Modeling Foraminifera in Framsticks. Genotype, phenotype, ecosystem

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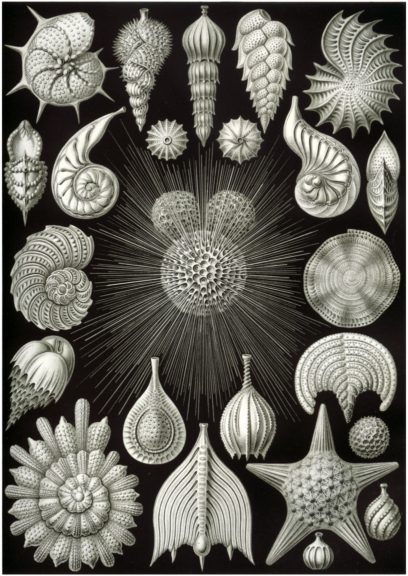
Outline

What are Foraminifera?



Ernst Haeckel, *Kunstformen der Natur*, 1904.

What are Foraminifera?

Foraminifera in the Indian Ocean, Southeast Coast of Bali. Field width = 5.5 mm.
Microphotographie personnelle by Psammophile.

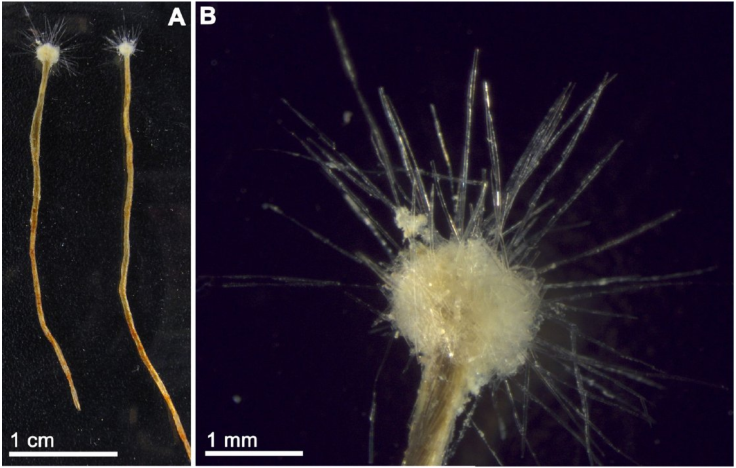
What are Foraminifera?

Tests of foraminifera extracted sand from the beach of Ngapali (Myanmar).
Microphotographie personnelle by Psammophile.

What are Foraminifera?

Star sand on Hoshizuna-no-hama, Iriomote, Okinawa.
Own work by Geomr.

What are Foraminifera?



Spiculosiphon oceana, a species of giant foraminiferan from the Mediterranean Sea. (A) General view of the holotype and the paratype (from left to right, respectively) of Spiculosiphon oceana. (B) Detail of capitate region of the holotype, showing the globelike, central structure and the radiating tracts of spicules.

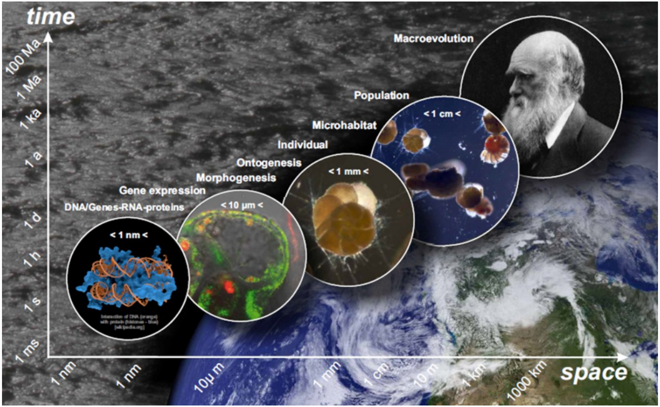
A giant foraminifer that converges to the feeding strategy of carnivorous sponges. Zootaxa 3669 (4): 571–584. doi:10.11646/zootaxa.3669.4.9

Motivations: why Foraminifera?

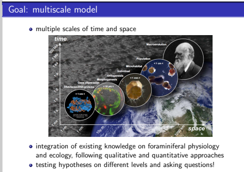
- single-celled organisms
- abundant as fossils for the last 540 million years (since the earliest Cambrian)
- diverse morphologies, from 100 micrometers to 20 centimeters
- catch their food with a network of thin pseudopodia
- 4,000 species: 40 species are planktonic (float in the water), others are benthic (bottom of the ocean)
- applications: biostratigraphy, paleoclimatology, paleoceanography, bioindicators, oil exploration
- much of our current knowledge about climate and past history of Earth comes from studies of foraminifera

Goal: multiscale model

- multiple scales of time and space



- integration of existing knowledge on foraminiferal physiology and ecology, following qualitative and quantitative approaches
- testing hypotheses on different levels and asking questions!



1. Testing hypotheses on different levels and asking questions – to make the model complete and to discover missing relationships.
2. The Framsticks simulator provides infrastructure needed to model and simulate Foraminifera.

