INVESTIGATING THE EVOLUTION OF DEVELOPMENTAL MECHANISMS IN DIGITAL MULTICELLULAR ORGANISMS

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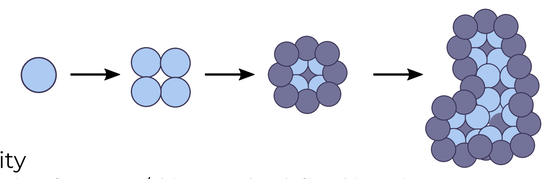
Abstract

Development in metazoan organisms is composed of a series of steps that give rise to intercellular heterogeneities and signalling capabilities. We have used Avida – an artificial life software platform to study how development associated processes change during evolution. Avida uses an agent-based model wherein autoreplicating evolvable computer programs compete for resources through innovation and deployment of a variety of mathematical tasks. In order to simulate multicellular clusters, we introduce spatially discrete and isogenic multicellular sub-populations in the world - called demes. Such a framework allows us to track the evolutionary dynamics of a series of quantifiable metrics, such as the number and diversity of distinct **unicellular phenotypes**, the **developmental time** as well as the degree to which organisms in the deme **communicate** and **sense** their surroundings. Our preliminary experiments indicate - perhaps unsurprisingly - towards a nonlinear disparate relationship between the evolution of the genomic complexity and what can be encapsulated by considering all the above phenotypic metrics as, developmental complexity.

Terminology

Development

Development of organisms is the process wherein cells divide, differentiate and proliferate in tissues, set up a body axis, and form organs. It is a well regulated process and this is usually summed up as the presence of a **developmental program** for the organism.



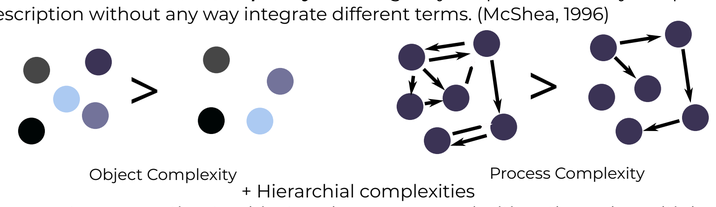
Complexity

The complexity of a system/object can be defined in various ways.

A. Kolomogorov Complexity : Length of the shortest computer program that produces the object as an output. (Used for sequences, Kolomogorov 1968)

B. Physical Complexity : Summation of amount of information stored at all sites in the genome based on their substitution frequencies. (Used for the genome, Adami 2000)

C. McShea Structural Complexity : Biologically inspired but only a qualitative description without any way integrate different terms. (McShea, 1996)

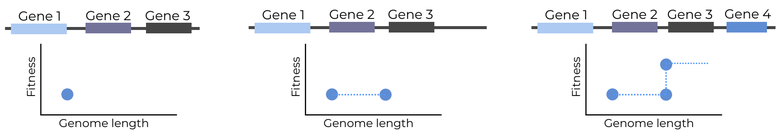


In our system, we estimate object and process complexities through multiple gross measures.

- Object Complexity : Number of cells, degree of differentiation.

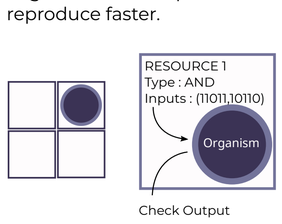
- Process Complexity : Number of communication channels.

Complexity ≠ Utility



Avida

- Agent based simulation framework with genotype-phenotype discretization (*A* - artificial, *-vida* - life)
- Genome is made of instructions from an instruction set. (Turing complete)
- Organisms that perform certain mathematical tasks acquire resources and reproduce faster.



Inst	AX	BX	CX	Stack	Output
1 IO	?	X	?	?	?
2 push	?	X	?	X, ?	
3 pop	?	X	X	?	
4 nop-C					
5 nand	?	~X	X	?	
6 IO	?	Y	X	?	~X

NOT

To model multi-cellular organism dynamics, the avida world is divided into subpopulation - or *demes*.

