

Modeling Foraminifera in Framsticks. Genotype, phenotype, ecosystem

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www.framsticks.com

Details of this research are available in [Kom+16; Kom+17]
and at www.framsticks.com/foraminifera.

Foraminifera in the Tree of Life

Foraminifera

Genotype-to-phenotype mapping

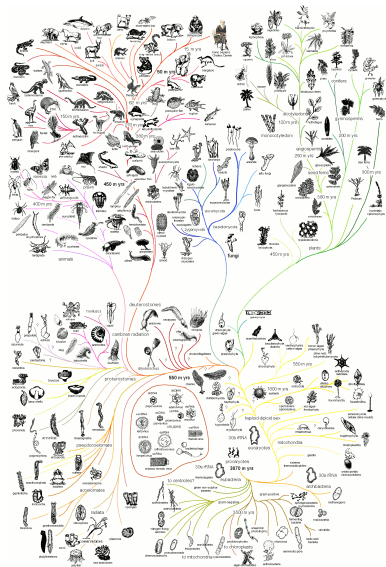
Similarity measure

Life cycle

Population dynamics

Conclusions

References



What are Foraminifera?

Foraminifera

Genotype-to-
phenotype
mapping

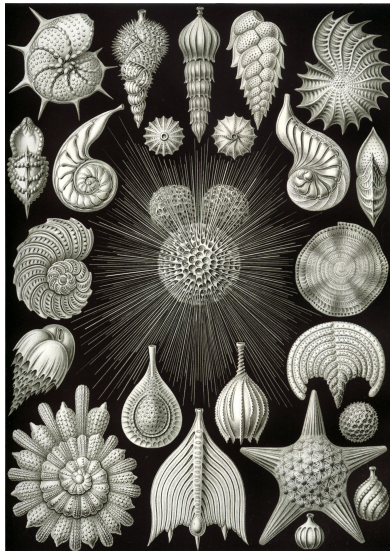
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Ernst Haeckel, *Kunstformen der Natur*, 1904.

What are Foraminifera?

Foraminifera

Genotype-to-phenotype mapping

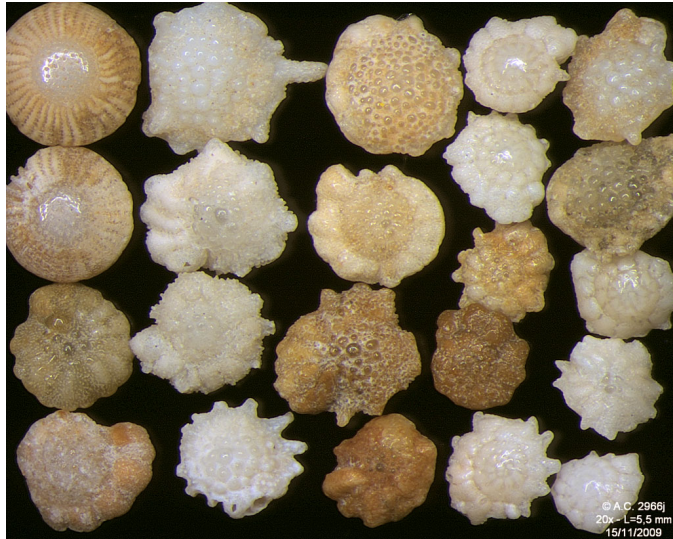
Similarity measure

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

What are Foraminifera?

Foraminifera

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

What are Foraminifera?

Foraminifera

Genotype-to-phenotype mapping

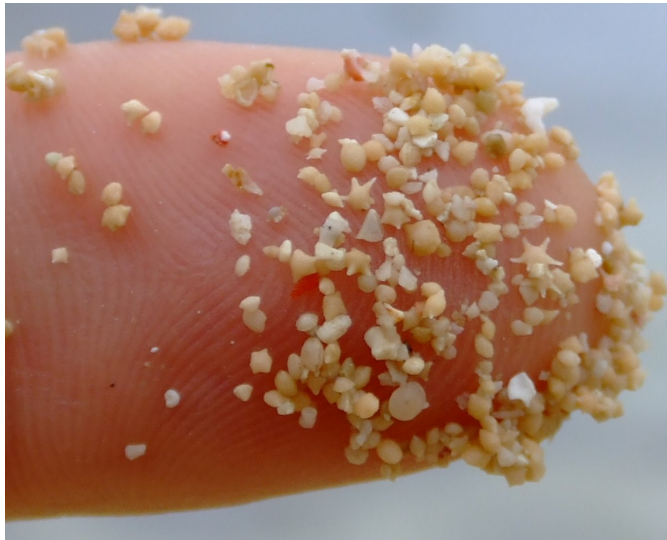
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Star sand on Hoshizuna-no-hama, Iriomote, Okinawa.
Own work by Geomr.

