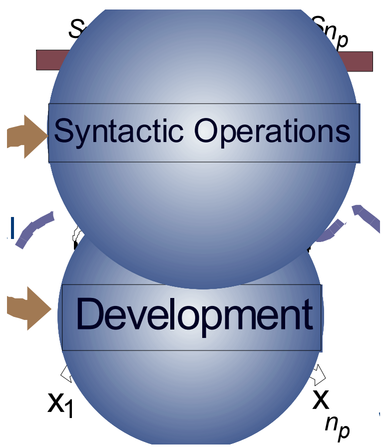
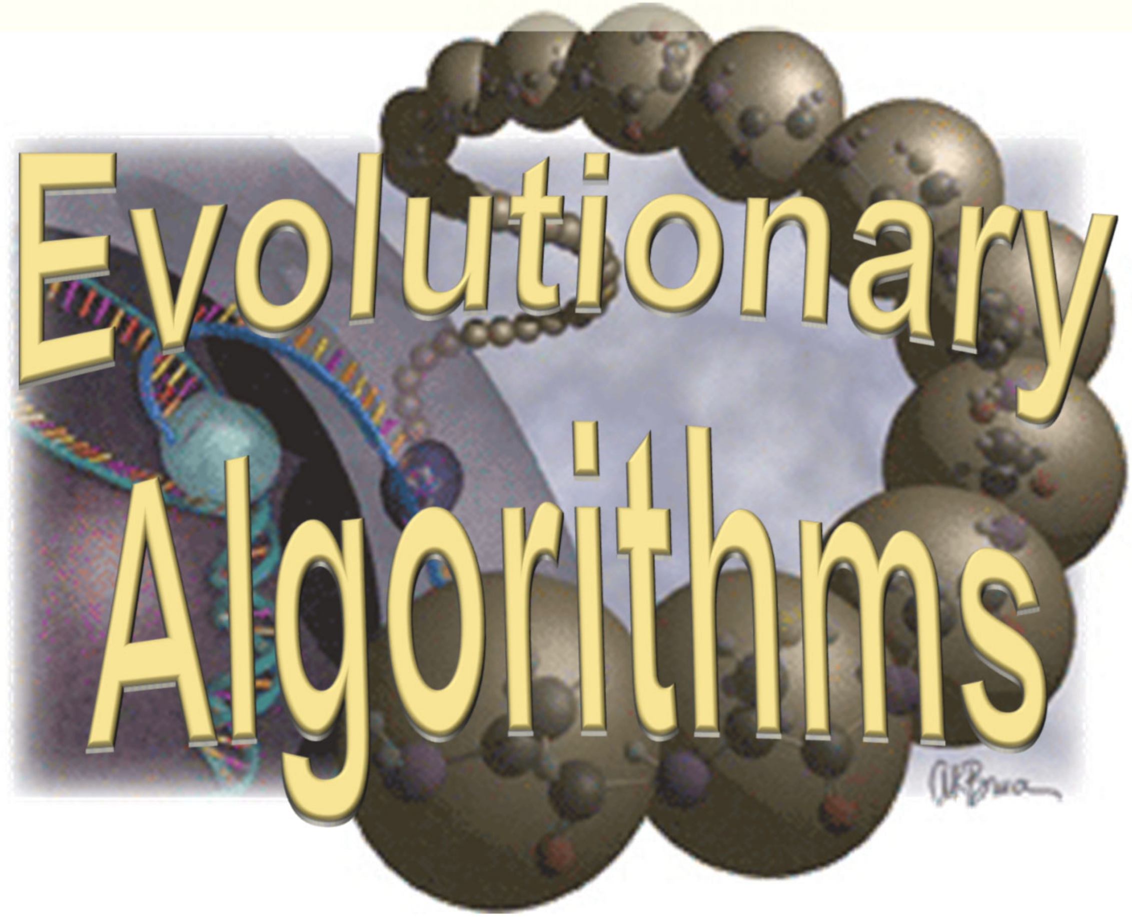
lecture 11 - Evolutionary Algorithms

