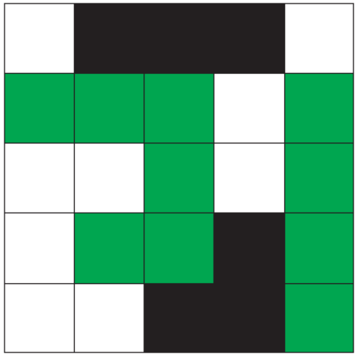

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UCNC 2012 - University of Orléans (France)

”Genome Parameters as Information to Forecast Emergent Developmental Behavior”

Stefano Nichele and Gunnar Tufte
2012, September 4

Goal

- Measure genome properties in EvoDevo systems to predict emergent phenotypic behaviors of artificial organisms

  EvoDevo:

  - Artificial Development (genotype – phenotype mapping)
  - Artificial Evolution (population, generations, genetic operators)

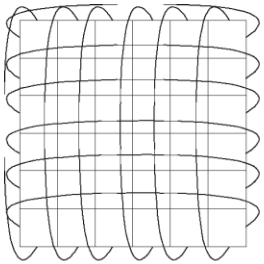
EvoDevo systems - CA

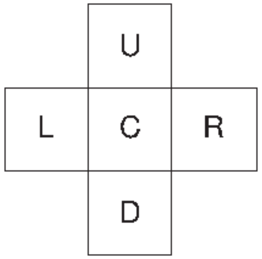
- A CA can be considered as a developmental system, in which an organism can develop (e.g. grow) from a zygote to a multi-cellular organism (phenotype) according to specific local rules, represented by a genome (genotype).

- The genome specifications and the gene regulatory information control the cells' growth and differentiation.

- The behavior of the CA is represented by the emergent phenotype, which is subject to shape and size modification, along the developmental process.

CA model





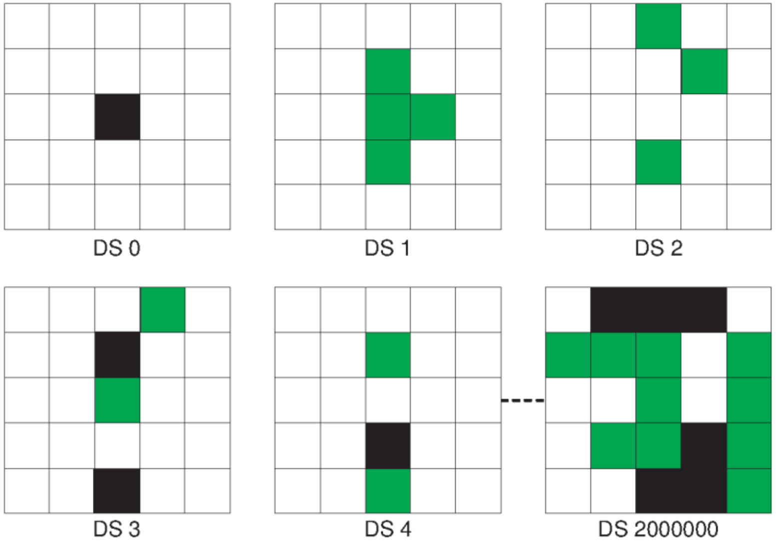
☐ : Void, type 0

■ : Type 1

🟩 : Type 2

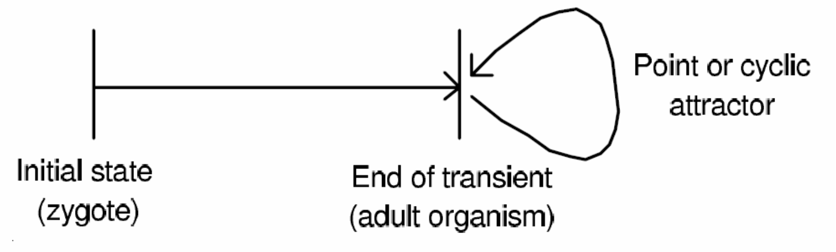
- minimalistic developmental system
- 3 cell types
  (type 0: quiescent, type 1 and type 2 for multicellularity)
- all possible 3^5 = 243 regulatory input combinations are represented in a development table