What are Foraminifera?

Foraminifera

Genotype-to-phenotype mapping

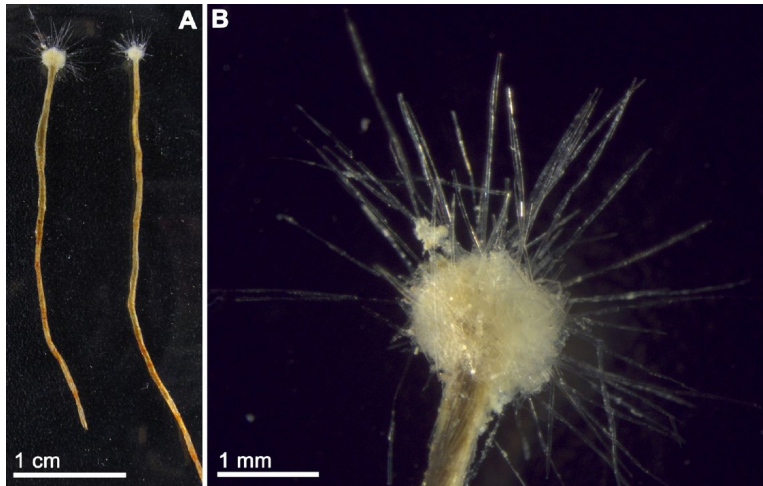
Similarity measure

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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?

Foraminifera

Genotype-to-phenotype mapping

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References

- 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

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

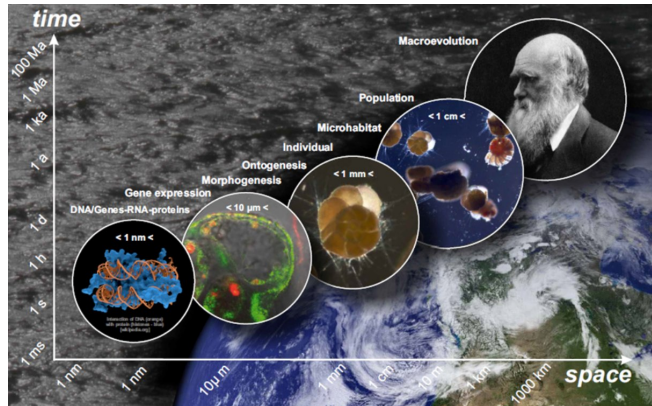
Life cycle

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- 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!

Genotypes and phenotypes

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

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References

$X(\text{XX}, \text{RX}(\text{X}, \text{X}))$

```
//3
```

```
5
```

```
aakyabzakvzaabzdyzzxyabcdforwizehaaaaabhzz
```

```
//0
```

```
p:sh=2,sx=0.6,sy=0.6,sz=0.3,z=3.4,vr=0.8,0.8,0.4
```

