

Morphogenesis and evolution of Foraminifera in Framsticks

Maciej Komosinski

www.framsticks.com

Details of this research are available in [Kom+16]
and at www.framsticks.com/foraminifera.

Foraminiferal
morphotypes

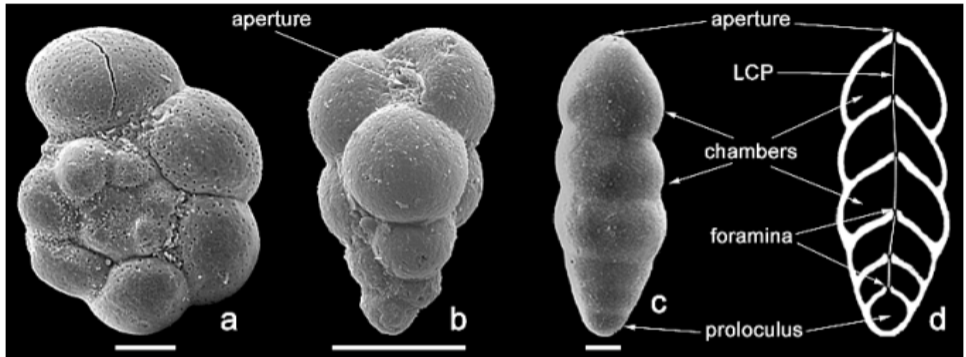
Growth
algorithm

Framsticks
genetics

Foraminifera representation

Evolution

Demo



Examples of foraminiferal morphotypes. Scale bar = 50 μm .

Some diagrams shown here come from, and the algorithm is based on [Lab+03].

Concepts used in the growth algorithm

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

The reference growth axis (2D example)

Foraminiferal
morphotypes

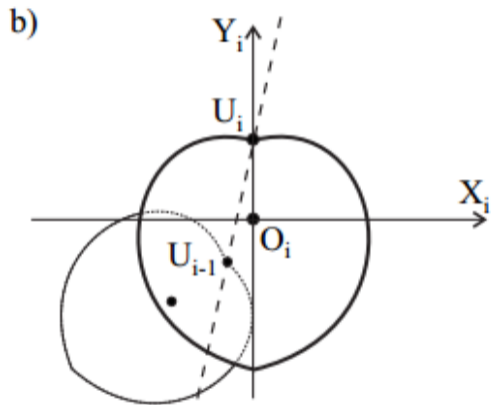
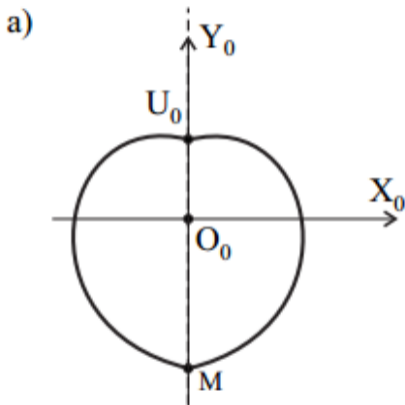
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Creation of a new chamber (2D example)

Foraminiferal morphotypes

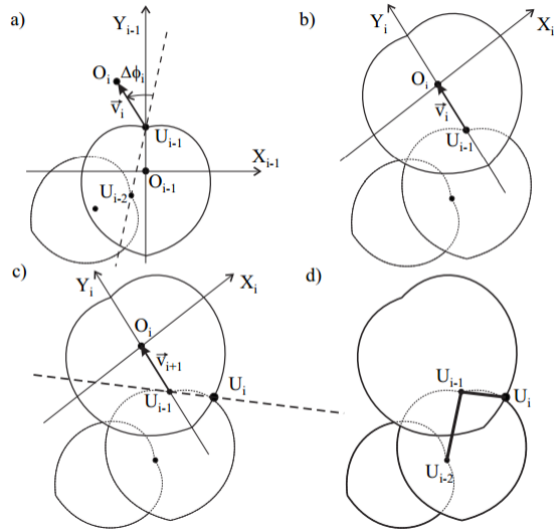
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Creation of a new chamber (3D example)

Foraminiferal morphotypes

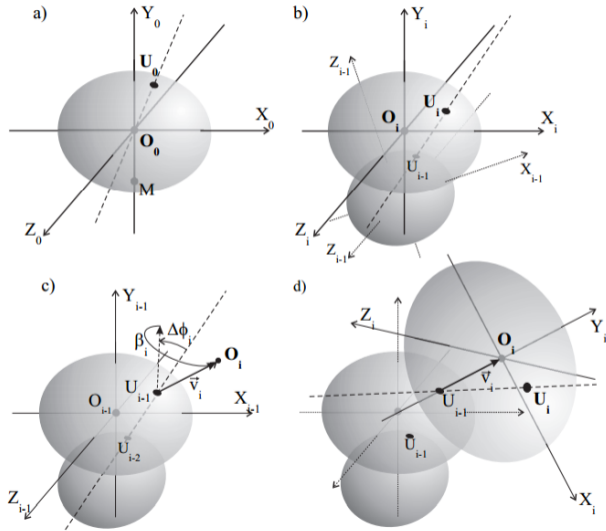
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Growth simulation parameters