- .Organisms in a deme reproduce independently of organisms in other demes and place offspring only within the same deme. There is no mutation during this process.
- Organisms can donate their accumulated resources to the deme. A deme that reaches a particular resource threshold reproduces by replacing a neighbor deme.

- We assay deme properties by isolating them in a test environment. The world geometry is periodic.

Method

Deme Runs

World size in X : 5
World size in Y : 1000
Deme size : 25 (5x5) - total max 200 demes
1. A single organism with an ancestral genotype is injected into an empty deme.
2. The organisms can incorporate instructions that allow them to **communicate** with neighbors, **sense their position** in the deme, and even exit or join the **germline** of their deme.
3. **Phenotypic heterogeneity** can arise due to formation of information processing pipelines.

Unicellular runs

World size in X : 5
World size in Y : 1000
Number of organisms : max 5000
These organisms reproduce as soon as they genome is completely executed.

Measurements

A single long evolutionary run is conducted for **1.5 million updates**. The demes organisms from each update are taken and analysed in a separate isolated environment where different properties are measured.

Fitness of an organism : Metabolic rate divided by gestation time of the organism

Fitness of a deme : Average rate of resource acquistion over lifetime.

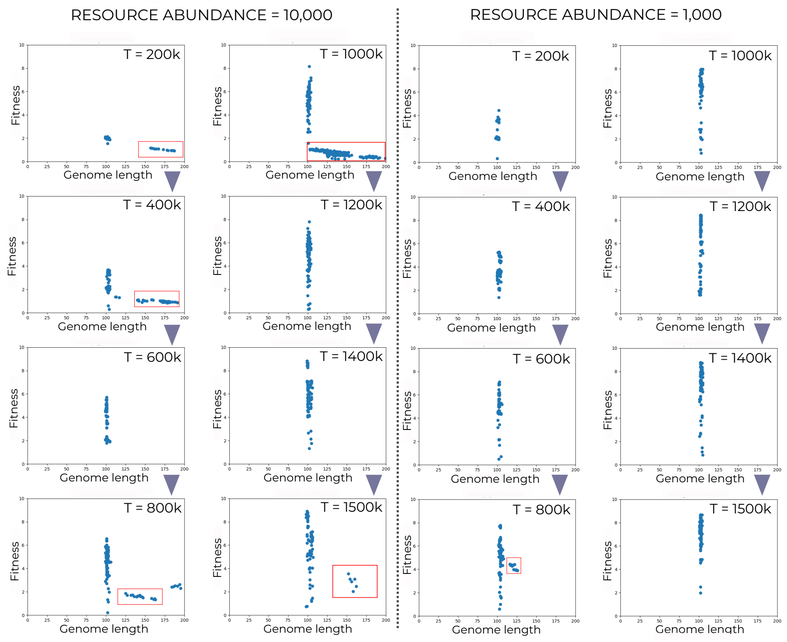
Results

Population fitness structure

The population fitness structure at a particular update is the scatter plot of a particular property of genotypes in the population against their fitness.

