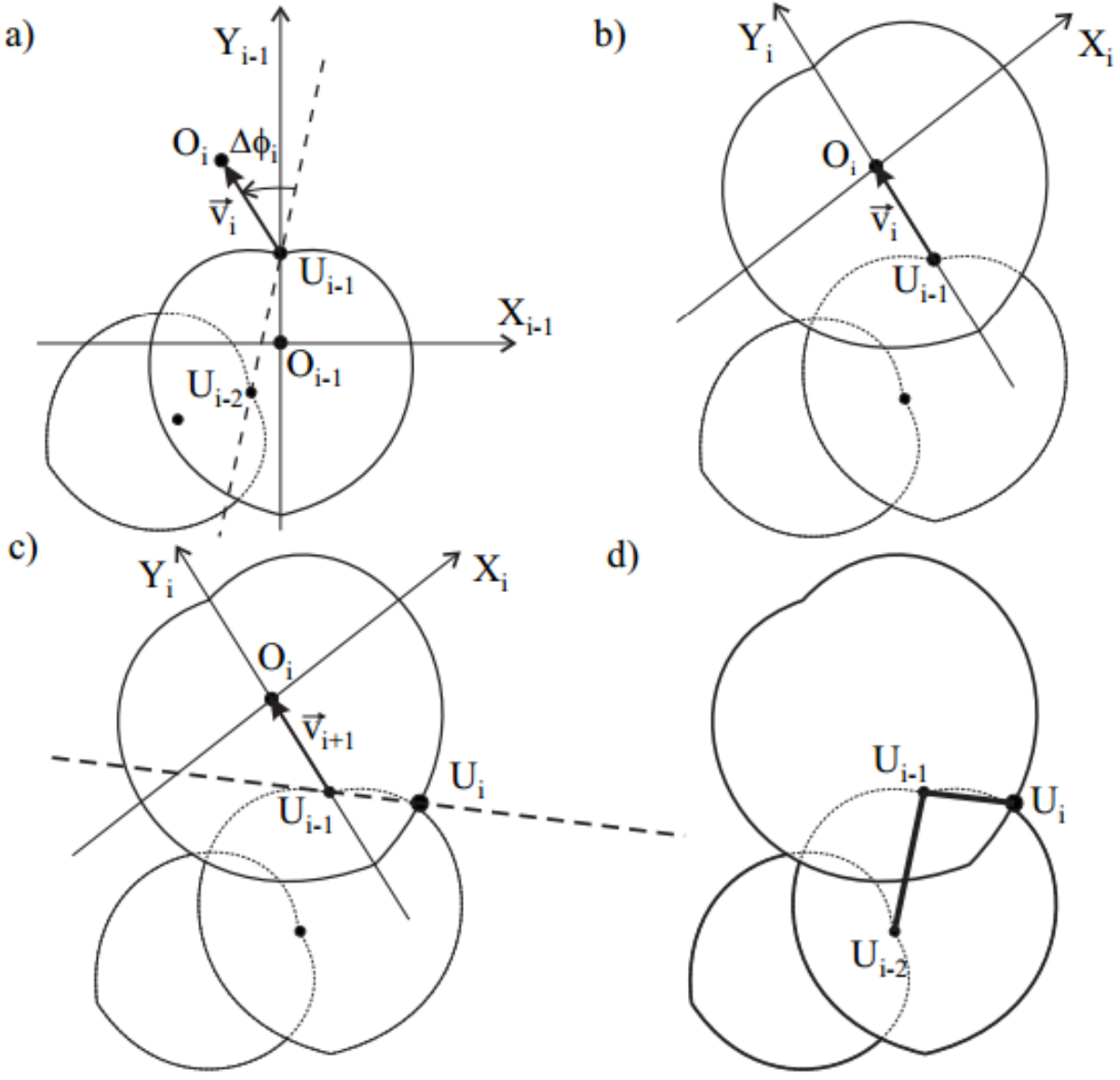
Concepts used in the growth algorithm

- O_i – center of the chamber
- U_i – aperture point
- v_i – growth vector
- reference growth axis