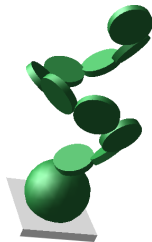
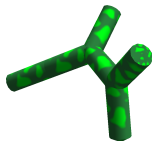
```
p:sh=2,sx=0.1,sy=0.1,sz=0.1,vr=0.8,0.8,0.4
```

```
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

Foraminifera

Genotype-to-phenotype mapping

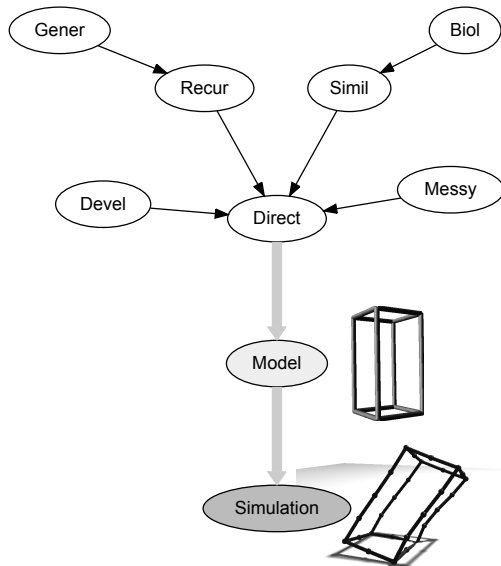
Similarity measure

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Specialized genetic operators for each genetic encoding

Foraminifera

Genotype-to-phenotype mapping

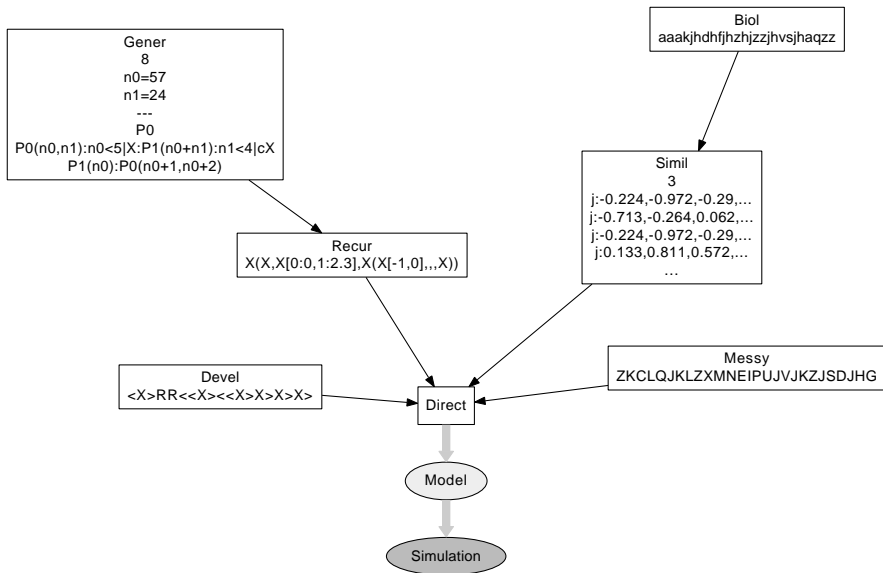
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Adding foraminiferal genetics to Framsticks

Foraminifera

Genotype-to-phenotype mapping

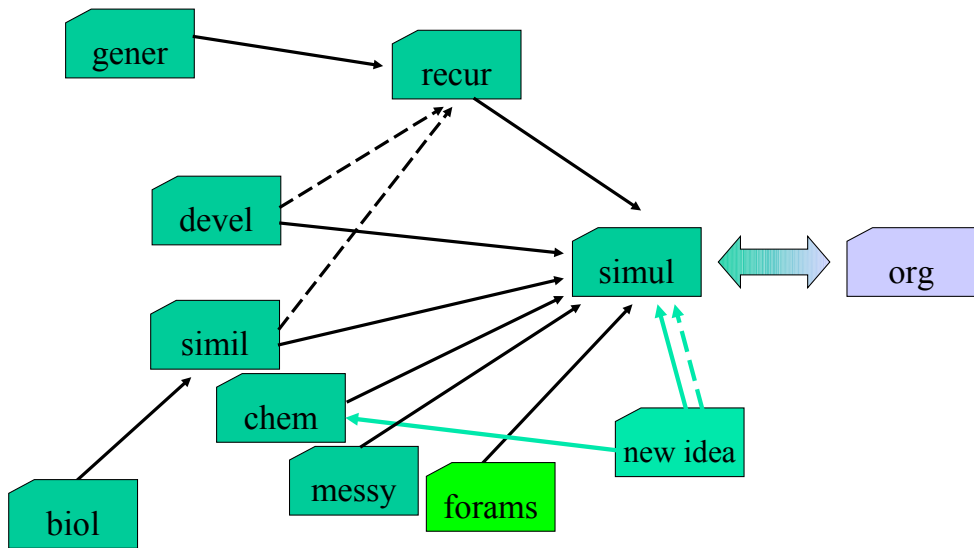
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Foraminifera morphology

Foraminifera

Genotype-to-phenotype mapping

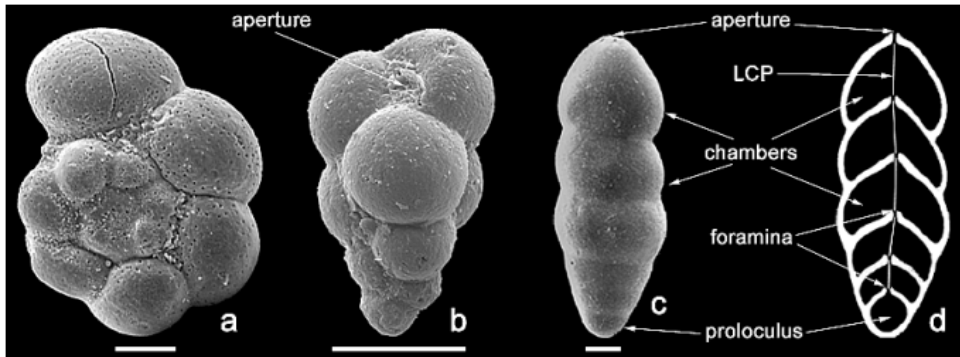
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References



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

Foraminifera growth model – 2D

Foraminifera

Genotype-to-phenotype mapping

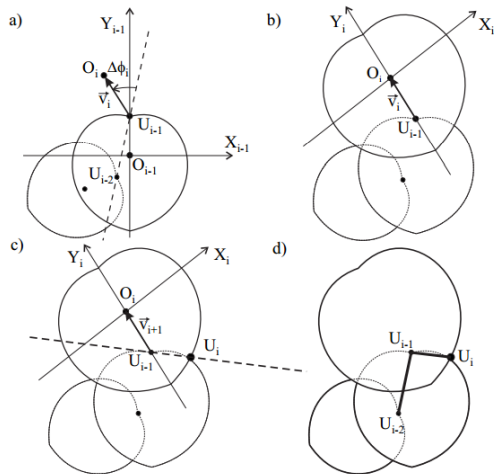
Similarity measure

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Conclusions

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

Foraminifera growth model – 3D