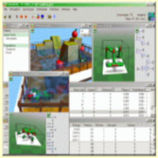
Framsticks simulation environment

Framsticks: general information

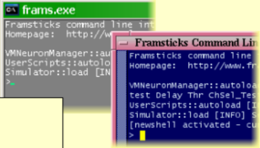
- simulation software: physics, “body” and “brain”, evolution
- developed since 1996
- authors and main developers: Maciej Komosinski and Szymon Ulatowski
- volunteers involved in technical support, development, and experiments
- `www.framsticks.com`

Framsticks software – desktop, mobile, client-server

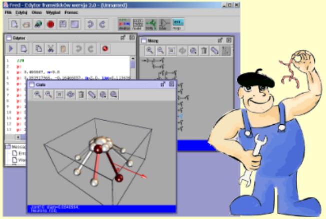
Simulator GUI



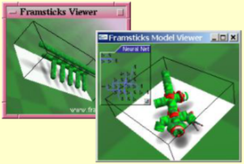
Simulator command-line



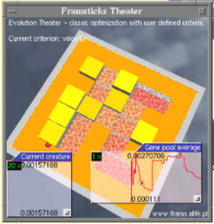
Visual Editor – FRED



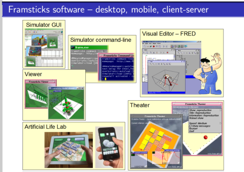
Viewer



Theater



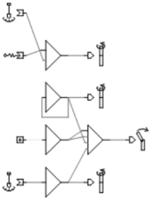
Artificial Life Lab

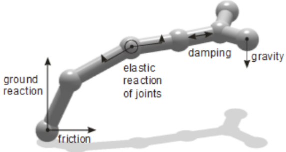


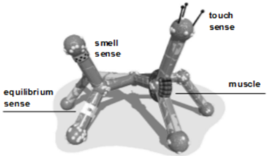
Command-line and server for intensive computation experiments, GUI for interactive investigation, client-server for distributed, parallel experiments, FRED and theater for beginners.

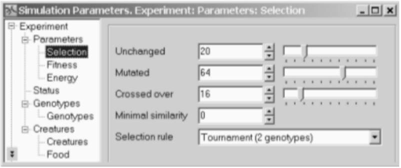
Main points of users' interest

- simulation
- biology, evolution
- robotics
- neuroscience
- cognitive science
- computer science
- visualization
- education and understanding
- simplicity / complexity
- entertainment
- versatility

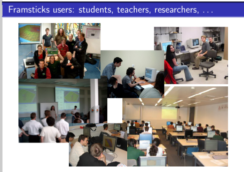








Framsticks users: students, teachers, researchers, . . .



Used in summer schools, e.g. recently in 2012: Princeton Institute for Advanced Study – Summer School in Computation and Biology.

Sample uses and experiments

- synthesizing (building) agents
- studying agents' behaviors
- optimizing agents
- designing genetic representations
- studying evolutionary dynamics, coevolution, migration, etc.
- evolving neural and fuzzy controllers
- understanding evolved brains
- evolving communication and cooperation
- designing custom user experiments

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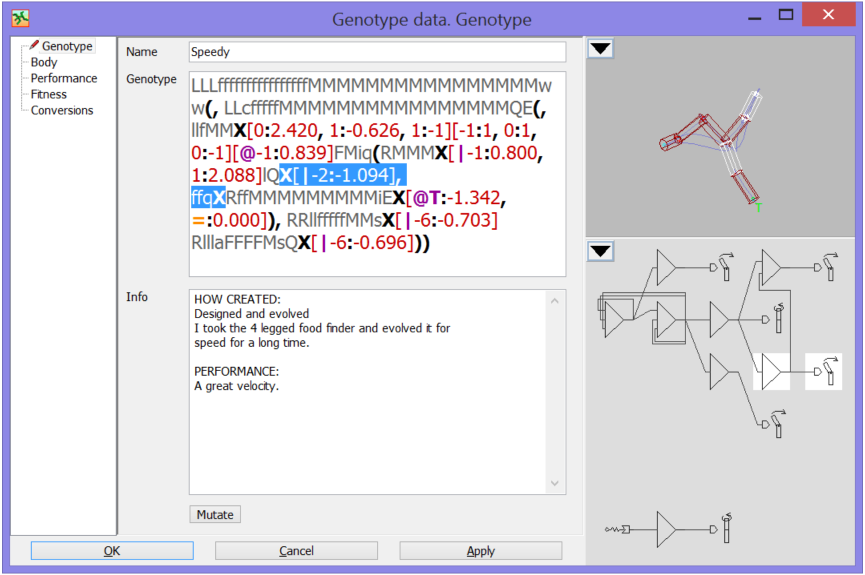
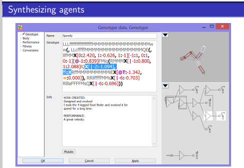
A very broad and open-ended range of experiments and uses!