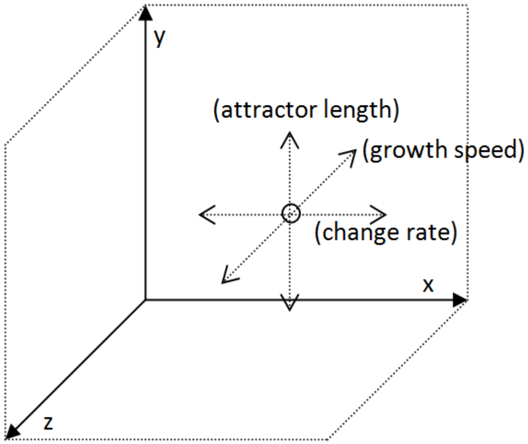
L	R	U	D	C	$C_{(t+1)}$
0	0	0	0	0	0
0	0	0	0	1	{0,1,2}
0	0	0	1	0	{0,1,2}
0	0	0	1	1	{0,1,2}
0	0	1	0	0	{0,1,2}
		:			:
1	1	1	1	1	{0,1,2}
0	0	0	0	2	{0,1,2}
0	0	0	2	0	{0,1,2}
0	0	0	2	1	{0,1,2}
0	0	0	2	2	{0,1,2}
		:			:
2	2	2	2	2	{0,1,2}



Genome Parameters

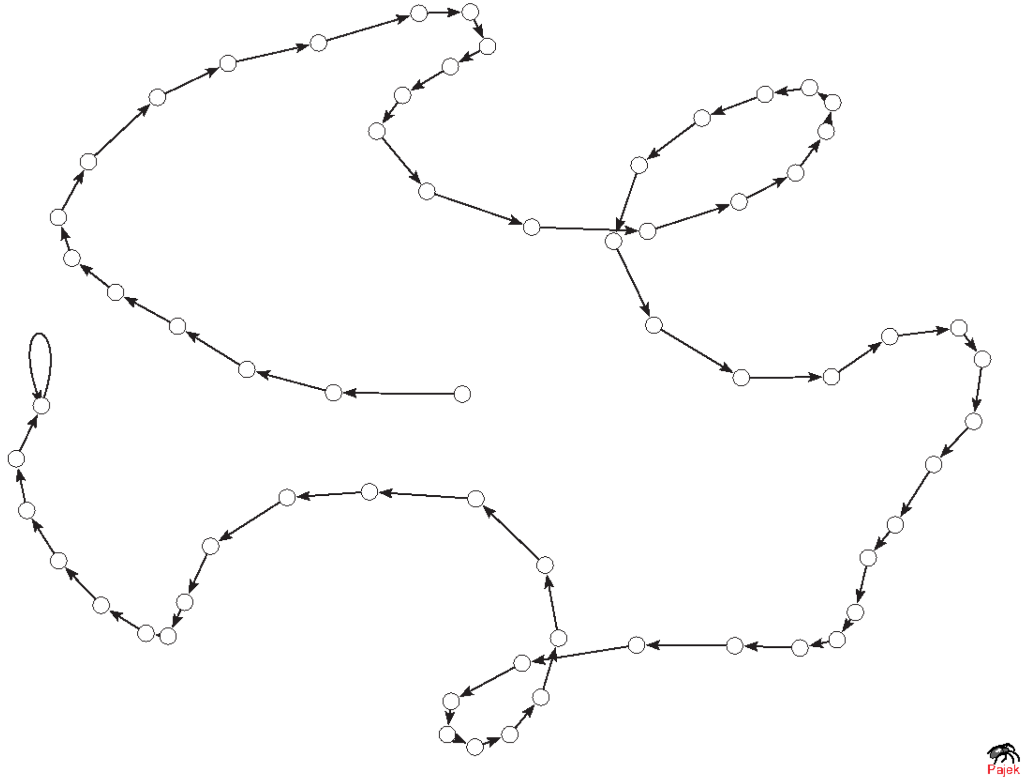
- Genome information to estimate the dynamic behavior of the system





- Each parameter may be better suited to describe specific developmental behaviors, e.g. long transient length, short attractor