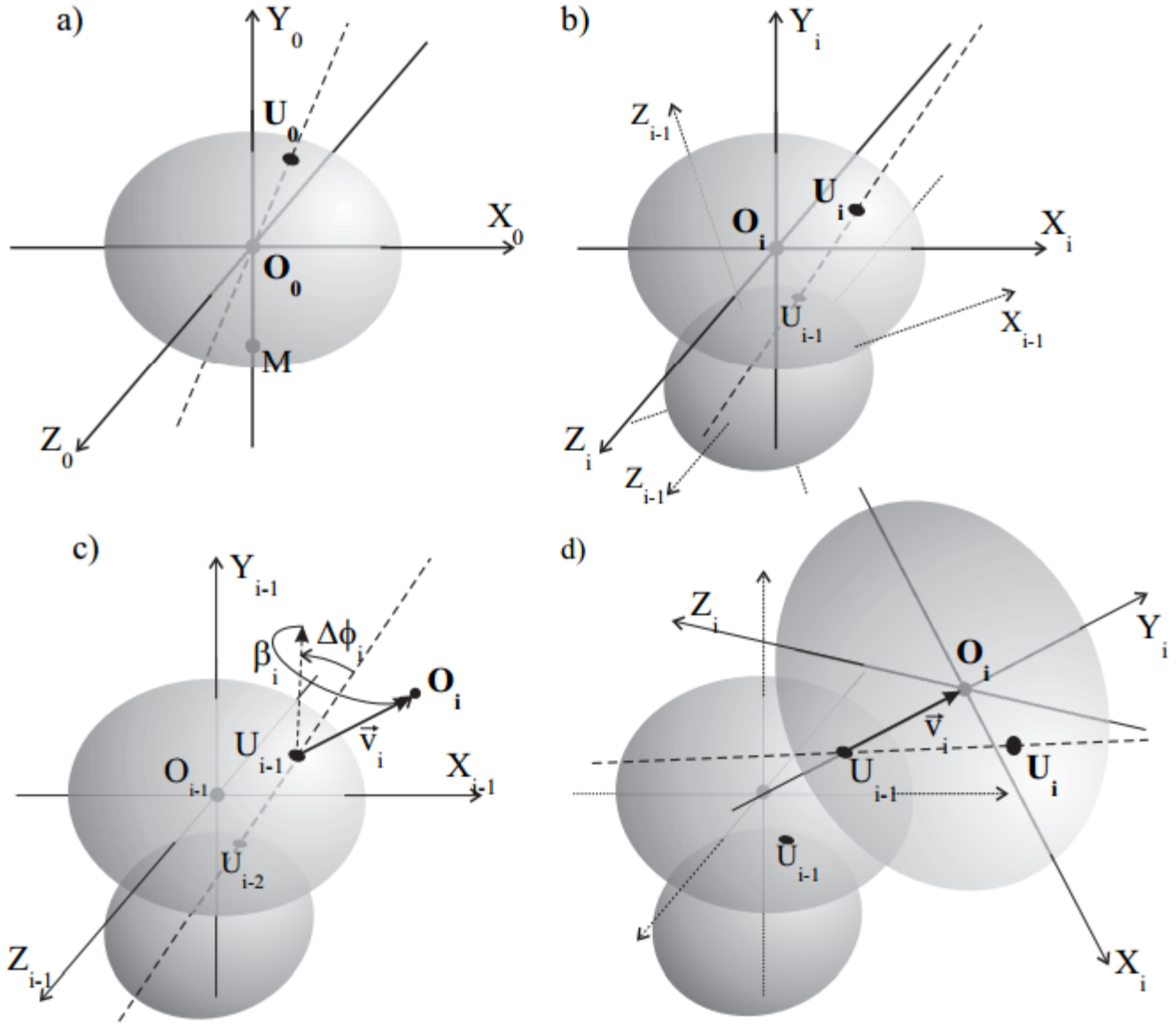
The reference growth axis (2D example)



Creation of a new chamber (2D example)