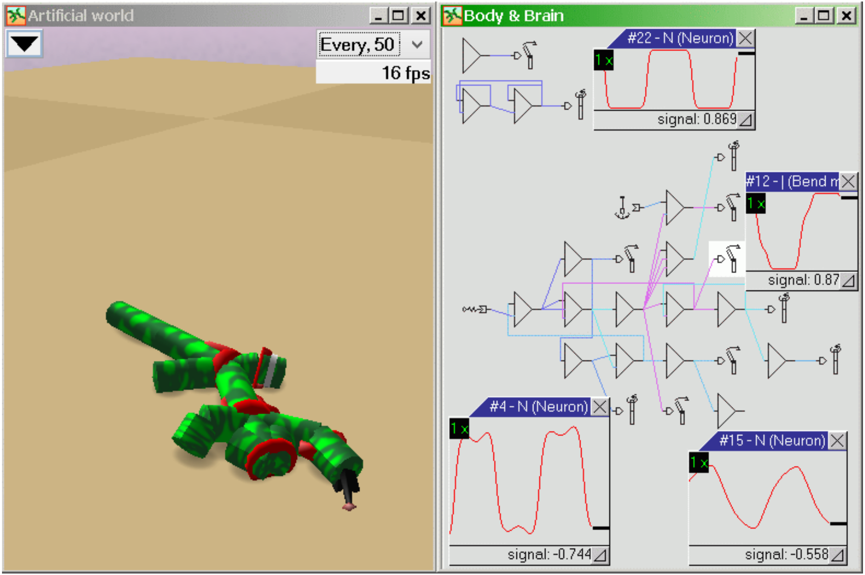
Synthesizing agents

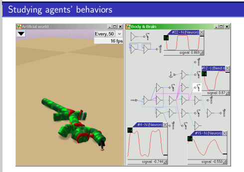




You can select parts of the genotype (genes) and see which parts of the phenotype (phenes) are affected by these genes. In this picture, body and brain parts that are shown in white are created from the selected genes. This also works the other way round: you can select phenes (parts of body and brain) and see which genes influence them.

Studying agents' behaviors

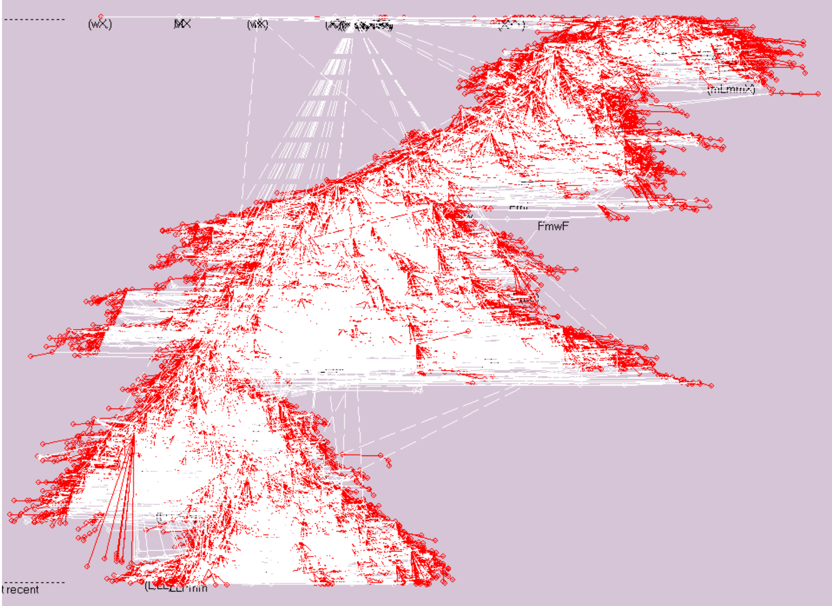


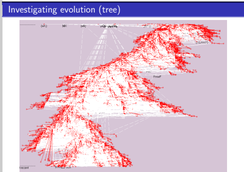


Even with optimization, evolved structures and control systems are extremely intertwined. Even for simple constructs with a few components and a few neurons, it is very hard to identify and understand their role... "everything is connected!"

Often parts that seem to be redundant influence indirectly other parts (receptor–effector loop), so usually nothing is entirely redundant even though many parts seem random and separate.

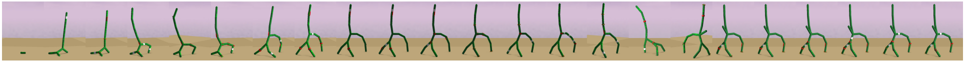
Investigating evolution (tree)

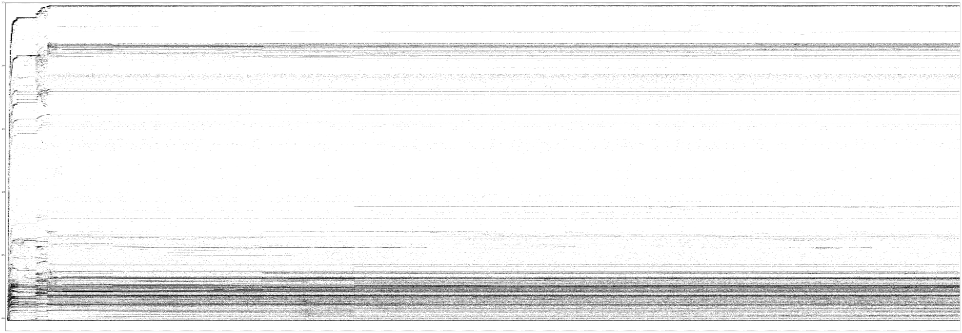


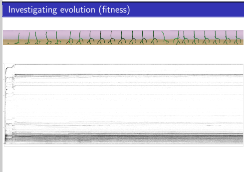


Red=mutation, White=crossover. Milestones are visible and these can be automatically detected.