Foraminifera

Genotype-to-phenotype mapping

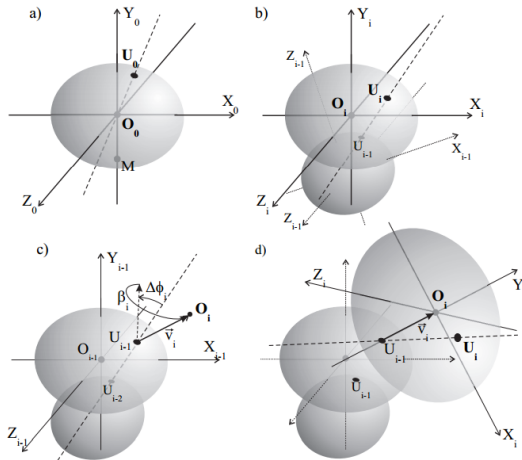
Similarity measure

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

Parameters of the model – genes

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

- 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

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

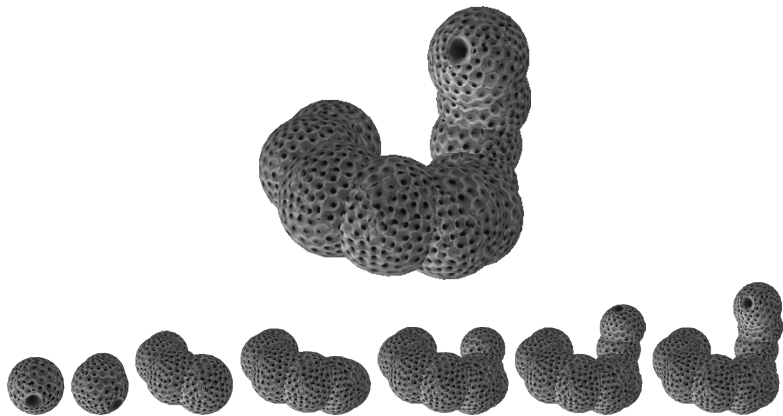
Life cycle

Population dynamics

Conclusions

References

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



Genotype-to-phenotype mapping analysis

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

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 $\Delta\beta$

Foraminifera

Genotype-to-phenotype mapping

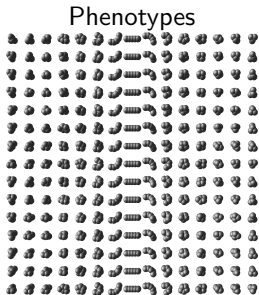
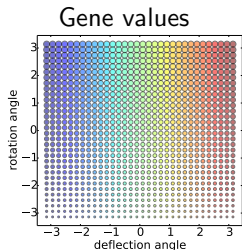
Similarity measure

Life cycle

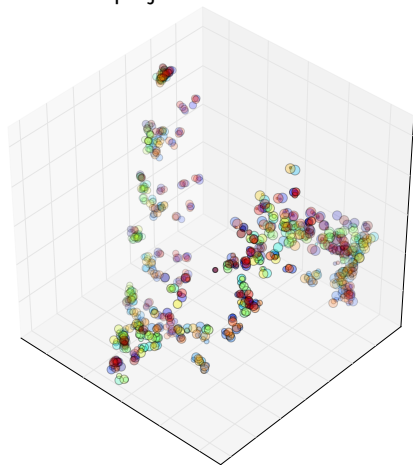
Population dynamics

Conclusions

References



Phenotype distances projected into 3D



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

Foraminifera

Genotype-to-phenotype mapping

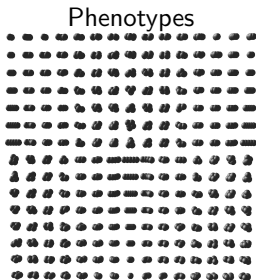
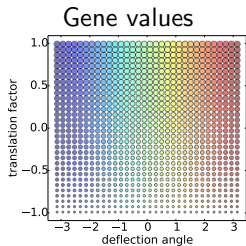
Similarity measure

Life cycle

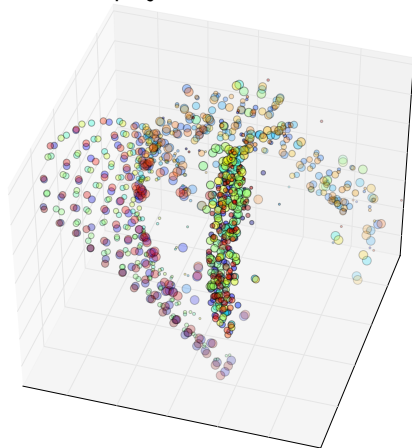
Population dynamics