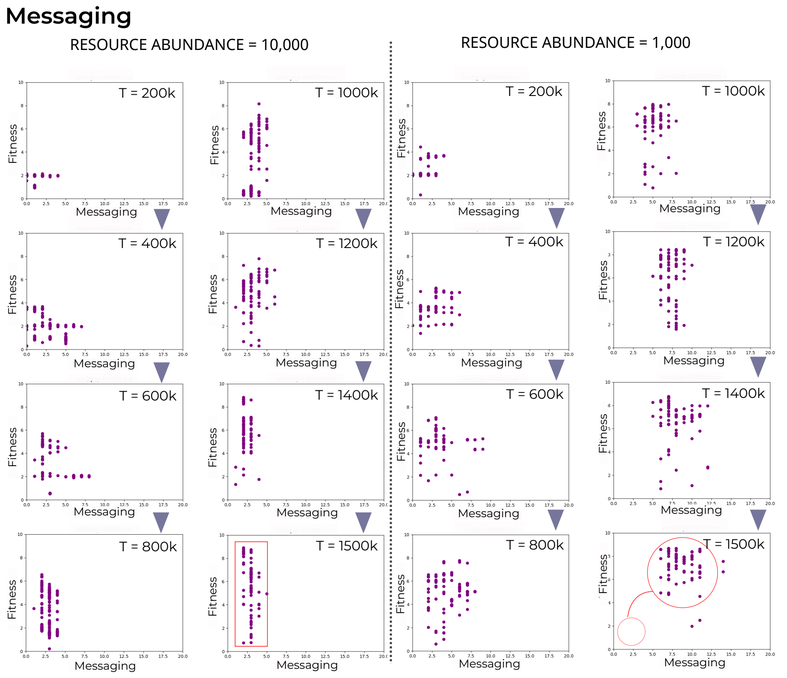
VARYING RESOURCE CONDITIONS

Genome length (genomic structural complexity)



Hypothesis 1 : *High resource abundance allows appearance of high complexity outliers. Low resource condition is highly selective and restrictive to changes in complexity. Genomic structural complexity is* ***relatively*** *tightly bound in both cases.*

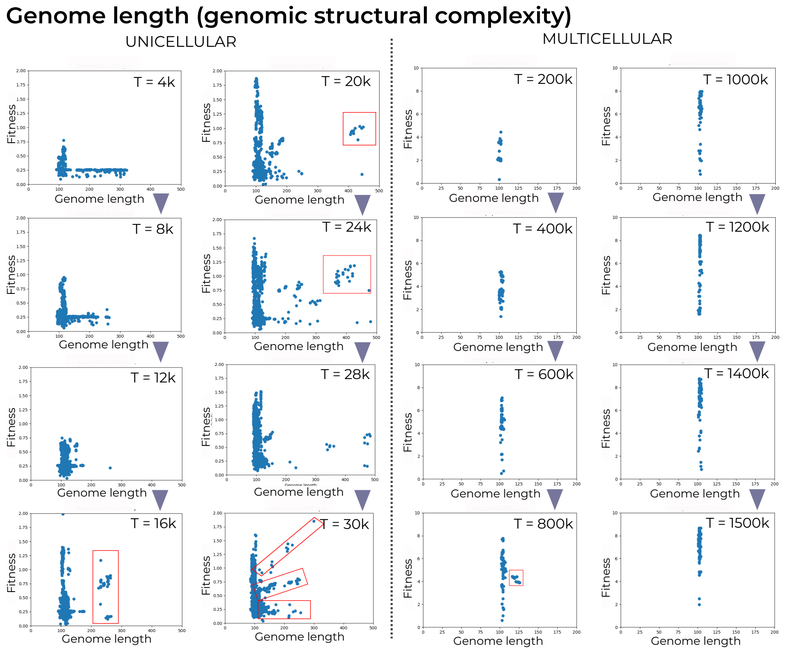
Messaging



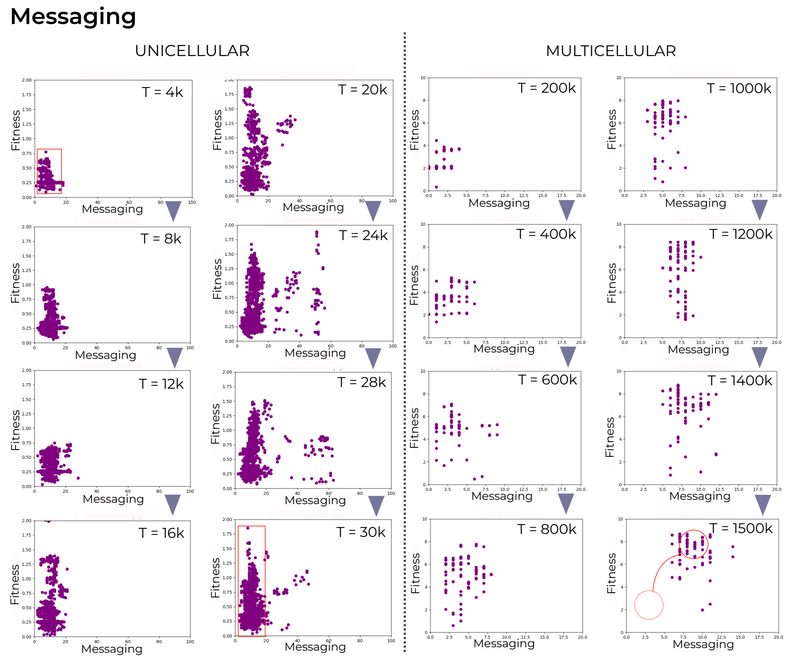
Hypothesis 2 *: Multicellular organisms in low resource environments develop higher instances of messaging and sensing required for division of labor (also seen previously in [2]). The messaging processes correlate well with fitness of these organisms.*