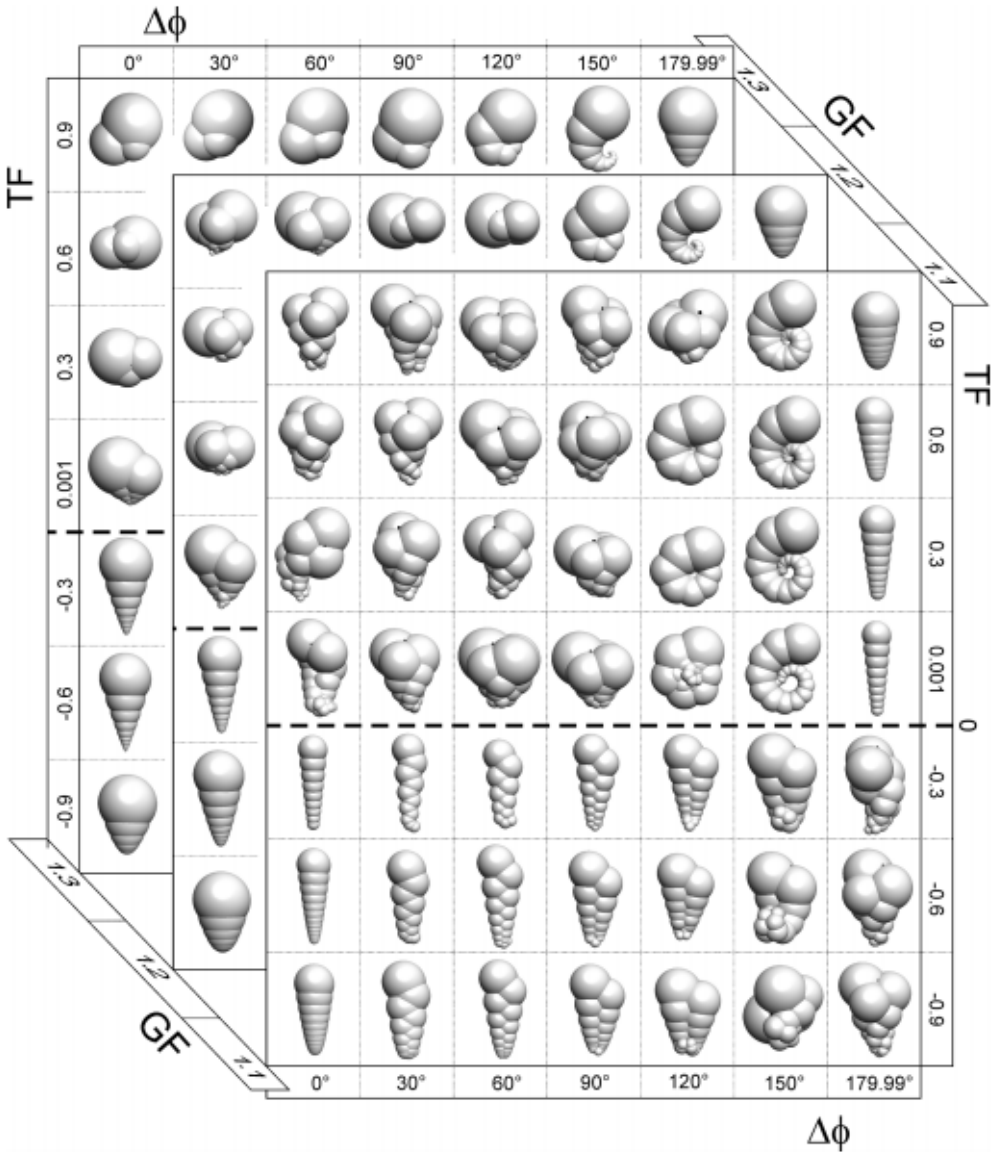
Creation of a new chamber (3D example)