Conclusions

References



Phenotype distances
projected into 3D



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

Foraminifera

Genotype-to-phenotype mapping

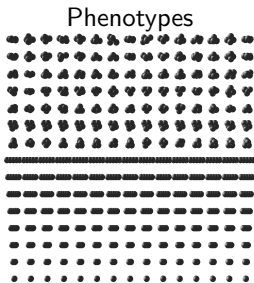
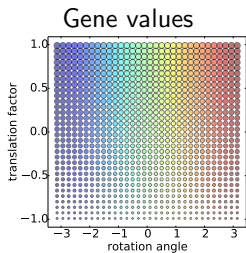
Similarity measure

Life cycle

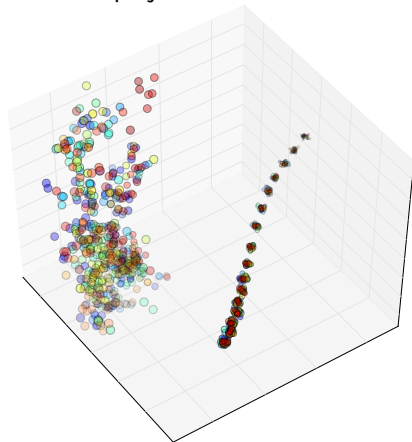
Population dynamics

Conclusions

References



Phenotype distances projected into 3D



Genotype-to-phenotype mapping – summary

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

- 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?

Results published in [Kom+16].

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

- Comparing individuals facilitates:
 - classifying morphologies
 - inferring dendrograms
 - discovering clusters
 - **phenotype-to-genotype mapping analysis**
- Other domains of application
 - computer vision
 - bioinformatics
 - chemistry

Similarity measure – the algorithm

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

- Organism model
 - Undirected graph
- Algorithm
 - Alignment of the structures
 - Construction of the matching function
 - Calculation of dissimilarity components



Algorithm – the matching function

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