Foraminiferal
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- 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, $\Delta\phi \in [-180^\circ, 180^\circ]$
- β – rotation angle, $\beta \in [-180^\circ, 180^\circ]$

Morphospace resulting from the model

Foraminiferal morphotypes

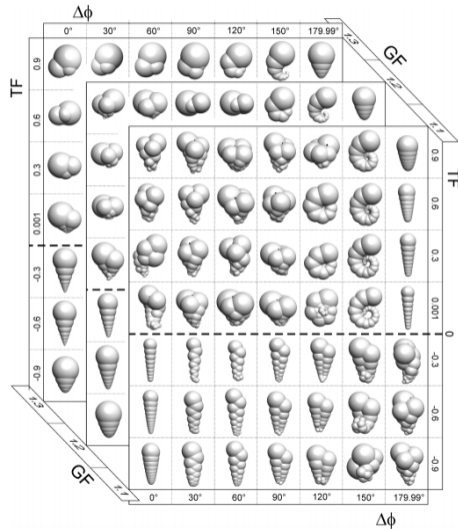
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The hierarchy of genetic encodings in Framsticks

Foraminiferal
morphotypes

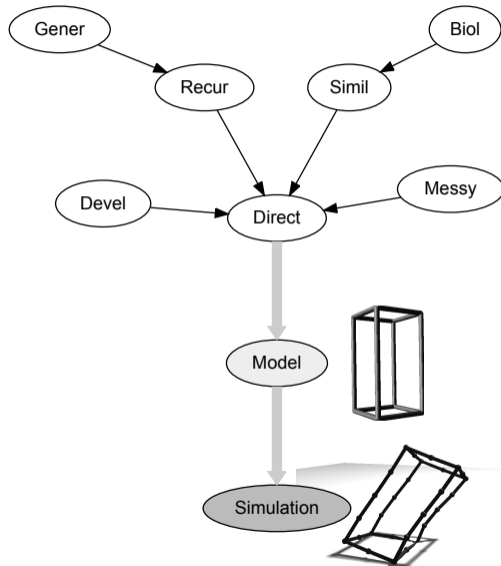
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Specialized genetic operators for each genetic encoding

Foraminiferal morphotypes

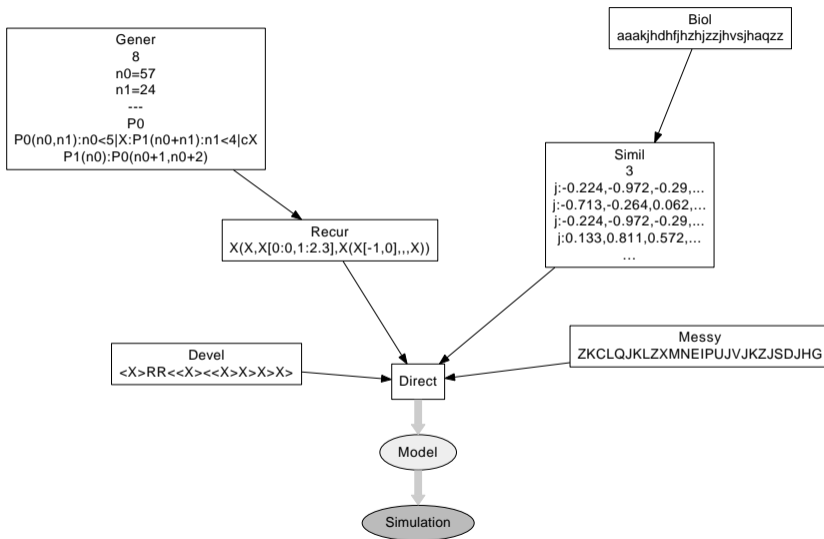
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Adding foraminiferal genetics to Framsticks

Foraminiferal morphotypes

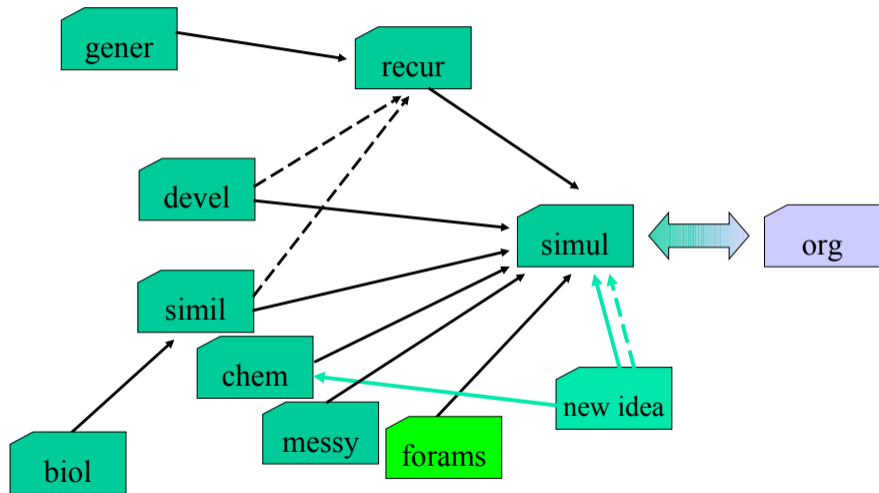
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Foraminiferal genotype in Framsticks

