ResearchGate

See discussions, stats, and author profiles for this publication at: https://www.researchgate.net/publication/318375058

Increasing the complexity of solutions produced by an evolutionary developmental system

Conference Paper · July 2017
DOI: 10.1145/3067695.3075999

CITATION
1

READS
21

4 authors:

Heather Goldsby
University of Washington Seattle
31 PUBLICATIONS **614** CITATIONS
SEE PROFILE

Becca Young
University of Texas at Austin
24 PUBLICATIONS **751** CITATIONS
SEE PROFILE

Hans A Hofmann
University of Texas at Austin
149 PUBLICATIONS **4,741** CITATIONS
SEE PROFILE

Arend Hintze
Michigan State University
86 PUBLICATIONS **895** CITATIONS
SEE PROFILE

Some of the authors of this publication are also working on these related projects:

Project evolution of artificial intelligence View project

Project Evolution of the neuromolecular substrates underlying vertebrate social behavio View project

All content following this page was uploaded by Hans A Hofmann on 15 February 2018.

The user has requested enhancement of the downloaded file.

Increasing the Complexity of Solutions Produced by an Evolutionary Developmental System

Heather J. Goldsby
Department of Computer Science and Engineering, Michigan State University
BEACON Center for the Study of Evolution in Action
hjg@msu.edu

Rebecca L. Young
Department of Integrative Biology, The University of Texas at Austin
Center for Computational Biology and Bioinformatics, The University of Texas at Austin
BEACON Center for the Study of Evolution in Action
youngrl@utexas.edu

Hans A. Hofmann
Department of Integrative Biology, The University of Texas at Austin
Center for Computational Biology and Bioinformatics, The University of Texas at Austin
Institute for Cellular and Molecular Biology, Institute for Neuroscience, The University of Texas at Austin
BEACON Center for the Study of Evolution in Action
hans@utexas.edu

Arend Hintze
Department of Integrative Biology, Michigan State University
Department of Computer Science and Engineering, Michigan State University
BEACON Center for the Study of Evolution in Action
hintze@msu.edu

ABSTRACT

Evolutionary computation and neuroevolution seek to create systems of ever increasing sophistication, such that the digitally evolved forms reflect the variety, diversity, and complexity seen within nature in living organisms. In general, most evolutionary computation and neuroevolution techniques do so by encoding the final form without any type of development. This is in contrast to nature, where most complex organisms go through a developmental period. Here we focus on an evolving digital tissues that develop from a single cell and unfold into a complex body plan. It quickly became evident that evolving developing forms is quite challenging. We compare four different techniques that have successfully been employed within evolutionary computation to evolve complex forms and behavior: scaffolding (i.e., gradually increasing the difficulty of the task rewarded by the environment over evolutionary time), stepping stones (i.e., rewarding easier tasks within an environment that can co-opted for the performance of more complex tasks), and island models (i.e., rewarding different fitness functions within different subpopulations with migration). We show the effect of these methods on the evolution of complex forms that develop from a single cell, the rate of adaptation, and different dimensions of robustness and variation among solutions.

KEYWORDS

Artificial life, Markov Brains, digital tissues

ACM Reference format:
Heather J. Goldsby, Rebecca L. Young, Hans A. Hofmann, and Arend Hintze. 2017. Increasing the Complexity of Solutions Produced by an Evolutionary Developmental System. In *Proceedings of GECCO '17 Companion, Berlin, Germany, July 15-19, 2017,* 2 pages.
DOI: http://dx.doi.org/10.1145/3067695.3075999

Permission to make digital or hard copies of all or part of this work for personal or classroom use is granted without fee provided that copies are not made or distributed for profit or commercial advantage and that copies bear this notice and the full citation on the first page. Copyrights for components of this work owned by others than ACM must be honored. Abstracting with credit is permitted. To copy otherwise, or republish, to post on servers or to redistribute to lists, requires prior specific permission and/or a fee. Request permissions from permissions@acm.org.
GECCO '17 Companion, Berlin, Germany
© 2017 ACM. 978-1-4503-4939-0/17/07…$15.00
DOI: http://dx.doi.org/10.1145/3067695.3075999