```
SORT( $P_i, i \in \{1, 2\}$ , descending by vertex degree)
SORT(groups in  $P_i, i \in \{1, 2\}$  with the same vertex degree descending by neuron_count)
REPEAT
    FIND  $U, V$  – groups of parts in  $P_1, P_2$  with the same, highest possible, degree and with
parts not matched yet
    COMPUTE  $DIST(U, V)$ 
    REPEAT
        FIND the first part  $u \in U$  which is yet unmatched
        FIND the first part  $v \in V$  which is yet unmatched
        FIND  $min\_for\_u = min(u, V)$ 
        FIND  $min\_for\_v = min(v, U)$ 
        MATCH( $u, min\_for\_u$ )
        MATCH( $v, min\_for\_v$ )
    UNTIL all parts in  $U$  or all parts in  $V$  are matched
UNTIL all parts in the smaller set are not matched
```

Dissimilarity components

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

- d_V – number of vertices
- d_D – vertex degree
- d_N – count of the neurons
- d_G – geometrical distance

$$dissim = w_V * d_V + w_D * d_D + w_N * d_N + w_G * d_G$$

Fuzzy vertex degree

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

	0	1	2	3	4	5	6	7	8
0	0	1	0	0	0	0	0	0	0
1	1	0	1	0	0	0	0	0	0
2	0	1	0	1	0	0	1	0	0
3	0	0	1	0	1	0	0	0	0
4	0	0	0	1	0	1	0	0	0
5	0	0	0	0	1	0	0	0	0
6	0	0	1	0	0	0	0	1	0
7	0	0	0	0	0	0	1	0	1
8	0	0	0	0	0	0	0	1	0

	I	II	III	IV	V	VI	VII	VII	IX
2	3.00	2.00	2.33	1.83	2.25	1.79	2.24	1.77	2.24
3	2.00	2.50	1.75	2.29	1.73	2.26	1.73	2.25	1.74
6	2.00	2.50	1.75	2.29	1.73	2.26	1.73	2.25	1.74
1	2.00	2.00	2.00	2.17	1.92	2.21	1.85	2.23	1.81
4	2.00	1.50	2.25	1.62	2.27	1.68	2.27	1.71	2.26
7	2.00	1.50	2.25	1.62	2.27	1.68	2.27	1.71	2.26
0	1.00	2.00	2.00	2.00	2.17	1.92	2.21	1.85	2.23
5	1.00	2.00	1.50	2.25	1.62	2.27	1.68	2.27	1.71
8	1.00	2.00	1.50	2.25	1.62	2.27	1.68	2.27	1.71

Fuzzy vertex degree

Foraminifera

Genotype-to-phenotype
mapping