Investigating evolution (fitness)

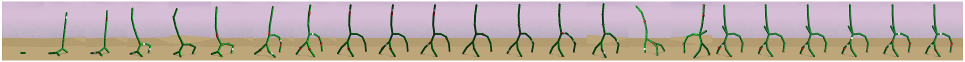


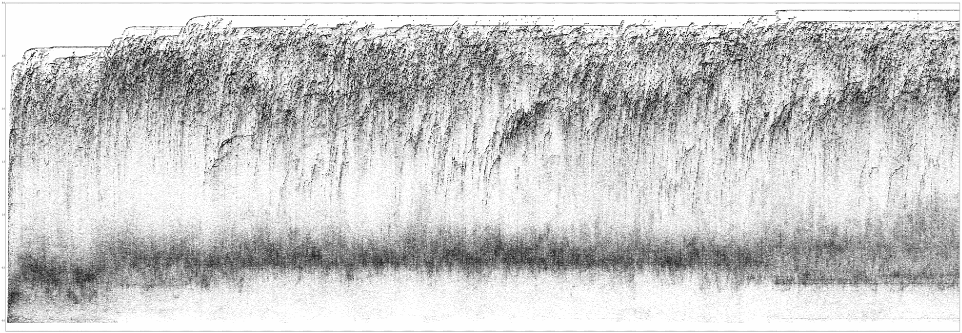


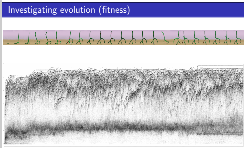


1. 3,000 individuals in each single vertical bar. Evolutionary optimization of the *vertpos* criterion.
2. Three different selection methods, balancing fitness (or not).
3. You can see many poor genotypes (as usual in EA).
4. You can also see that fitness is “quantized”: mutations of best individuals have specific fitness values.

Investigating evolution (fitness)







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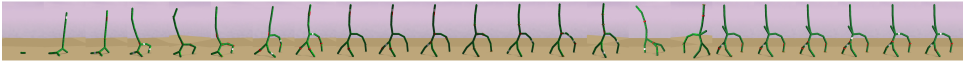

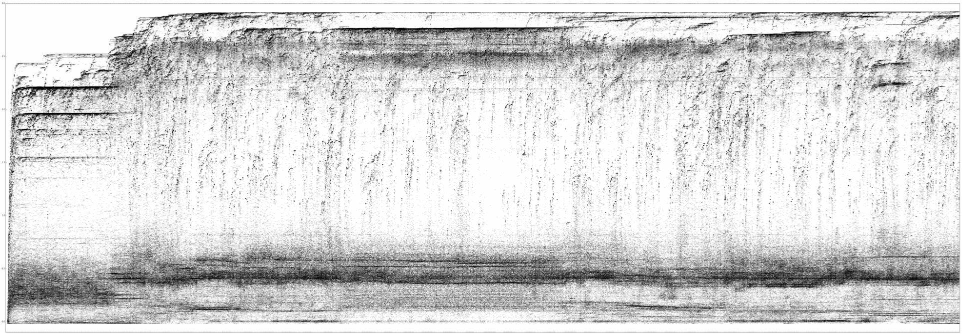

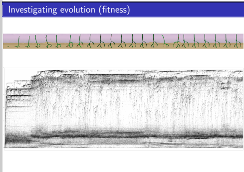

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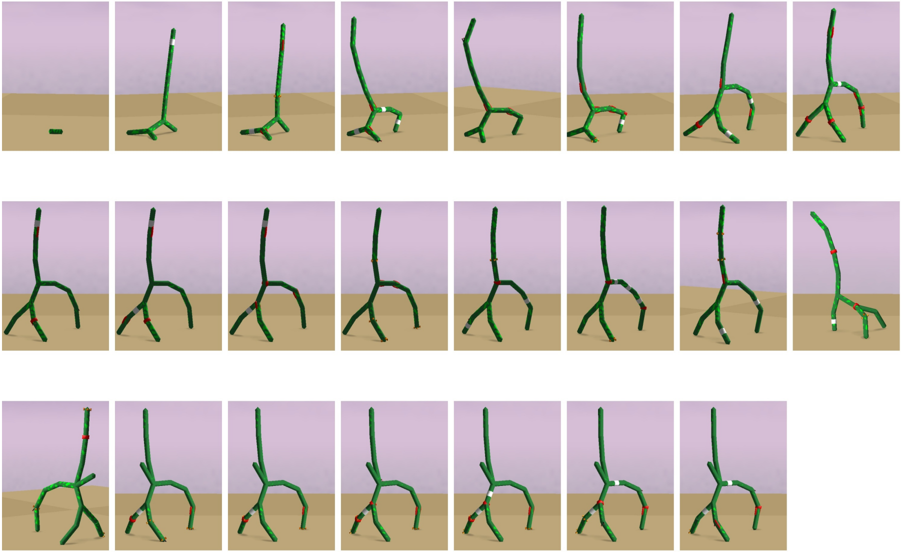
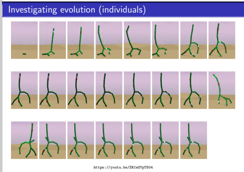
Investigating evolution (individuals)



https://youtu.be/ZRIeOYpTS04



These are the same individuals as in the “stripe” on the previous slide (best from each gene pool snapshot), just shown bigger.