UNICELLULAR VS MULTICELLULAR

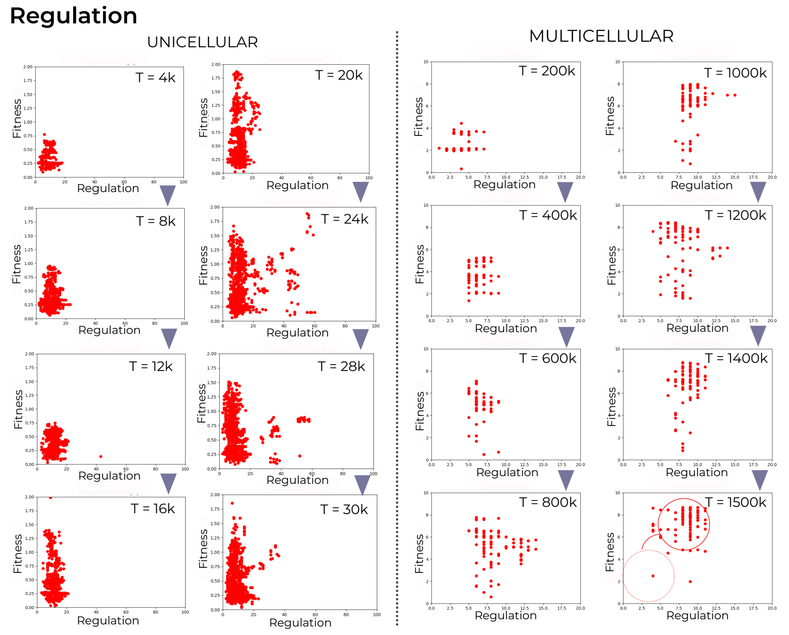
Genome length (genomic structural complexity)



Messaging



Regulation



No population shift is observed in the case of unicellular populations. The fitness of these populations increase over time but they do not incorporate new regulation/ sensing instructions in a stable fashion while at the same time increasing their fitness.

Hypothesis 3 *: Unicellular organisms rely majorly on changes in genomic complexity to bring about evolutionary innovations as compared to multicellular organisms - that rely on regulation and signalling to innovate new solutions.*

Conclusion

In this work, we present a new framework to answer questions involving the evolution of developmental pathways in multi-cellular organisms and present preliminary results indicating the relative importance of genomic complexity and extra-genomic pathways in unicellular and multicellular organisms.

Our results indicate that low resource conditions hinder the appearance of high complexity genomes and facilitates messaging to be incorporated as a functional process.

They also hint towards the relatively important but disparate roles of genomic complexity and other developmental functions in unicellular and multicellular evolving organisms.

Future work

- Use metrics to quantify the contribution of the genome and non-genome to fitness.
- Develop a concise methodology that takes in account these rough complexity measures and integrates them into a single "developmental complexity".
- Study how network topologies evolve in demes where messaging plays a major role in fitness acquistion.
- Use the physical complexity metric (*sensu* Adami) to see if developmental features allow major transitions without increase in genomic complexity.

References

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