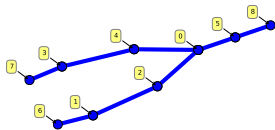
Similarity
measure

Life cycle

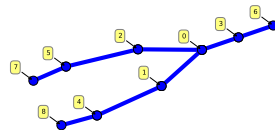
Population
dynamics

Conclusions

References



(a) Sorting by vertex degree



(b) Sorting by fuzzy vertex degree

Fuzzy vertex degree

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

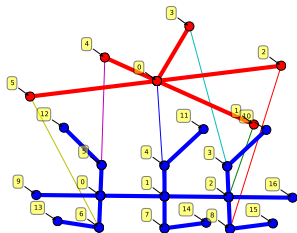
Life cycle

Population dynamics

Conclusions

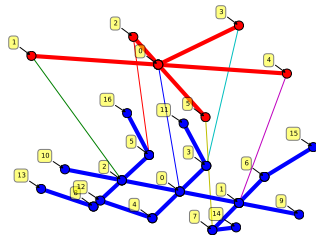
References

distance=25.81



(a) Old matching

distance=24.42



(b) New matching

Dissimilarity matrix

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

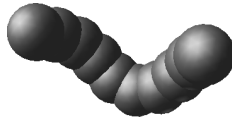
Population dynamics

Conclusions

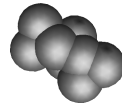
References



(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

Foraminifera reproduction cycle

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

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Population dynamics

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References

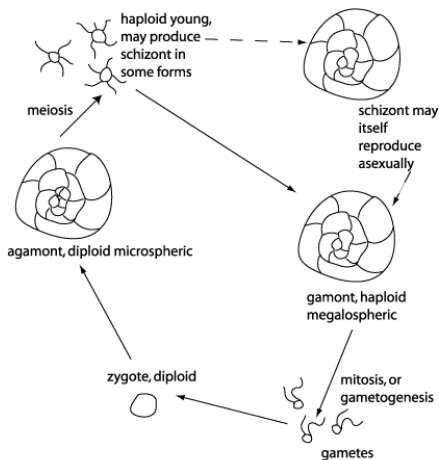


Diagram showing a generalised foraminifera life cycle note alternation between a haploid megalospheric form and a diploid microspheric form.

Redrawn from Goldstein 1999.

Algorithm

Foraminifera

Genotype-to-phenotype mapping

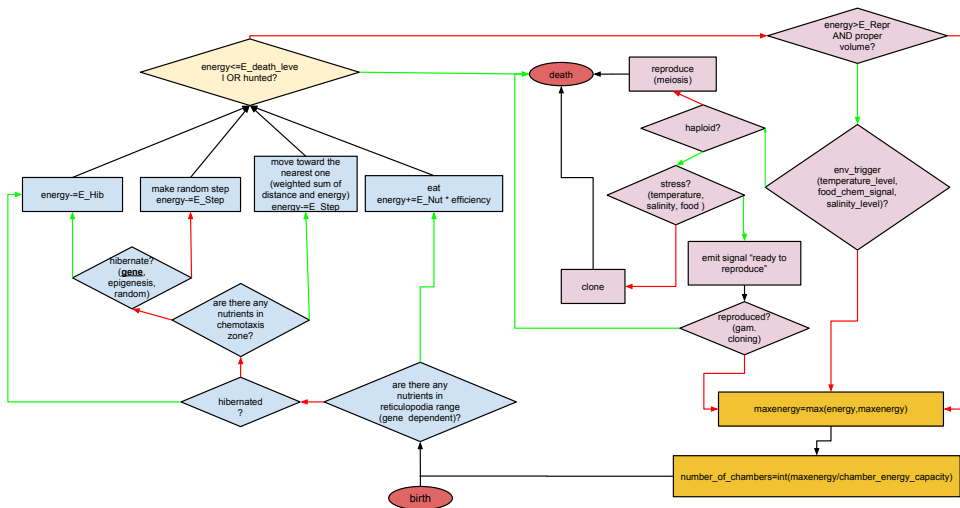
Similarity measure

Life cycle

Population dynamics

Conclusions

References



Investigation of population dynamics – assumptions

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

- 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)

Experiments were performed on the eVolutus platform [[Top+16](#)].

Population dynamics – experiments

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

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