Potential evolved behaviors

- walking/swimming/jumping/rolling/...
- memory
- predation, prey
- symbiosis, cooperation
- mutual identification and location
- preferences, group/social behaviors
- communication
- feelings, consciousness, ...?

- ...they discover, learn and exploit simulator imperfections!

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- ...they discover, learn and exploit simulator imperfections!

1. These are ordered from the most basic to the most complex; going down on the list makes it more and more difficult for a human to identify these phenomena, especially in spontaneous evolution. We see them but we need to spend time to identify them, and it is "another world" so these phenomena often have a different "implementation" than among humans/animals.
2. Last item: they abuse bugs, gain energy from leaks, used oscillations to move etc.

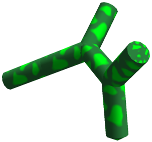
Research and experiments

- Selected publications:
  `http://www.framsticks.com/biblio`
- Sample videos:
  - `https://youtu.be/CrWj_l-UrN4?t=60`
  - `https://youtu.be/r5RfTmx3S4g`

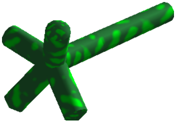
Foraminifera: genotype-to-phenotype mapping

Genotypes and phenotypes

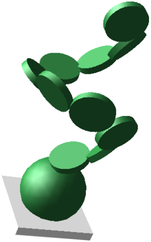
X(XX,RX(X,X))



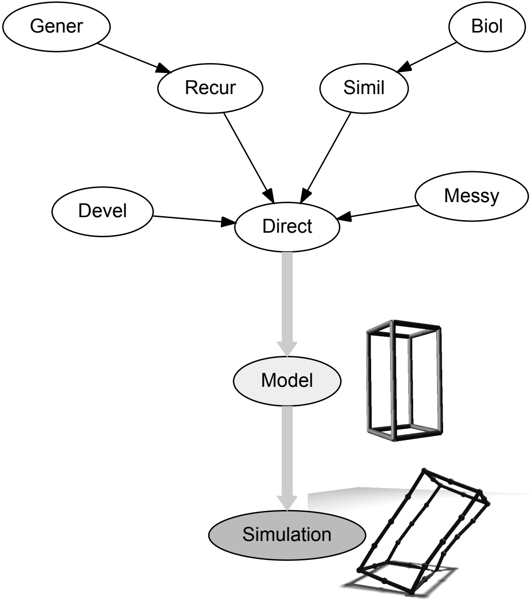
//3
5
aakyaabzakvzaabzdyzzxyabcdforwizehaaaaabhzz

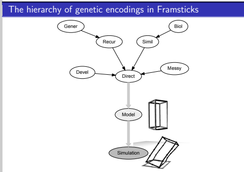


//0
p:sh=2,sx=0.6,sy=0.6,sz=0.3,z=3.4,vr=0.8,0.8,0.4
p:sh=2,sx=0.1,sy=0.1,sz=0.1,vr=0.8,0.8,0.4
p:sh=2,sx=0.1,sy=0.1,sz=0.1,vr=0.8,0.8,0.4
j:0,1,sh=1,dx=0.45,dy=0.45,dz=−0.4
j:0,2,sh=1,dx=−0.45,dy=0.45,dz=−0.4
...



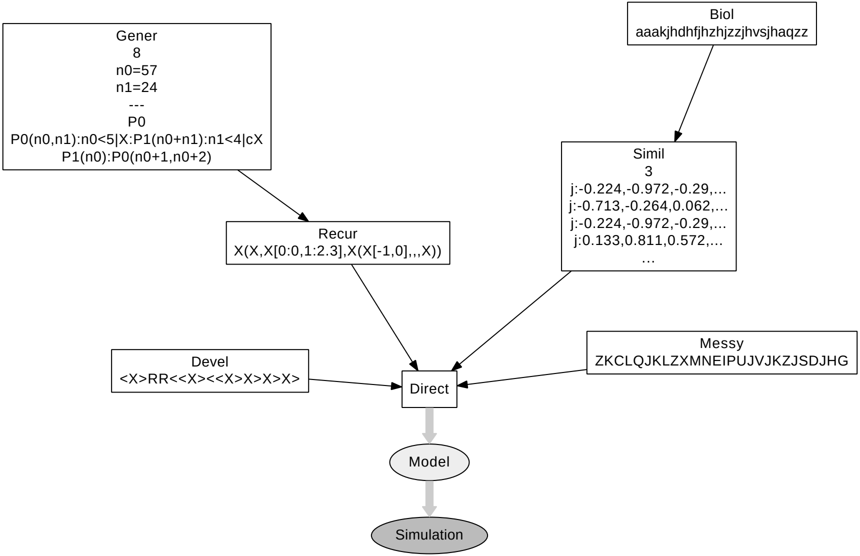
The hierarchy of genetic encodings in Framsticks