1 INTRODUCTION

Within biology there are many pressing topics surrounding our understanding of how developmental systems evolve. These include understanding major transitions in evolution, such as the transition from unicellular to multicellular organisms [3, 11, 12], the effects and possible treatments for lesions [8, 13] and cancers [1, 7] within multicellular organisms, and the evolution of the many complex and fascinating body plans we see in the world around us [4]. A central aspect of each of these topics is the nuanced interplay between the development of an individual organism, which determines how it changes throughout its lifetime, and evolutionary pressures, which shape how generations of organisms change throughout time at a larger scale. Here, we address the need for an evolutionary system in which the organisms also exhibit development by creating a computational evo-devo model that can be used to tackle the evolutionary-developmental questions faced by biologists.

For this work, we designed a computation model that allows us to evolve multicellular organisms (called *digital tissues*), where each digital tissue starts as a single cell that develops into a 2D tissue of differentiated cells (similar to [6]). The behavior of the cells are controlled by evolving Markov Brains, which are networks of deterministic and probabilistic logic gates encoded in an evolvable fashion [5, 10]. These 2D tissues of differentiated cells evolve in response to selection for a particular target pattern or body plan. Figure 1 provides an example of four such target patterns. Each large square represents a body plan or pattern. Each smaller square represents a cell, where cell fate is indicated by color. Each cell within the tissue has several capabilities: reproduce to form another cell, migrate to an adjacent location, sense properties of its environment (including whether it is on the edge of the tissue space, whether its location has been marked with any resources, and the cell fates of its cardinal neighbors), and communicate with neighboring cells (by sending and receiving messages from its cardinal

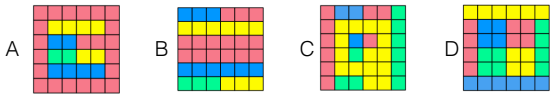

Figure 1: Four two-dimensional target patterns used as digital analogs for body plans. Each large square represents one pattern, each smaller square represents a cell. Cell fate is denoted by color.

neighbors). This information can be used by the cell to express its own cell fate (depicted as color), which is the only aspect of the cell to effect the body pattern of the tissue and its fitness. The evolutionary success (or failure) of the digital tissue is determined by the degree to which its cells express a target pattern rewarded so that more matching cells give an exponential increase in fitness.

Using this system we address the question: What evolutionary techniques can be used to produce complex patterns, thus enabling us to tackle questions surrounding evolutionary-developmental systems? In particular, we compare: (1) Direct evolution, where the fitness of each digital tissue is how closely it matches the target pattern. (2) Stepping stone evolution, where in addition to providing fitness incentives for matching the desired target pattern, the digital tissue also receives fitness rewards for matching simpler patterns that should serve as stepping stones to the more complex pattern [9]. We use two different weighting schemes – **stepping stones - flat**: a naive weighting scheme, where all patterns received the same weight, and **stepping stones - exp**: an exponential weighting scheme, where each pattern was weighted according to its complexity. (3) Scaffolding, where digital tissues are placed under different selective pressures over evolutionary time that build from selecting for simple patterns to more complex patterns [2], and (4) Island model evolution, where distinct subpopulations reward for different patterns [14]. For the first treatment (**island**), we created four islands for the desired four patterns (A, B, C, and D). For the second treatment (**island - many**), we included islands for the intermediary patterns we created for the scaffold approach.

We compare the performance of these various evolutionary techniques along three different dimensions, which are the quality of the complex pattern evolved, the rate of adaptation (or number of evaluations required to evolve a complex pattern), and the robustness of the evolved patterns to environmental sensor perturbation. In general, the island models produced the highest quality complex patterns (Figure 2). The island model that just had islands for the four target patterns provided the best blend of quality of result, number of evaluations, and number of updates. Neither island models nor scaffolding had a stronger effect on robustness or diversity of the solutions than any other technique. This suggests that either technique can be used, without biasing the resulting developmental process to have any particular preferences.