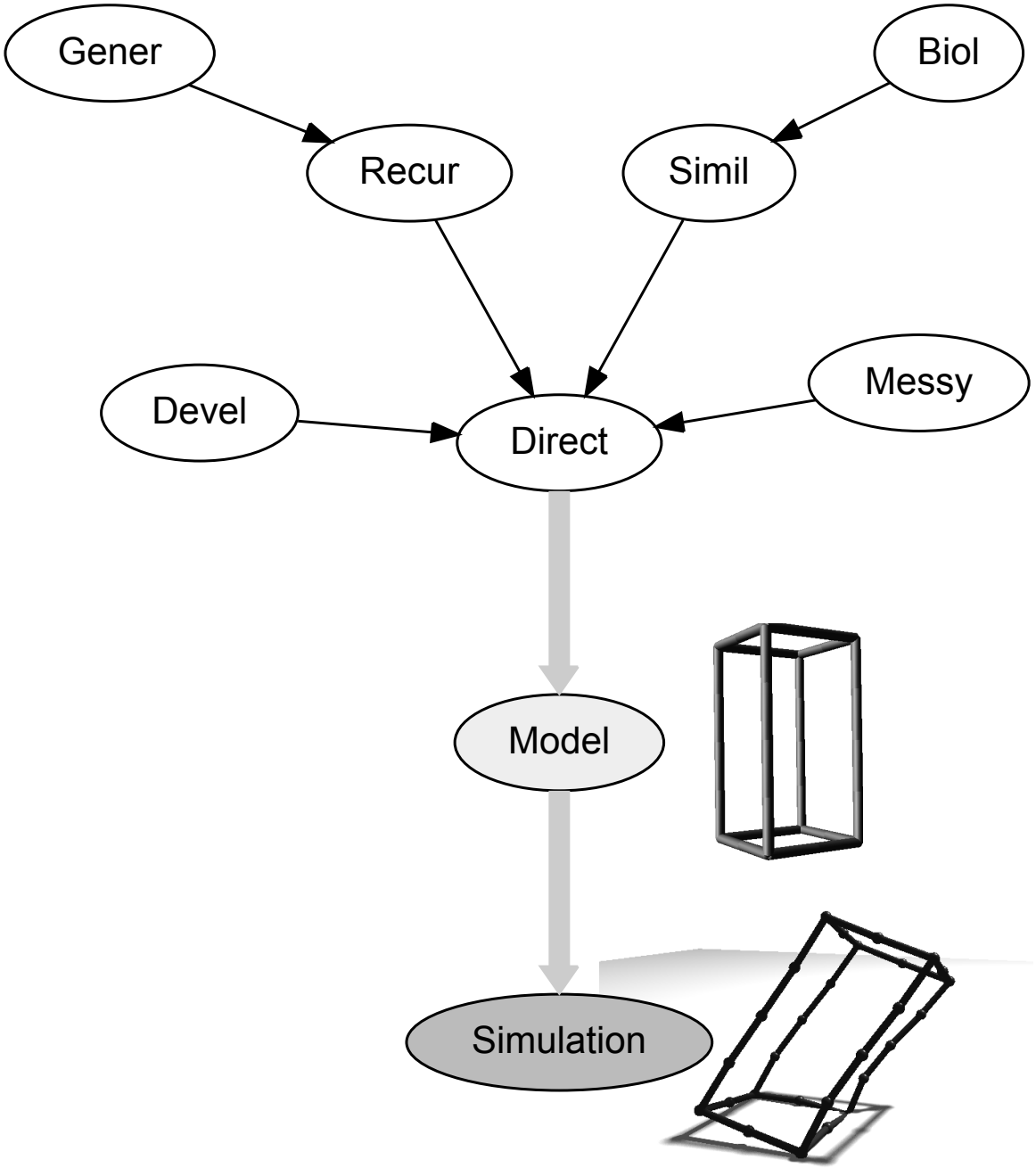
Growth simulation parameters

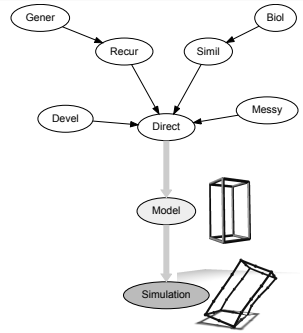
- k_x, k_y, k_z – chamber scaling rates
  (can be assumed equal: growth factor $GF = k_x = k_y = k_z$)
- TF – translation factor, $TF \in [-1, 1]$
- $\Delta\phi$ – deviation angle, $\Delta\phi \in [-180°, 180°]$
- β – rotation angle, $\beta \in [-180°, 180°]$