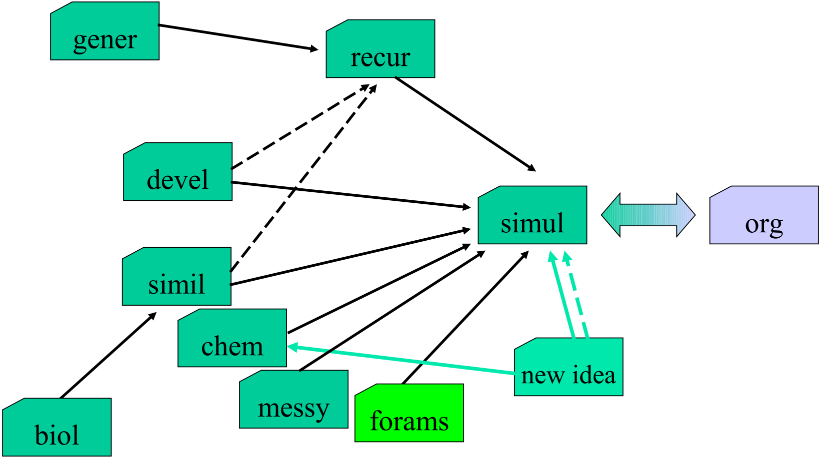


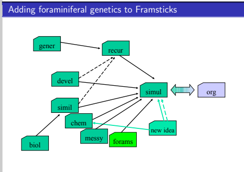
Evolution (search) works in genetic spaces – different topologies that influence performance of evolution!

Specialized genetic operators for each genetic encoding



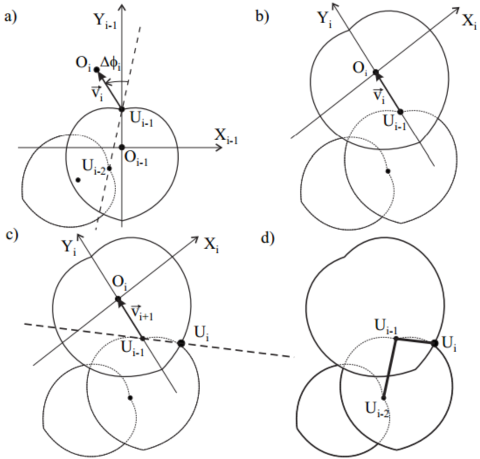
Adding foraminiferal genetics to Framsticks





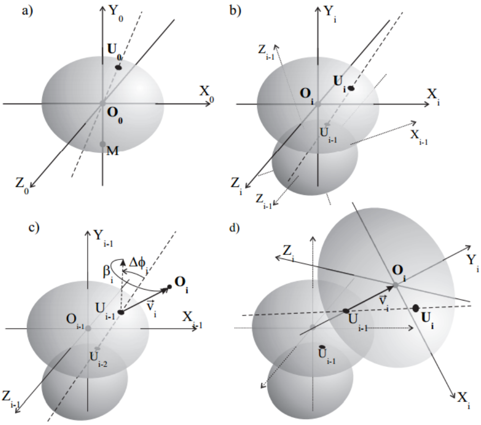
Adding foraminiferal genetics to Framsticks was easy – it becomes one of many existing genetic representations, and a framework supporting various genetic representations exists. This is because one of the major research areas in Framsticks is investigation of genetic encodings, genotype-phenotype mappings,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

Foraminifera growth model – 2D



2D and 3D numerical models of the growth of foraminiferal shells (Labaj, Topa, Tyszka, and Alda. *Computational Science*, ICCS, 2003)

Foraminifera growth model – 3D



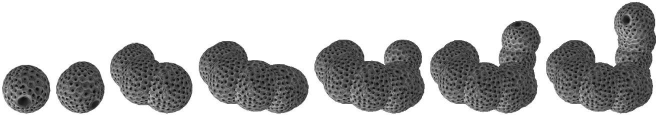
2D and 3D numerical models of growth of foraminiferal shells (Labaj, Topa, Tyszka, and Alda. *Computational Science*, ICCS, 2003)

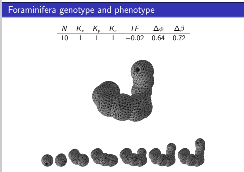
Parameters of the model – genes

- N – number of chambers
- K_x – scaling factor
- K_y – scaling factor
- K_z – scaling factor
- TF – translation factor
- $\Delta\phi$ – deflection angle
- $\Delta\beta$ – rotation angle

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





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

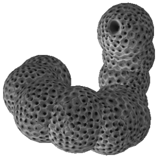
Similarity measure

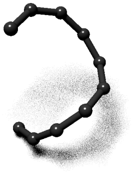
Comparing individuals facilitates:

- classifying morphologies
- inferring dendrograms
- discovering clusters
- **phenotype-to-genotype mapping analysis**

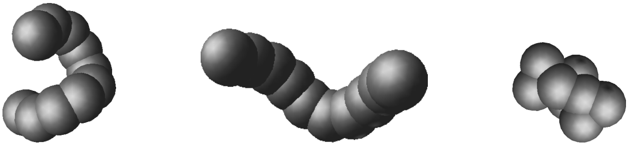
Similarity measure – the algorithm

- organism model: undirected graph
- matching of the vertices of compared structures
- components of the similarity (dissimilarity):
  - difference in the number of vertices
  - difference in vertex degrees
  - difference in the number of control units
  - difference in vertex coordinates in 3D