bit.ly/atBIC





BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

key events coming up

- Labs: 35% (ISE-483)
  - Complete 5 (best 4 graded) assignments based on algorithms presented in
    - Lab 3: **March 31st**
      - Cellular Automata and Boolean Networks (Assignment 3)
        - Delivered by Kaeli Ahn and Erik Fiolkoski
        - Due: **April 7th**
    - Lab 4 : April 22nd (Tuesday after Easter break)????
      - Evolutionary Algorithms, (Assignment 4)
        - Delivered by Kristen Beideman
        - Due April 29th
- SSIE – 583 -Presentation and Discussion: 25%
  - Present and lead the discussion of an article related to the class materials
    - Enginet students post/send video or join by Zoom
  - April 22, 2025
    - Rik Pardun
      - Conrad, M. [1990]. "The geometry of evolution." *Biosystems* **24**: 61-81.
    - Kiet Ngo Tuan
      - Garg, Shivam, Kirankumar Shiragur, Deborah M. Gordon, and Moses Charikar. "Distributed Algorithms from Arboreal Ants for the Shortest Path Problem." *PNAS* **120**, no. 6 (February 7, 2023): e2207959120.
    - Eric Fiolkoski
      - Schmidt, M. and H. Lipson [2009]. "Distilling Free-Form Natural Laws from Experimental Data". *Science*, **324**: 81-85.

bit.ly/atBIC

sheepfilms.co.uk

rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

final project schedule

- Projects
  - **Due by May 7th** in Brightspace, "Final Project 483/583" assignment
    - ALIFE 2025
      - Not necessarily to submit to actual conference due date
        - May 4 full paper, July 4, abstract
      - https://2025.alife.org/
      - Max 8 pages, author guidelines:
      - https://2025.alife.org/calls#paper-call
      - MS Word and Latex/Overleaf templates
    - Preliminary ideas **by March 7**
      - Submit to "Project Idea" assignment in Brightspace.
  - Individual or group
    - With very definite tasks assigned per member of group

ALIFE 2025

Tackle a real problem using bio-inspired algorithms, such as those used in the labs.

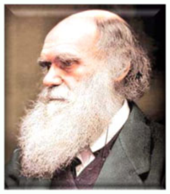
bit.ly/atBIC

Reusing and expanding labs is highly encouraged.

BINGHAMTON UNIVERSITY
STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

until now

- Class Book
  - Floreano, D. and C. Mattiussi [2008]. *Bio-Inspired Artificial Intelligence: Theories, Methods, and Technologies*. MIT Press. Preface**, Chapters 1 and 4.**
- Lecture notes
  - Chapter 1: What is Life?
  - Chapter 2: The logical Mechanisms of Life
  - Chapter 3: Formalizing and Modeling the World
  - Chapter 4: Self-Organization and Emergent Complex Behavior
  - Chapter 5: Reality is Stranger than Fiction
  - Chapter 6: Von Neumann and Natural Selection
    - posted online @ http://informatics.indiana.edu/rocha/i-bic