Morphospace resulting from the model



The hierarchy of genetic encodings in Framsticks

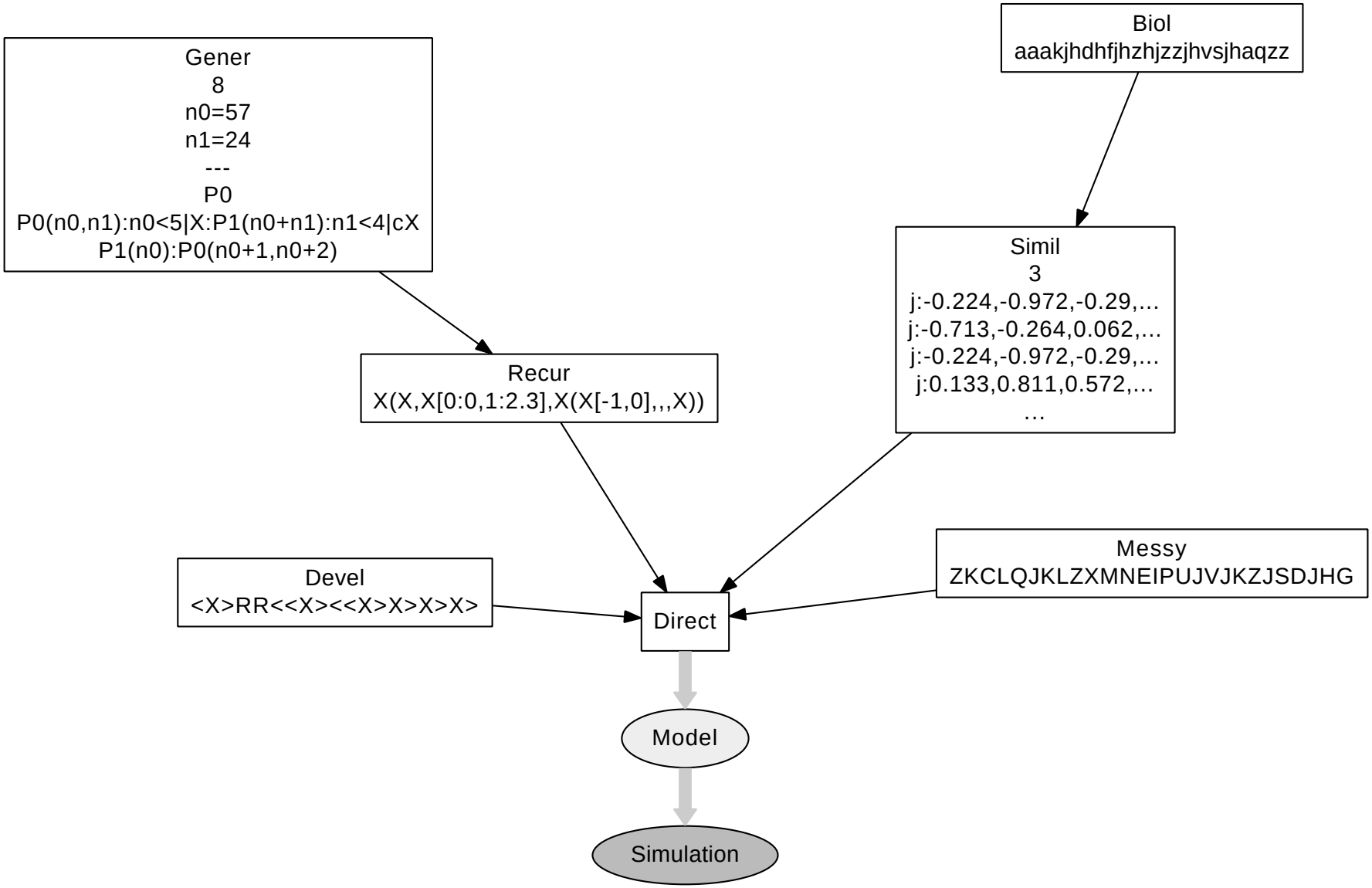




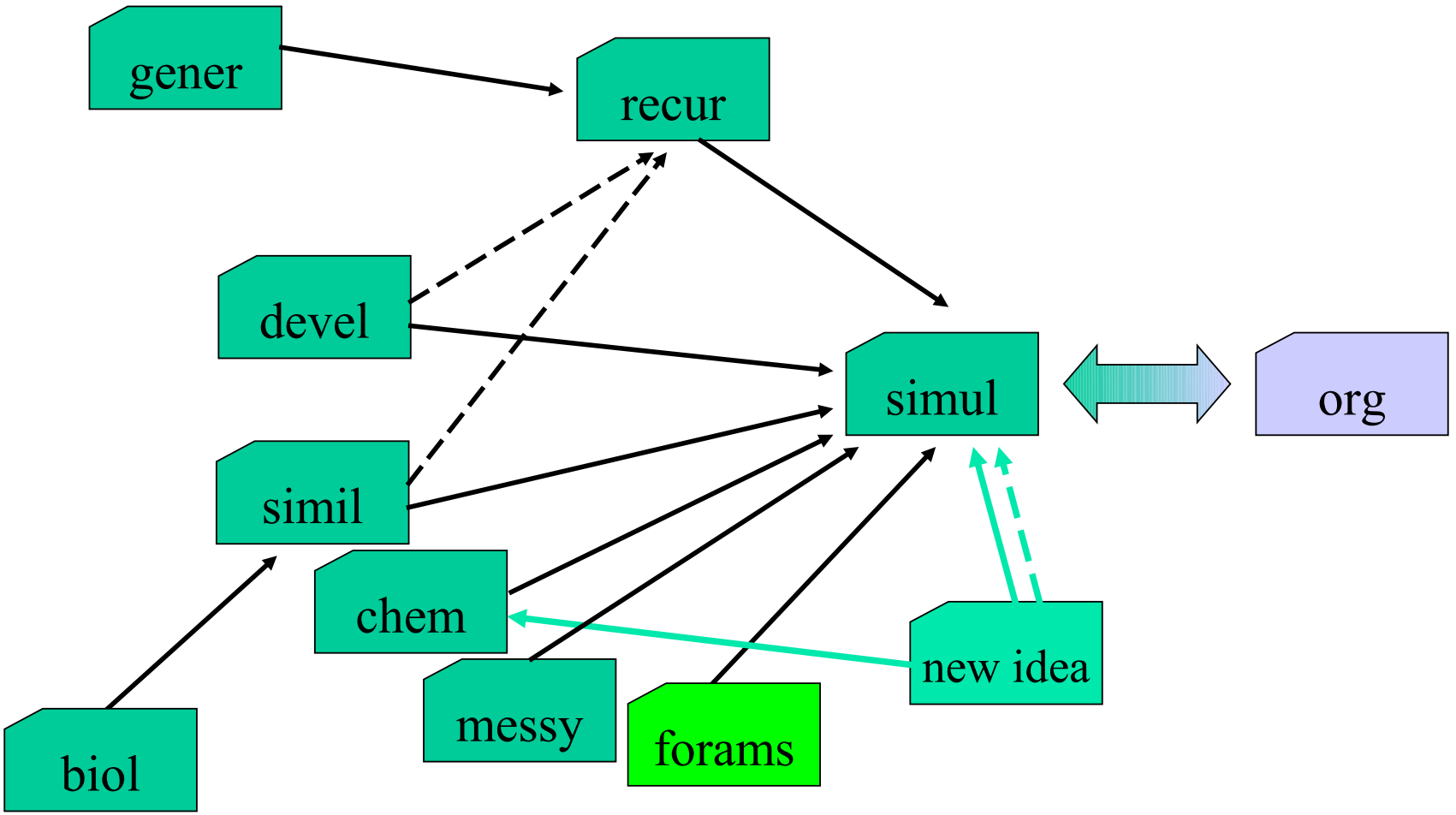
The hierarchy of genetic encodings in Framsticks