Dissimilarity matrix



(a) (b) (c)

	(a)	(b)	(c)
(a)	0.00	6.87	10.83
(b)	6.87	0.00	14.01
(c)	10.83	14.01	0.00

Genotype-to-phenotype mapping analysis

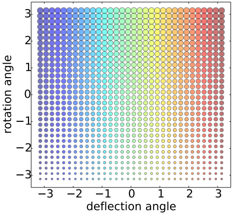
In each visualization:

- 32 x 32 genotypes were generated
- 5 out of 7 genes were kept constant
- 2 genes were varied

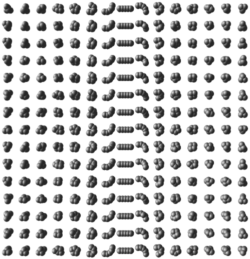
Visualization	N	K_x	K_y	K_z	TF	$\Delta\phi$	$\Delta\beta$
1	5	1	1	1	-0.1	$[-3.14; 3.14]$	$[-3.14; 3.14]$
2	5	1	1	1	$[-0.99; 0.99]$	$[-3.14; 3.14]$	0
3	5	1	1	1	$[-0.99; 0.99]$	0	$[-3.14; 3.14]$

Genotype-to-phenotype mapping – $\Delta\phi$ and $\Delta\beta$

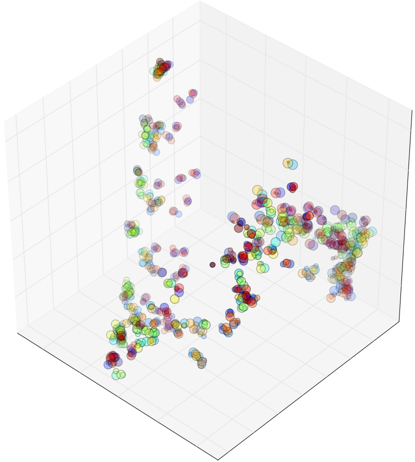
Gene values



Phenotypes

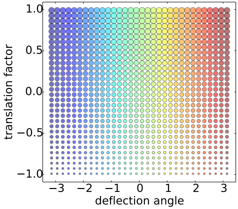


Phenotype distances projected into 3D

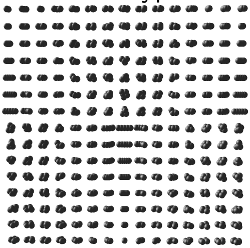


Genotype-to-phenotype mapping – *TF* and $\Delta\phi$

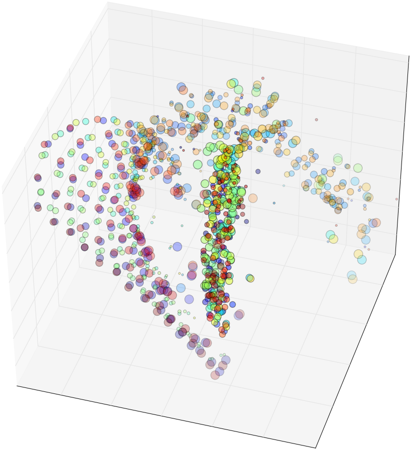
Gene values



Phenotypes

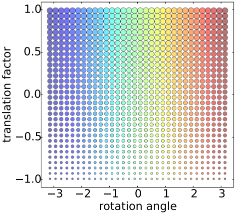


Phenotype distances projected into 3D

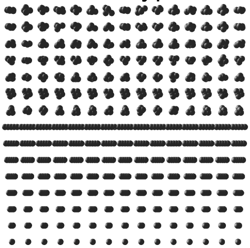


Genotype-to-phenotype mapping – *TF* and $\Delta\beta$

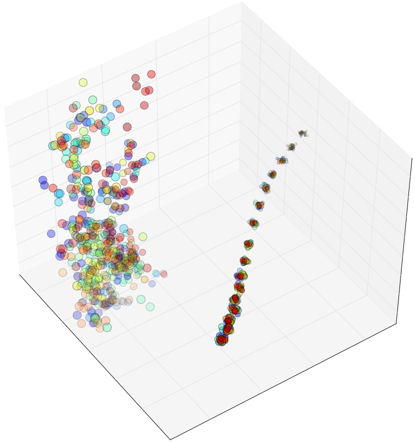
Gene values



Phenotypes



Phenotype distances projected into 3D



Genotype-to-phenotype mapping – summary

- low *locality* of the mapping (different topologies of genetic and phenetic spaces; many discontinuities)
- discontinuities are disadvantageous from search and optimization point of view – a smooth landscape is good for evolution
- locality of biological genotype-to-phenotype mapping?

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.