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"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++)

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```
// 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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```
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```

```
ParamEntry fF_growth_params::paramtab[] =  
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  { "sx" , 0, CANOMITNAME, "scale x", "f 1.0 1.1 1.05", FIELD(scalex), },  
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};
```

Sample genotypes:

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

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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

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  { "sy" , 0, CANOMITNAME, "scale y", "f 1.0 1.1 1.05" , FIELD(scaley), },  
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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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  { "sy" , 0, CANOMITNAME, "scale y", "f 1.0 1.1 1.05" , FIELD(scaley), },  
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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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  { "sz" , 0, CANOMITNAME, "scale z", "f 1.0 1.1 1.05" , FIELD(scalez), },  
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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
- /*F*/ 6, 1.05, 1.05, 1.038, 0.312, 0.0, 0.0

Source code: https://www.framsticks.com/trac/framsticks/browser/cpp/frams/genetics/fF/fF_genotype.cpp

Foraminifera genotype and phenotype

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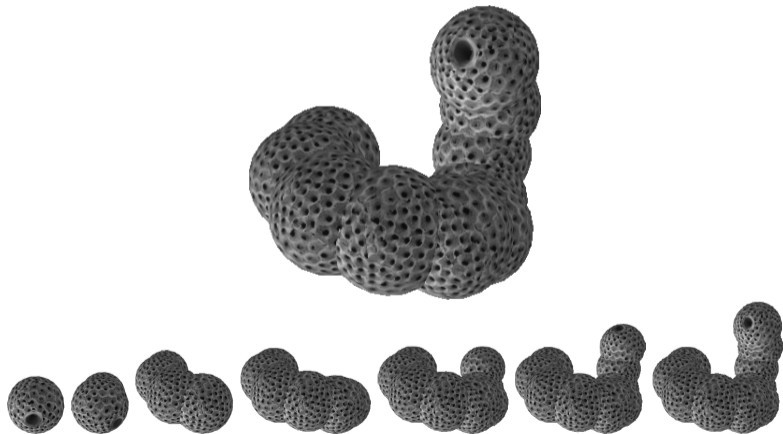
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N	K_x	K_y	K_z	TF	$\Delta\phi$	$\Delta\beta$
10	1	1	1	-0.02	0.64	0.72



Genotype → Phenotype

Foraminiferal
morphotypes

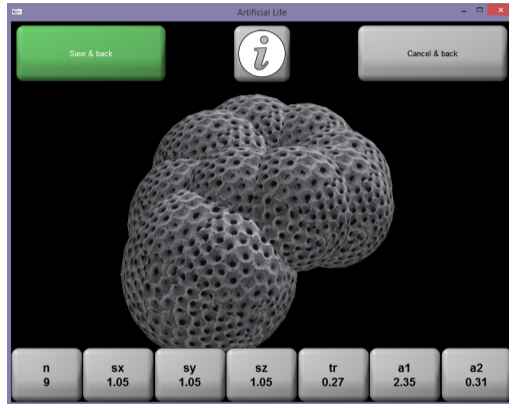
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The phenotype development process and its properties are described in more detail in [Kom+16].

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

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

- Genotype consists of values (numbers)
- Mutation
- Crossing over

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- 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

- 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

**Foraminiferal
morphotypes**

**Growth
algorithm**

**Framsticks
genetics**

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Let's see how it works!

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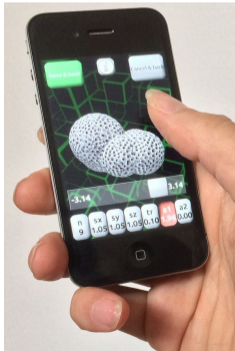
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Let's see how it works!



References I

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- [Kom+16] Maciej Komosinski et al. "Application of a morphological similarity measure to the analysis of shell morphogenesis in Foraminifera". In: *Man–Machine Interactions 4*. Ed. by Aleksandra Gruca et al. Vol. 391. Advances in Intelligent Systems and Computing. Springer, 2016, pp. 215–224. ISBN: 978-3-319-23436-6. DOI: [10.1007/978-3-319-23437-3_18](https://doi.org/10.1007/978-3-319-23437-3_18). URL: <http://www.framsticks.com/files/common/ForaminiferaGenotypePhenotypeMapping.pdf>.
- [Łab+03] Paweł Łabaj et al. "2D and 3D numerical models of the growth of foraminiferal shells". In: *LNCS 2657 (ICCS 2003: International Conference Proceedings)*. Springer. 2003, pp. 669–678.