Point Attractor



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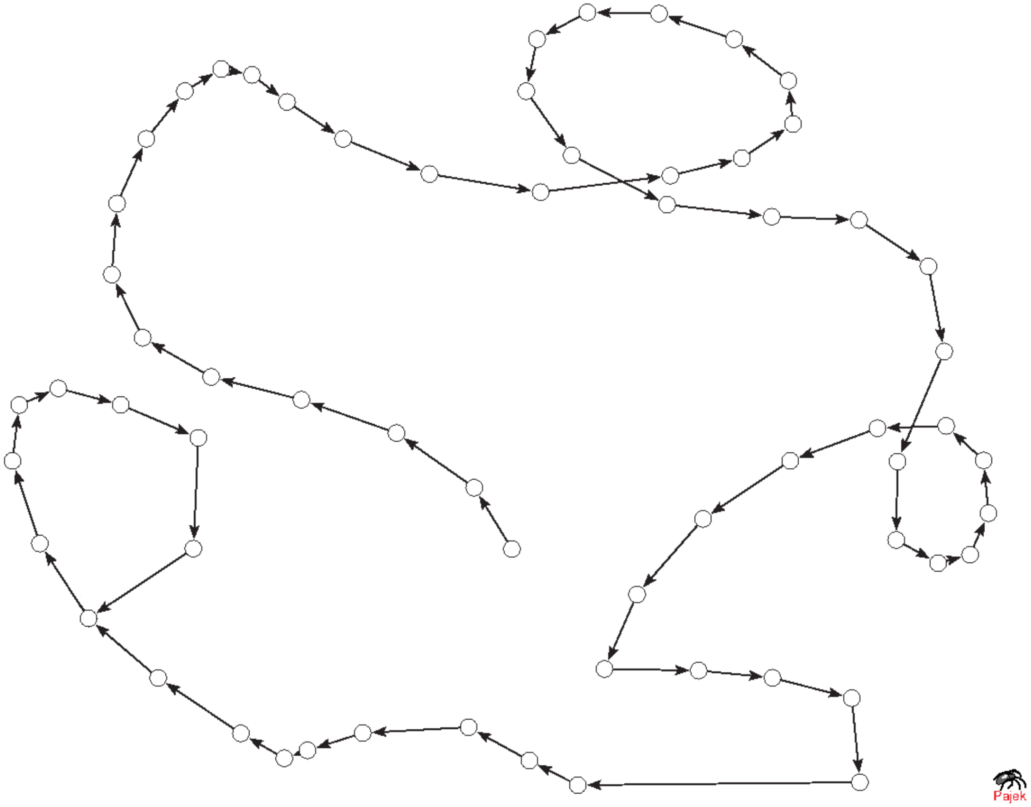
Cyclic Attractor



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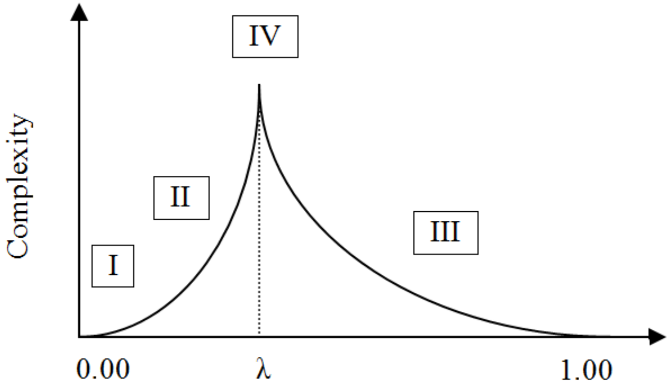
Lambda Parameter

$$\lambda = \frac{K^N - n}{K^N}$$

- n = number of transitions to the quiescent state (state 0)
- K = number of cells types = 3 (in our model)
- N = neighborhood size = 5 (Von Neumann neighborhood)



Majority Parameter

- how many neighborhood configurations in the rule table follow the majority state to determine the next state

$$M = \sum_{(V1V2\ldots Vm)} [V(m+1) = maj(V1V2\ldots Vm)]$$

- m = number of cells in the neighborhood
- V(m+1) = value of the cell being considered, at the next time step
- maj() = function that retrieves the most present cell type (or the set of most present cell types) in the neighborhood

Sensitivity Parameter

- measures the number of changes in the output of the transition table based on a change in the neighborhood, one cell at a time, over all the possible neighborhoods of the rule being considered

$$\mu = \frac{1}{n * m * (\mathrm{K} - 1)} \sum_{(V1V2\ldots Vm)} \sum_{q=1}^{m} \frac{\delta\varphi}{\delta Vq} \longrightarrow \frac{\delta\varphi}{\delta Vq} = \begin{cases} 1 \; if \; \varphi(V1 \ldots Vq \ldots Vm) \neq \varphi(V1 \ldots \overline{Vq} \ldots Vm) \\ 0 \; otherwise \end{cases}$$

