The evolution of information representation in biological networks

Cameron Ray Smith¹, Aviv Bergman^{1,2,3}

¹ Department of Systems and Computational Biology,

² Dominick P. Purpura Department of Neuroscience,

³ Department of Pathology, Albert Einstein College of Medicine,

1301 Morris Park Ave, Bronx, NY 10461, USA

(Dated: September 30, 2012)

Abstract text

Contents

I. Hierarchy in logic 1 A. Russell's paradox 1 1 B. A type theoretic resolution C. Categorical type theory 1 II. Information representation 1 A. Information theory 1 B. Signaling games 1 C. Domain theory 1 III. Biological information 1 A. Niche construction and multilevel selection 1 2 B. The structure of molecular networks 1. Endo-genetics, genetics, epi-genetics, and 2 n-epi-genetics C. Hierarchical organization and evolution 2 2 Acknowledgements 2 A. Category theory for tourists 2 References

I. HIERARCHY IN LOGIC

A. Russell's paradox

A theorem due to Cantor states that given a set X and a map of sets f it is impossible to find a mapping

$$f: X \to 2^X$$

where 2^X represents the set of all subsets of X also referred to as the powerset of X.

B. A type theoretic resolution

C. Categorical type theory

See [1].

II. INFORMATION REPRESENTATION

A. Information theory

See [2] and [3].

B. Signaling games

See [4].

C. Domain theory

See [5], [6].

III. BIOLOGICAL INFORMATION

A. Niche construction and multilevel selection

The concept of selection is foundational to evolutionary theory. More recently, a concept referred to as niche construction that we consider to be complementary to selection, in a sense to be made precise, has been introduced [7, 8]. An organism experiences a situation similar to that represented in diagram A.1.

The molecular interaction network that underlies an arbitrary type of organism is represented by a category \mathcal{D} and the environment is represented by a category \mathcal{C} . Due to the dependence of selection on the environment, those organisms capable of survival are those that most closely approximate a natural transformation $\eta: F \circ G \Rightarrow H$. Why might this be the case?

To answer this question requires consideration of the necessity of the category \mathcal{J} in this conceptual framework. From the perspective of any organism, we can

roughly think of \mathcal{D} as "internal" and \mathcal{C} as "external" in a sense that can be likened but not yet clearly identified with "known" and "unknown" respectively. The selection process can be thought of as requiring the organism to establish a representation of properties of \mathcal{C} so as to enable its existence to remain complementary, and thus stable, relative to its environment. The molecular network underlying the various biochemical functions of the organism has no direct access to the processes that determine the causal structure of the environment. In this case we consider the organism to have direct access only to the structure contained in \mathcal{D} , but nevertheless being implicitly assigned, as a result of its relationship to the environment, the seemingly impossible task of establishing the structure of C. If C were internalized by the organism then relationships between \mathcal{D} and \mathcal{C} that preserve structure, specifically the functors labelled $H: \mathcal{D} \to \mathcal{C}$, could also be directly internalized. Since \mathcal{C} is external to \mathcal{D} , the organism must find another way of determining the relationship between its internal structure and that which is external, even if local.

One way to address this apparently paradoxical situation is to consider the relationship between endofunctors on \mathcal{D} and those like H. In the case of A.1, \mathcal{J} is considered

to be a subcategory of $\mathcal D$ that contains all the domains (in the sense of complete partial orders) of $\mathcal D$. This scenario allows functors $F:\mathcal J\to\mathcal D$ to index diagrams in $\mathcal D$

See [9] for information on multilevel selection.

B. The structure of molecular networks

- 1. Endo-genetics, genetics, epi-genetics, and n-epi-genetics
 - C. Hierarchical organization and evolution

See [10], [11].

Acknowledgements

CRS was supported by . AB was supported by .

Appendix A: Category theory for tourists

- Roy L. Crole. Categories for Types (Cambridge Mathematical Textbooks). Cambridge University Press, 1994.
 I C
- [2] David Ellerman. Counting distinctions: on the conceptual foundations of Shannons information theory. Synthese, 168(1):119–149, March 2008. II A
- [3] Thomas M. Cover and Joy A. Thomas. Elements of Information Theory 2nd Edition (Wiley Series in Telecommunications and Signal Processing). Wiley-Interscience, 2006. II A
- [4] Simon M Huttegger. Evolution and the Explanation of Meaning. *Philosophy of Science*, 74(1):1–27, January 2007. II B
- [5] Samson Abramsky. Information, Processes, and Games. 2008. II C
- [6] Samson Abramsky and Achim Jung. Domain Theory. In Samson Abramsky, Dov M. Gabbay, and T. S. E. Maibaum, editors, *Handbook of Logic in Computer Science Volume 3. Semantic Structures*, volume 3, chapter 3,

- pages 1–168. Oxford University Press, 1995. II C
- [7] F. John Odling-Smee, Kevin N. Laland, and Marcus W. Feldman. Niche Construction: The Neglected Process in Evolution (MPB-37) (Monographs in Population Biology, 37.). Princeton University Press, 2003. III A
- [8] David C Krakauer, Karen M Page, and Douglas H Erwin. Diversity, dilemmas, and monopolies of niche construction. The American naturalist, 173(1):26–40, January 2009. III A
- [9] Samir Okasha. Evolution and the levels of selection. Oxford University Press, USA, New York, 2006. III A
- [10] S J Gould. Tempo and mode in the macroevolutionary reconstruction of Darwinism. PNAS, 91(15):6764-71, July 1994. III C
- [11] A.J. Arnold and Kurt Fristrup. The theory of evolution by natural selection: a hierarchical expansion. *Paleobiology*, 8(2):113–129, 1982. III C