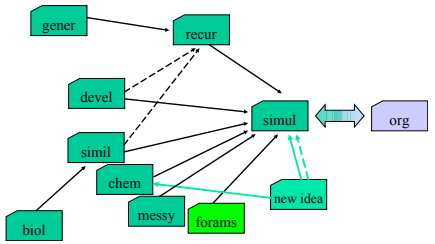
Evolution (search) works in genetic spaces – different topologies that influence performance of evolution!

Specialized genetic operators for each genetic encoding



Adding foraminiferal genetics to Framsticks





Adding foraminiferal genetics to Framsticks was easy – it becomes one of many existing genetic representations, and a framework supporting various genetic representations exists. This is because one of the major research areas in Framsticks is investigation of genetic encodings, genotype-phenotype mappings, fitness landscapes, and evolutionary performance.

Foraminiferal genotype in Framsticks

"n"	"number of chambers"	d	1	15	6
"sx"	"scale x"	f	1.0	1.1	1.05
"sy"	"scale y"	f	1.0	1.1	1.05
"sz"	"scale z"	f	1.0	1.1	1.05
"tr"	"translation factor"	f	−1	1	0
"a1"	"angle 1"	f	−3.14	3.14	0
"a2"	"angle 2"	f	−3.14	3.14	0

Foraminiferal genotype in Framsticks (C++)

```
// This file is a part of the Framsticks GDK.

ParamEntry fF_growth_params::paramtab[] =
{
 { "n" , 0, CANOMITNAME, "number of chambers", "d 1 15 6", FIELD(number_of_chambers), },
 { "sx", 0, CANOMITNAME, "scale x",       "f 1.0 1.1 1.05", FIELD(scalex), },
 { "sy", 0, CANOMITNAME, "scale y",       "f 1.0 1.1 1.05", FIELD(scaley), },
 { "sz", 0, CANOMITNAME, "scale z",       "f 1.0 1.1 1.05", FIELD(scalez), },
 { "tr", 0, CANOMITNAME, "translation factor", "f -1 1 0", FIELD(translation), },
 { "a1", 0, CANOMITNAME, "angle 1",  "f -3.1415 3.1415 0", FIELD(angle1), },
 { "a2", 0, CANOMITNAME, "angle 2",  "f -3.1415 3.1415 0", FIELD(angle2), },
};
```

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Sample genotypes:

- /*F*/ 6, 1.05, 1.05, 1.05, 0.0, 0.0, 0.0

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 { "a2", 0, CANOMITNAME, "angle 2",  "f -3.1415 3.1415 0", FIELD(angle2), },
};
```

Sample genotypes:

- /*F*/ 6, 1.05, 1.05, 1.05, 0.0, 0.0, 0.0
- /*F*/ 6, 1.05, 1.05, 1.05, 0.312, 0.0, 0.0

Foraminiferal genotype in Framsticks (C++)

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ParamEntry fF_growth_params::paramtab[] =
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```

Sample genotypes:

- /*F*/ 6, 1.05, 1.05, 1.05, 0.0, 0.0, 0.0
- /*F*/ 6, 1.05, 1.05, 1.05, 0.312, 0.0, 0.0
- /*F*/ 6, 1.05, 1.05, 1.038, 0.312, 0.0, 0.0

Foraminiferal genotype in Framsticks (C++)

```
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Sample genotypes:

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- /*F*/ 6, 1.05, 1.05, 1.05, 0.312, 0.0, 0.0
- /*F*/ 6, 1.05, 1.05, 1.038, 0.312, 0.0, 0.0

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Sample genotypes:

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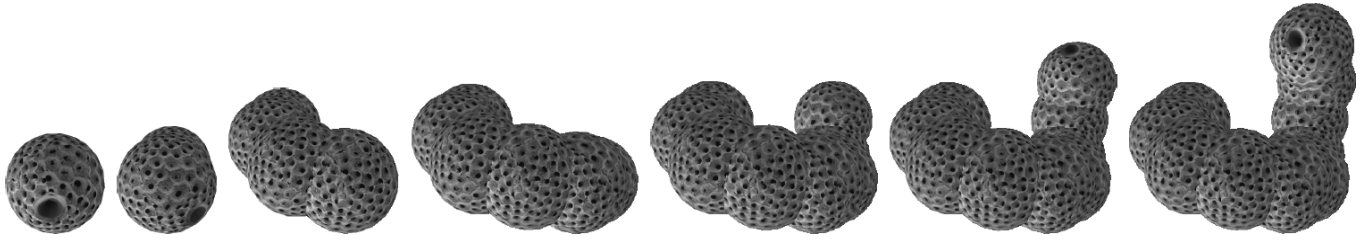
- /*F*/ 6, 1.05, 1.05, 1.05, 0.312, 0.0, 0.0
- /*F*/ 6, 1.05, 1.05, 1.038, 0.312, 0.0, 0.0

Source code:

http://www.framsticks.com/trac/framsticks/browser/cpp/frams/genetics/fF/fF_genotype.cpp

Foraminifera genotype and phenotype

N	K_x	K_y	K_z	TF	$\Delta\phi$	$\Delta\beta$
10	1	1	1	-0.02	0.64	0.72



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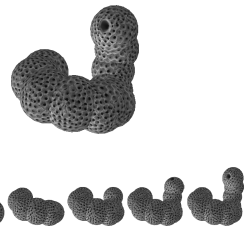
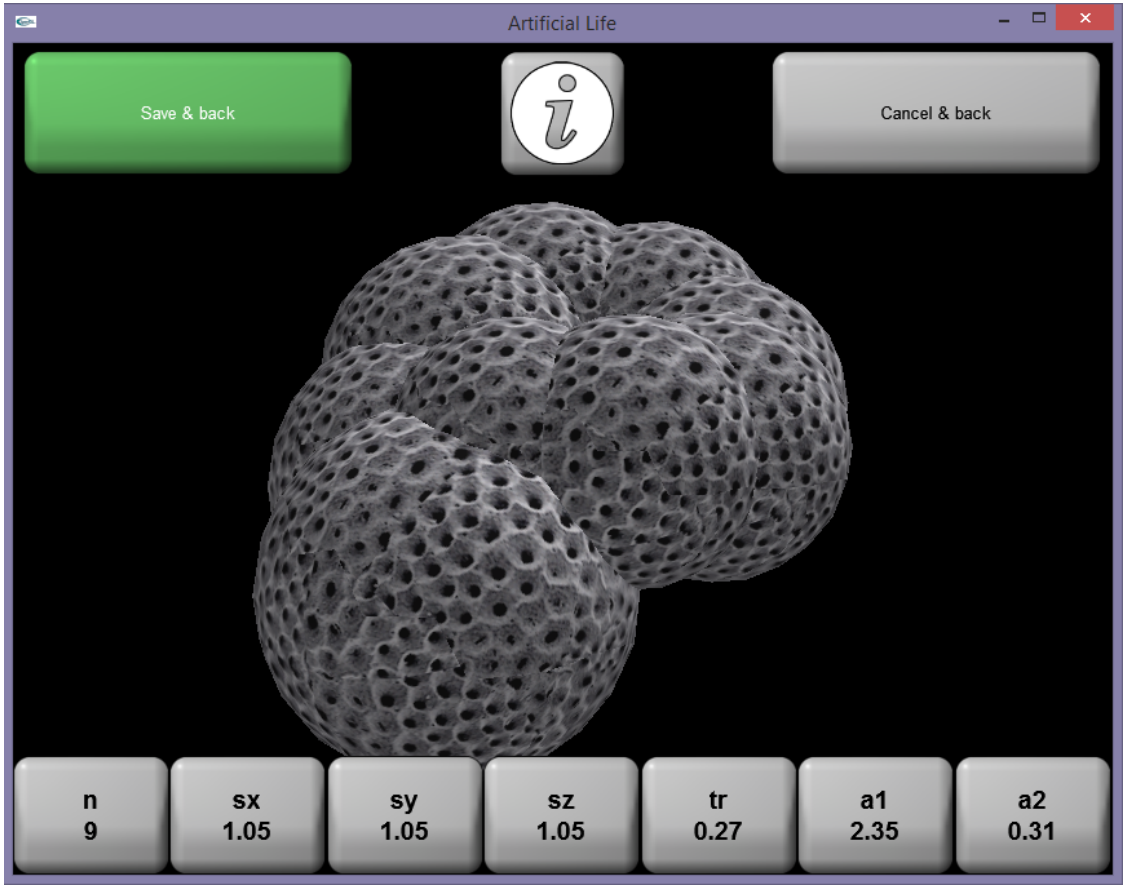