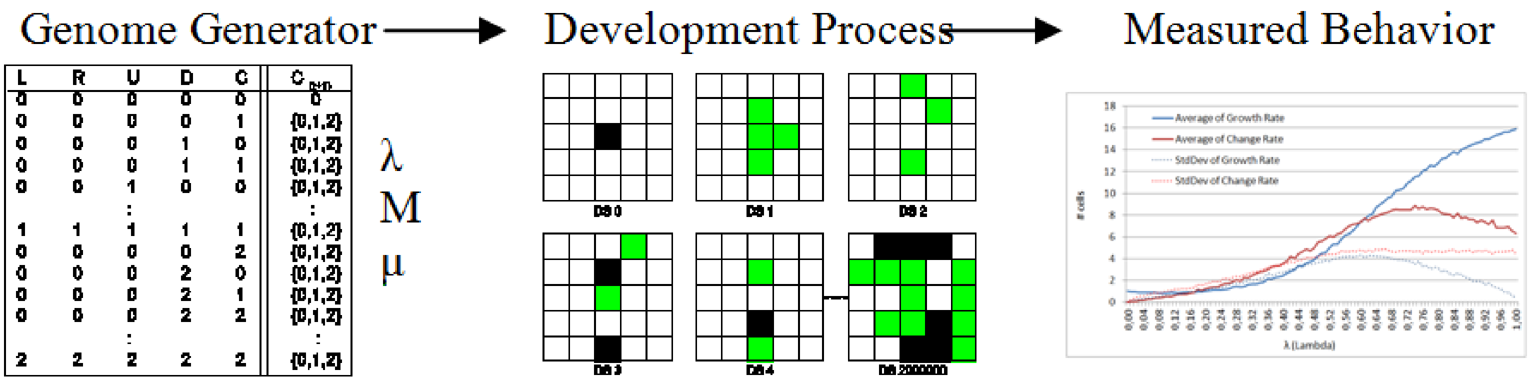
- m = number of cells in the neighborhood
- n = possible neighborhood configurations (V1V2…Vm = 3^5 = 243)
- K = number of cell types

Genome Parameters – Recap

Evaluation of the genetic information

- λ (Lambda): purely regulatory output
- M (Majority): regulatory input and relative output, each entry considered independently
- µ (Sensitivity): overall parameter calculated out of genetic dependency properties

Experimental Setup



Genome Generator → Development Process → Measured Behavior

L	R	U	D	C	C_{t+1}
0	0	0	0	0	0
0	0	0	0	1	{0,1,2}
0	0	0	1	0	{0,1,2}
0	0	0	1	1	{0,1,2}
0	0	1	0	0	{0,1,2}
		:			:
1	1	1	1	1	{0,1,2}
0	0	0	0	2	{0,1,2}
0	0	0	2	0	{0,1,2}
0	0	0	2	1	{0,1,2}
0	0	0	2	2	{0,1,2}
		:			:
2	2	2	2	2	{0,1,2}

λ
M
μ

State space:
3by3 = 3^9 = 19.683
4by4 = 3^16 = 43.046.721
5by5 = 3^25 = 847.288.609.443

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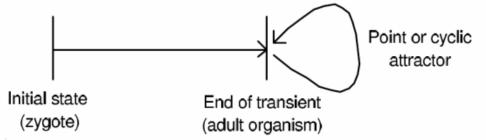
Measurements of the Phenotypic Behavior

- Measure characteristics of the developmental organism:
  - information regarding the development process as a whole
  - Information on phenotypic changes that occur during each development stage