Foraminifera: investigation of population dynamics

Foraminifera reproduction cycle

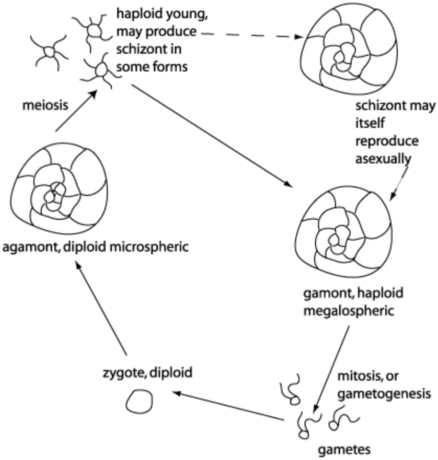


Diagram showing a generalised foraminifera life cycle note alternation between a haploid megalospheric from and a diploid microspheric form.

Redrawn from Goldstein 1999.

Investigation of population dynamics – assumptions

- foraminifers and nutrients are simulated as agents
- foraminifers can actively move
- they must accumulate a sufficient amount of energy to reproduce
- haploid and diploid generations alternate
- two species with different behavioral strategies: hibernating and/or moving randomly in shortage of nutrients (food)

Paweł Topa, Maciej Komosinski, Jarosław Tyszka, Agnieszka Mensfelt, Maciej Bassara, and Sebastian Rokitta. eVolutus: a new platform for evolutionary experiments. Lecture Notes in Computer Science, Springer, 2015.

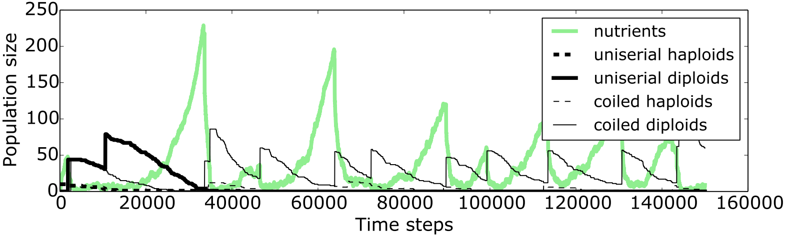
Population dynamics – experiments

The number of runs in which a given species (moving:hibernating) survived for each combination of parameter values.

		Reticulopodia and sensing ranges [mm]	
		3,6	5,8
Feeding rate	0.05	5:0	3:2
	0.1	2:3	0:5

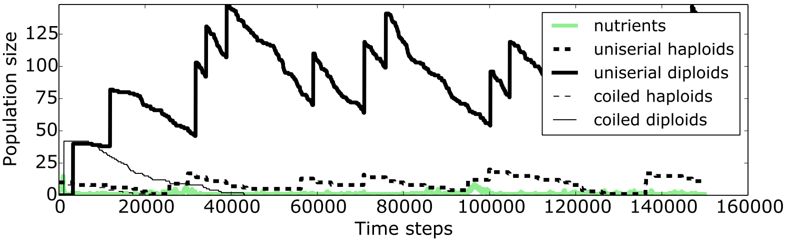
Population dynamics – experiments

feeding rate = 0.1 ranges = 3,6



Population dynamics – experiments

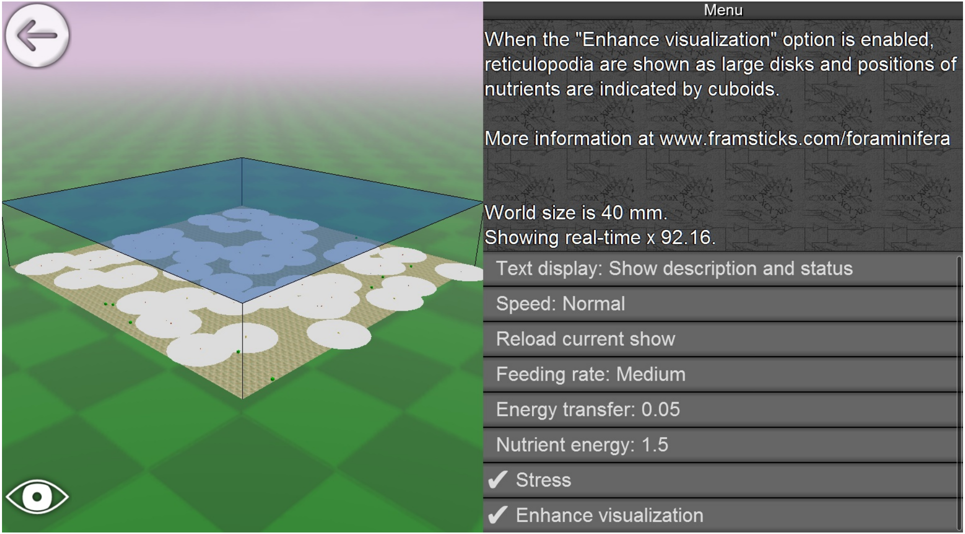
feeding rate = 0.1 ranges = 5,8



Live demo (desktop) http://www.framsticks.com/foraminifera

Live demo (mobile)

http://www.framsticks.com/foraminifera



Conclusions

- Experiments
  - populations generally follow Lotka-Volterra dynamics
  - competition for food tends to eliminate less adapted species
  - revealed differences and discontinuities in topologies of genetic and phenetic spaces
- The model
  - initial stage of research, needs further calibration
  - integrates existing knowledge on foraminiferal physiology and ecology
  - enables testing of hypotheses on different levels and across scales