Taking all of this into account, we would propose to use an island model to evolved the highest level of complexity. The methods all differed in their effect on robustness, but the different kind of patterns influenced theses differences much more. In the future

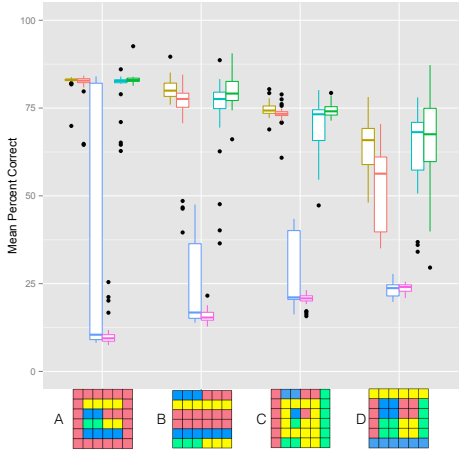

Figure 2: The mean performance of the various techniques for the four target patterns. Performance is measured in terms of the percentage of cells that exactly match the target pattern. The results are grouped by pattern, where each bar represents the performance of a particular treatment on a specific pattern. Color denotes treatment.

we will explore the role the actual complexity of the pattern plays in the evolution of a developmental process. In addition, we are working to leverage this developmental model to test evolutionary developmental hypotheses.

REFERENCES

[1] Bogenrieder, T., and Herlyn, M. Axis of evil: molecular mechanisms of cancer metastasis. *Oncogene 22*, 42 (2003), 6524–6536.
[2] Bongard, J. Morphological change in machines accelerates the evolution of robust behavior. *Proceedings of the National Academy of Sciences 108*, 4 (2011), 1234–1239.
[3] Calcott, B., and Sterelny, K., Eds. *The major transitions in evolution revisited.* MIT Press, 2011.
[4] Carroll, S. B. *Endless forms most beautiful: The new science of evo devo and the making of the animal kingdom.* No. 54. WW Norton & Company, 2005.
[5] Edlund, J. A., Chaumont, N., Hintze, A., Koch, C., Tononi, G., and Adami, C. Integrated information increases with fitness in the evolution of animats. *PLoS Comput Biol 7*, 10 (2011), e1002236.
[6] Federici, D., and Downing, K. Evolution and development of a multicellular organism: scalability, resilience, and neutral complexification. *Artificial life 12*, 3 (2006), 381–409.
[7] Hanahan, D., and Weinberg, R. A. Hallmarks of cancer: the next generation. *cell 144*, 5 (2011), 646–674.
[8] Kragl, M., Knapp, D., Nacu, E., Khattak, S., Maden, M., Epperlein, H. H., and Tanaka, E. M. Cells keep a memory of their tissue origin during axolotl limb regeneration. *Nature 460*, 7251 (2009), 60.
[9] Lenski, R. E., Ofria, C., Pennock, R. T., and Adami, C. The evolutionary origin of complex features. *Nature 423* (2003), 139–144.
[10] Marstaller, L., Hintze, A., and Adami, C. The evolution of representation in simple cognitive networks. *Neural computation 25*, 8 (2013), 2079–2107.
[11] Maynard Smith, J., and Szathmáry, E. *The major transitions in evolution.* Oxford University Press, New York, NY, USA, 1997.
[12] Ratcliff, W. C., Denison, R. F., Borrello, M., and Travisano, M. Experimental evolution of multicellularity. *Proceedings of the National Academy of Sciences 109*, 5 (2012), 1595–1600.
[13] Vaughan, R., and Trinkaus, J. Movements of epithelial cell sheets in vitro. *Journal of cell science 1*, 4 (1966), 407–413.
[14] Whitley, D., Rana, S., and Heckendorn, R. B. The island model genetic algorithm: On separability, population size and convergence. *Journal of Computing and Information Technology 7* (1998), 33–47.

View publication stats