Measurements of the Phenotypic Behavior - 2

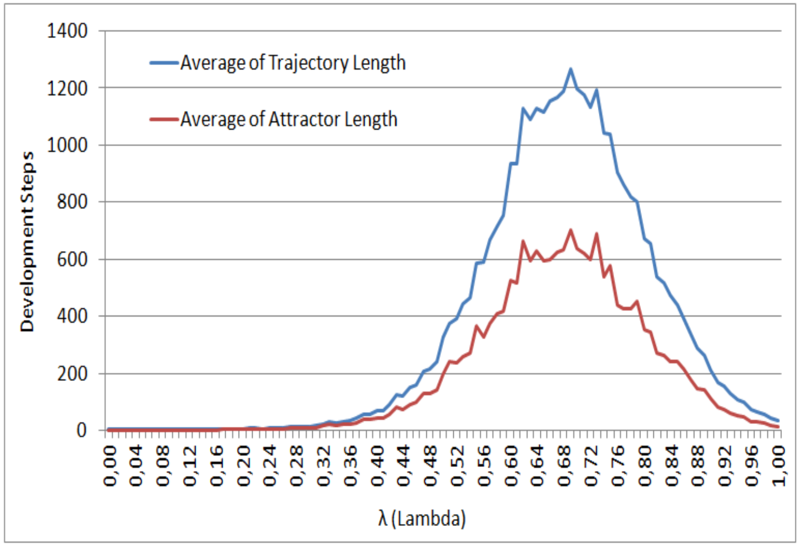


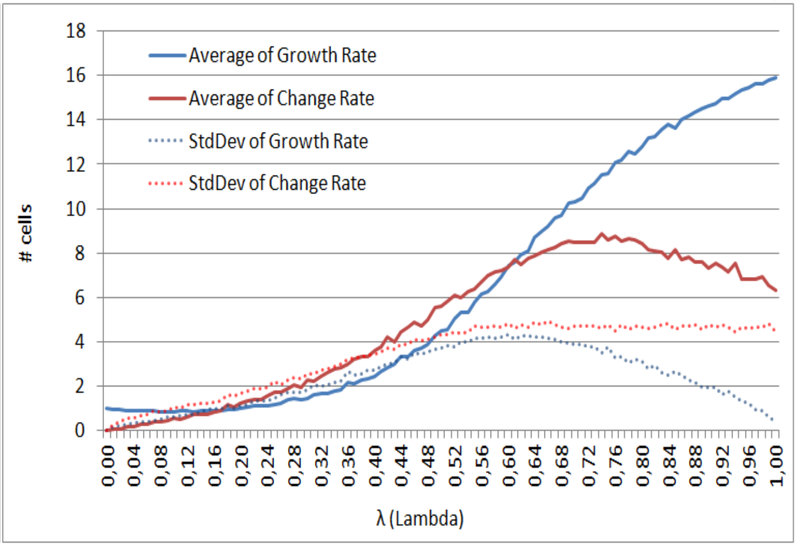
- trajectory and attractor length: may indicate information about structural and adaptive properties of the organism
  - does development create a stable organism (point attractor) or does the organism end with a self-reorganizing structure that changes form in a cyclic manner (cyclic attractor)?

- growth and change rate: may give information on the activity (internal properties) of the developmental processes
  - growth phase: the organism expand in size toward an ”adult” form
  - change phase: changes in the adult organism (measurement of the adult life of the organism)