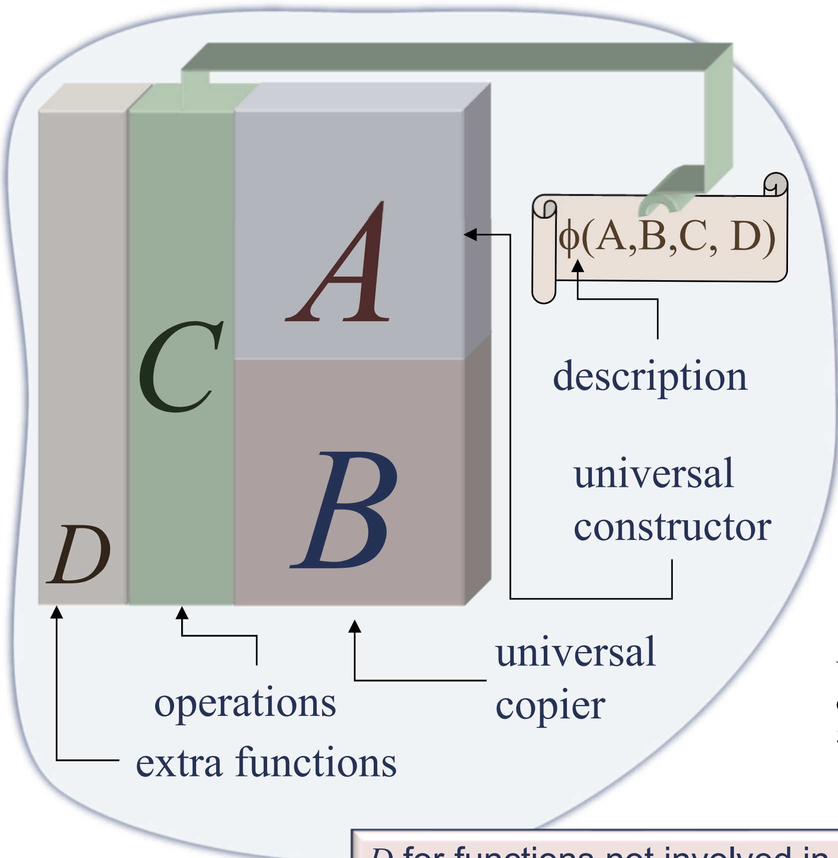


- Papers and other materials
  - Optional
    - Nunes de Castro, Leandro [2006]. *Fundamentals of Natural Computing: Basic Concepts, Algorithms, and Applications*. Chapman & Hall.
      - Chapter 2, 7, 8
      - **Chapter 3, sections 3.1 to 3.5**

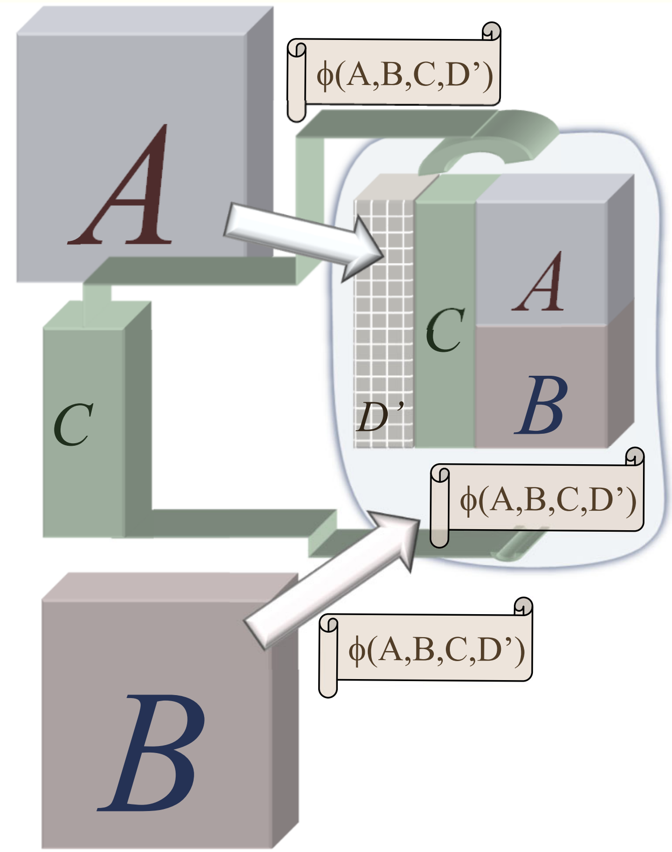
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

Von Neumann's generalization of Turing's tape

as a general principle (system) of evolution or **open-ended complexity**



Von Neumann, J. [1949]. "**Theory and organization of complicated automata**."
5 lectures at University of Illinois