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

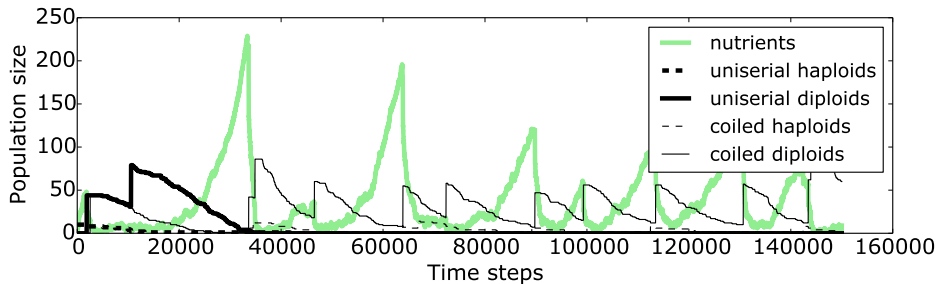
Life cycle

Population dynamics

Conclusions

References

feeding rate = 0.1 ranges = 3,6



Population dynamics – experiments

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

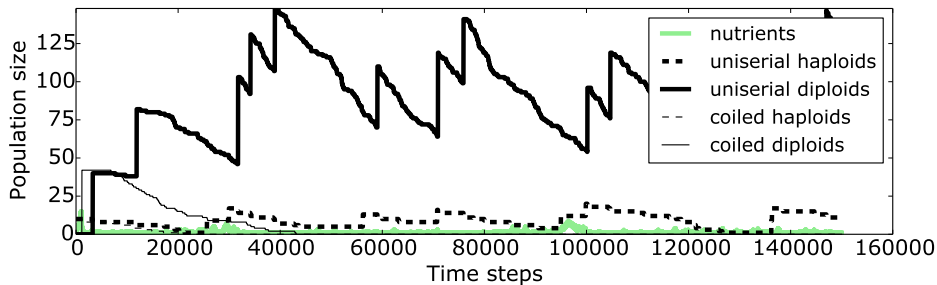
Population dynamics

Conclusions

References

feeding rate = 0.1

ranges = 5,8



Foraminifera

Genotype-to-phenotype mapping

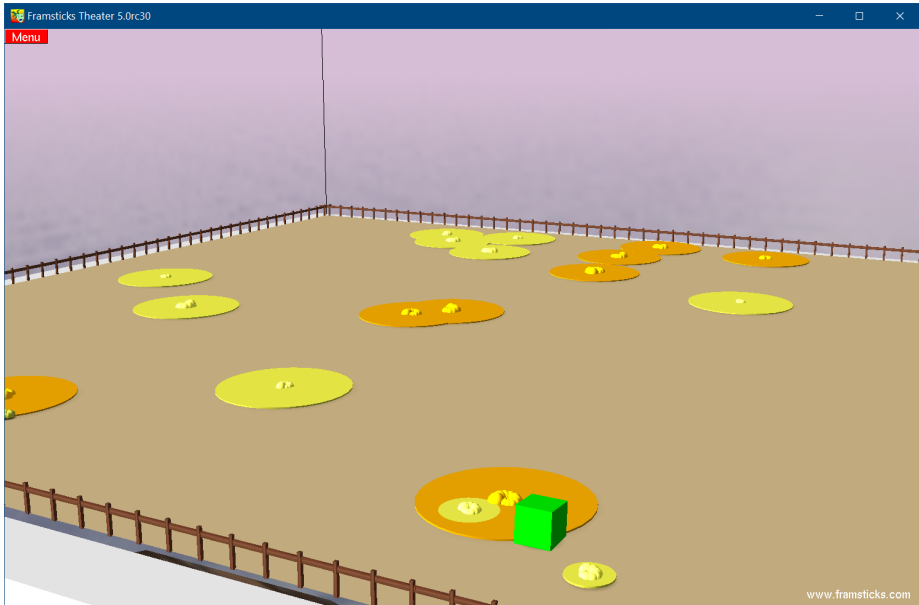
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Life cycle

Population dynamics

Conclusions

References



Foraminifera

Genotype-to-phenotype mapping

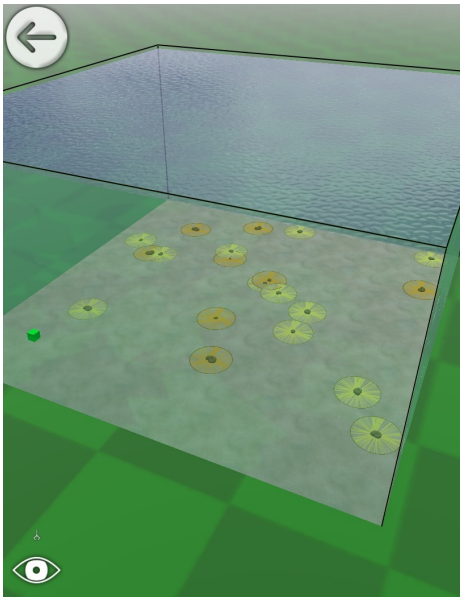
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Life cycle

Population dynamics

Conclusions

References



Menu
✕ Enhance visualization" option is enabled, reticulopodia are shown as large disks and positions of nutrients are indicated by cuboids.

More information at
www.framsticks.com/foraminifera

World size is 10 mm.
Showing real-time x 2400.

Text display: Show description and status >

Speed

Paused	Very slow	Slow	Normal
Fast		Very fast	

Reload current show

Food flux

Low	Medium	High
-----	--------	------

Energy transfer per second

0.0005	0.001	0.002
--------	-------	-------

Nutrient energy [ng Corg]

≈29	≈109	≈189
-----	------	------

Stress



- Results of 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
- Further work
 - development of foraminifera genetic representation
 - voxel-based similarity measure
 - comparison of similarity measures
 - development of foraminifera algorithmic model

References I

Foraminifera

Genotype-to-phenotype mapping

Similarity measure

Life cycle

Population dynamics

Conclusions

References

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