Results - λ

Measurements in correlation to λ, average over 1000 tests for each λ value



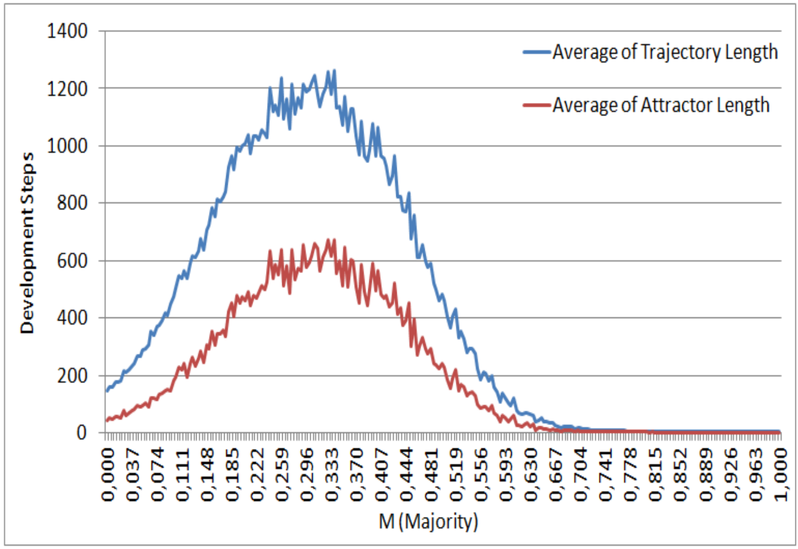


Average trajectory and attractor length

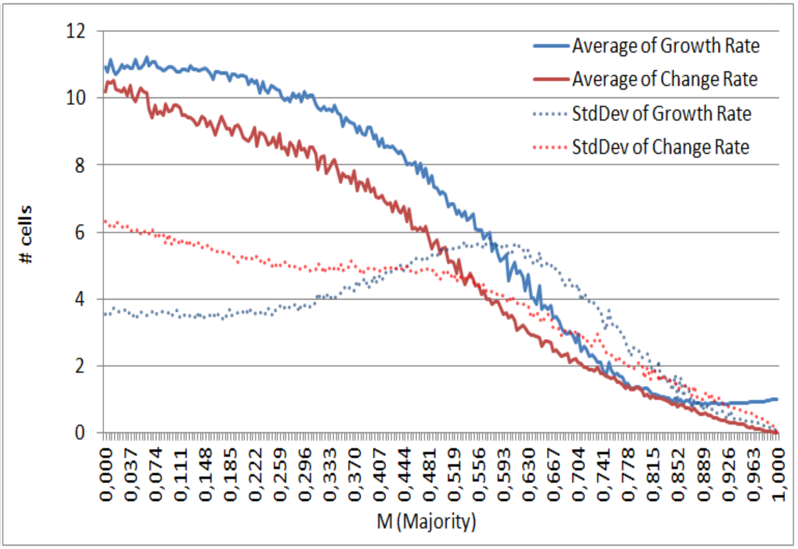
Average growth and change rate

Results - M

Measurements in correlation to M, average over 1000 tests for each M value



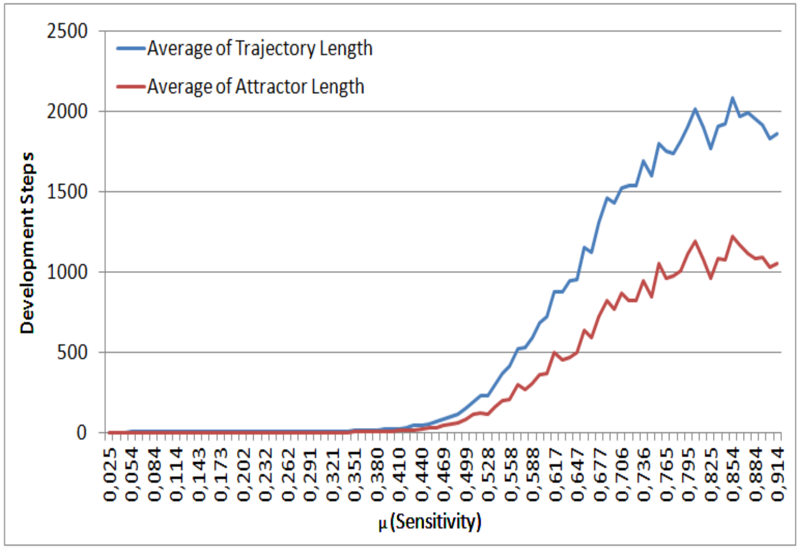
Average trajectory and attractor length



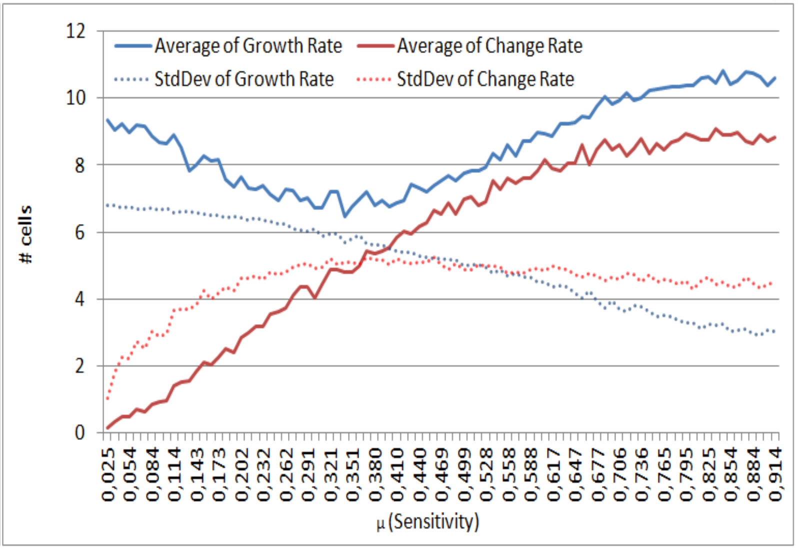
Average growth and change rate

Results - µ

Measurements in correlation to µ, average over 1000 tests for each µ value



Average trajectory and attractor length



Average growth and change rate

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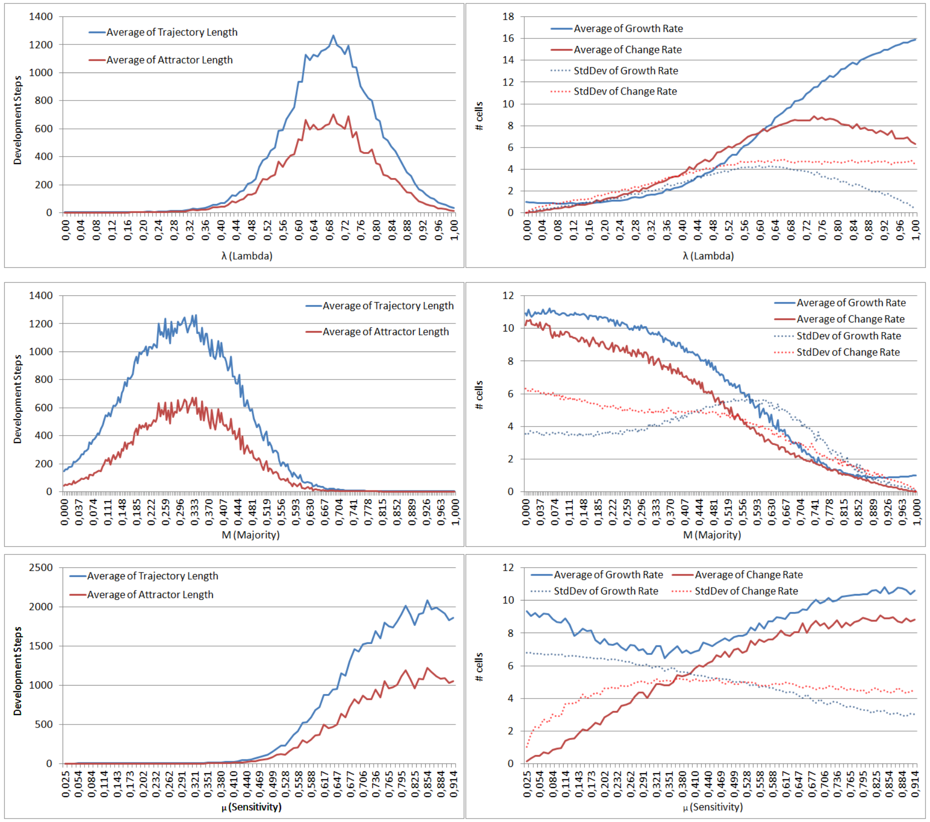
Comparison



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Conclusion

- Each genome parameter has a specific ability to measure properties of the resulting organism
- Knowledge of probable developing properties may be helpful at the design stage of an EvoDevo system, if information on the desired target phenotype is known
- Possible to use more parameters together to compose desired developmental behaviors, not achevable with a single parameter
- Adaptivity and evolution: genomes with a given parameter value will most likely mutate to genomes with similar developmental behavior, as long as the mutation results in an offspring with similar parameter value
- Guide evolution towards favorable areas of the solution space where desired developmental behaviors are more likely to be found

Future Work

- Other phenotypic measures of complexity, e.g. structural complexity
- Use parameters to drive evolution in desired areas of the search space
- Use parameters to supervise genetic operators
- ......

Genomes generation with λ parameter

Genomes generated with predefined values of λ

Similar method to Langton’s random table method

For every entry in the development table:

- with probability (1- λ) the cell type at the next developmental step is quiescent (type 0)
- with probability (λ), the cell type at the next developmental step is generated by a uniform random distribution among the other cell types (type 1 or 2)

Genomes generation with *M* parameter

- if there are more than 3 occurrences of a cell type:
  - with probability M the cell type at the next developmental step follows the most present cell type in the neighborhood
  - with probability 1-M the cell type at the next developmental step is generated by a uniform random distribution among the other two cell types (the minority in the neighborhood)
- If there are 2 cell types with occurrence 2
  - with probability M/2 one of those 2 cell types is chosen
  - with probability 1–M the cell type at the next developmental step has the same type as the less present cell type in the neighborhood

Genomes generation with *μ* parameter

μ is easily computable for a specific development table

Much harder to generate a development table with a target μ value, because of entry dependencies

A Genetic Algorithm is used