An extremely simple model, but reality is so complex and intertwined that there is (yet) no reasonable, more detailed model.

Genotype → Phenotype



Maciej Komosinski, Agnieszka Mensfelt, Paweł Topa, and Jarosław Tyszka. Application of a morphological similarity measure to the analysis of shell morphogenesis in Foraminifera. In Aleksandra Gruca et al., editors, Advances in Intelligent Systems and Computing. Springer, 2015.

Evolution

- Changes in genotype (genotype space)
- ...affect fitness of the corresponding phenotype (in phenotype space)
- “fitness landscape”

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- Mutation
- Crossing over

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- Mutation: creep
- Crossing over: average

Evolution

- Changes in genotype (genotype space)
- ...affect fitness of the corresponding phenotype (in phenotype space)
- "fitness landscape"

- Genotype consists of values (numbers)
- Mutation: creep
- Crossing over: average

- Fitness:
  - model: length, width, depth, body volume, surface area, ...
  - simulation: height, speed, ...

Putting it all together

Genetics, morphology, simulation, evolution

Let's see how it works!

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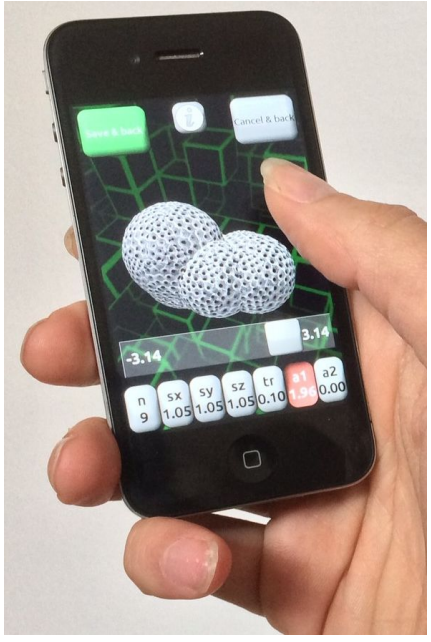

Putting it all together
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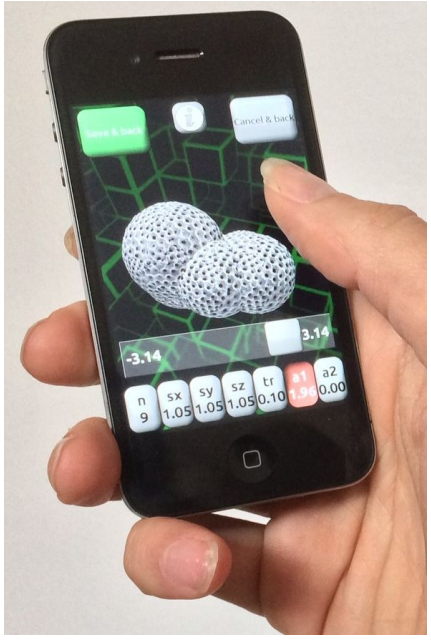
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