Artificial Life

Study of the Evolutionary/Pragmatics of BioSemiotics

- Life as it could be
- Abstract Simulations

Luis Rocha
2001

http://www.c3.lanl.gov/~rocha/bioinformatics
The Origin of Codes

Reproduction is Possible Without Codes

Why Are codes important for evolution?

Dynamics
Rate-Dependent
Catalytic

Memory
Rate-Independent
Inheritable

- Both peptide [Ghadiri et al] and nucleic acid chains are capable of template replication.
  - Only a small fraction of peptide sequences can though – occasional templates. RNA is an obligatory template
Coded Reproduction

Open-ended Evolution

- Can consistently produce any configuration from a stable, inheritable description
  - Not Just those whose initial conditions are recoverable
- Variation on descriptions
  - Not on phenotypes
- Can reproduce complicated, developed phenotypes
- Open-ended evolution

Self-Organizing Agent + Description

Initial Conditions

Self-Organization and Development

Constructor

Memory

Dynamics

Transcription

Copier

Interpreter

Reader

Self-Organizing Agent + Description

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49
Coded vs. Noncoded Agents

Simulations of Evolutionary Potential

FDP Agent Evolution via Self-Inspection

FDP Agent Evolution with Genetic Algorithm

Initial Conditions

Self-Organizing Agent

Constructor

Transcription

Memory

Dynamics

Self-Organizing Agent

Description

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Coded Vs. Noncoded Agents

Simulations of Evolutionary Potential

Evolution with both types of agents

Under most conditions and types of evolutionary algorithms, coded agents overtake the population in a small number of generations.  /pattee/rocha.html

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Coded vs. Noncoded Agents

With high values of variation

Evolution with both types of agents

With too much genetic variation, the stability of descriptions is lost, resulting in occasional taking over of the population by noncoded agents.

/pattee/rocha.html
The Origin of Codes

How would an RNA code work?

- How can a dual-function RNA molecule induce an evolutionary process?
  - They need to be stable (non-reactive) to carry information, while at the same time they need to be reactive to perform some (auto) catalytic function.

- Pure catalytic world (no code)
  - Requires some reader/constructor such as the self-organizing agents of previous simulations (self-inspection)
  - Protein world would offer richer dynamics

- Template Reproduction (no code)
  - Enzyme-free template-induced synthesis of long RNA molecules from monomers has not been achieved. Dissociation problem.
  - The more complex a ribozyme is, the more difficult it is to reproduce it as a template. A reader/constructor would be needed (self-inspection)
A Primordial RNA Editing Code?

- Inheritable RNA fragments with assembly (development) of complex catalytic ribozymes
  - Arts and Benne [1996] suggested RNA editing as a mechanism to integrate non-reactive, inheritable small RNA molecules into reactive ribozymes.
  - Small fragments can be ligated [von Kiedrowski, 1986]
The RNA Editing Code

How would it work?

The Self-Reproducing Unit

May even include aminoacid cofactors

Catalysis

Editor

Copy

Memory

Code

Dynamics

Self-Organization and Development

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The RNA Editing Code

How to Study it Computationally

- How easy is it to obtain a given functional RNA structure?
  - There are typically a small set of very large Neutral networks (common structures), and a large set of very small ones.
    - The fraction of sequences folding into common structures increases with length (100% in the limit).
- What does editing do to neutral networks?
- Are memory/functional sequences common?

- Need of collaborative effort in biocomputing

[References]

[URL]
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The Sequence Editing Code

An Artificial Life Experiment

Self-organizing process

\[ S = 10011010 \ldots 101 \]

\[ 1 - p_{\text{functional}} \]

Catalysis

\[ p_{\text{catalysis}} = p_{\text{functional}} \]

Catalyzes matching unfolded sequences

- Autocatalysis is possible
  - But the higher the probability and intensity of obtaining a catalyst, the lower the probability of finding an unfolded target to catalyze

Note: Ribozyme catalysis requires sequence complementarity, thus their specificity is predominantly defined by complementarity, not 3-d structure

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Experiments

Low $p$ sequences in a population

Editors

$1/4$

$+1$

$-1$

$+11$

Different Concentrations (probabilities)

- If a family of editors is found which converts sequences from low to high $p$, for certain values of editors concentration, self-reproduction is viable.
  - With high concentrations, all low $p$ sequences may be converted

- Simulations
  - Found longer complex catalytic networks highly dependent on life-span of sequences

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