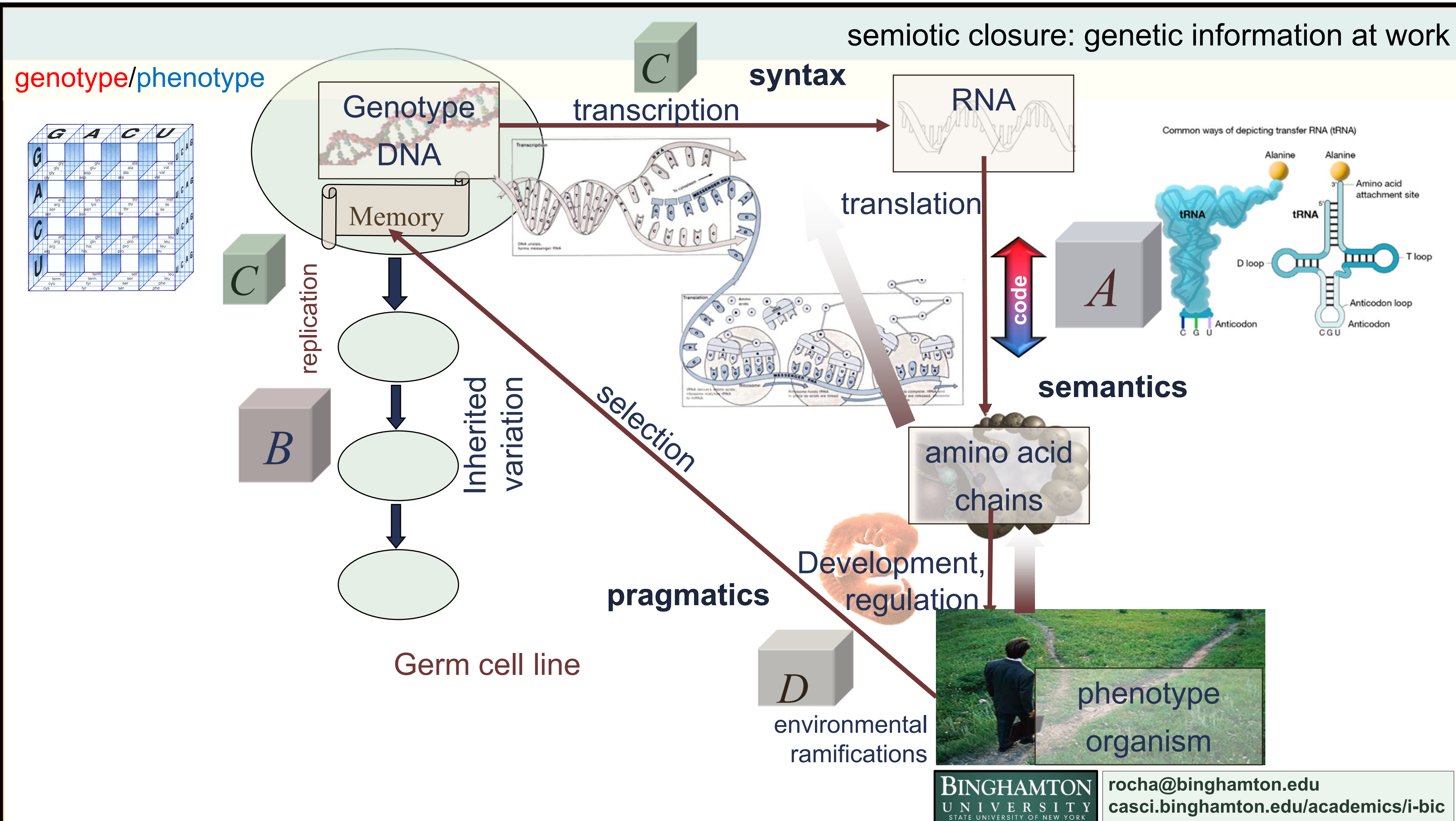


D for functions not involved in reproduction

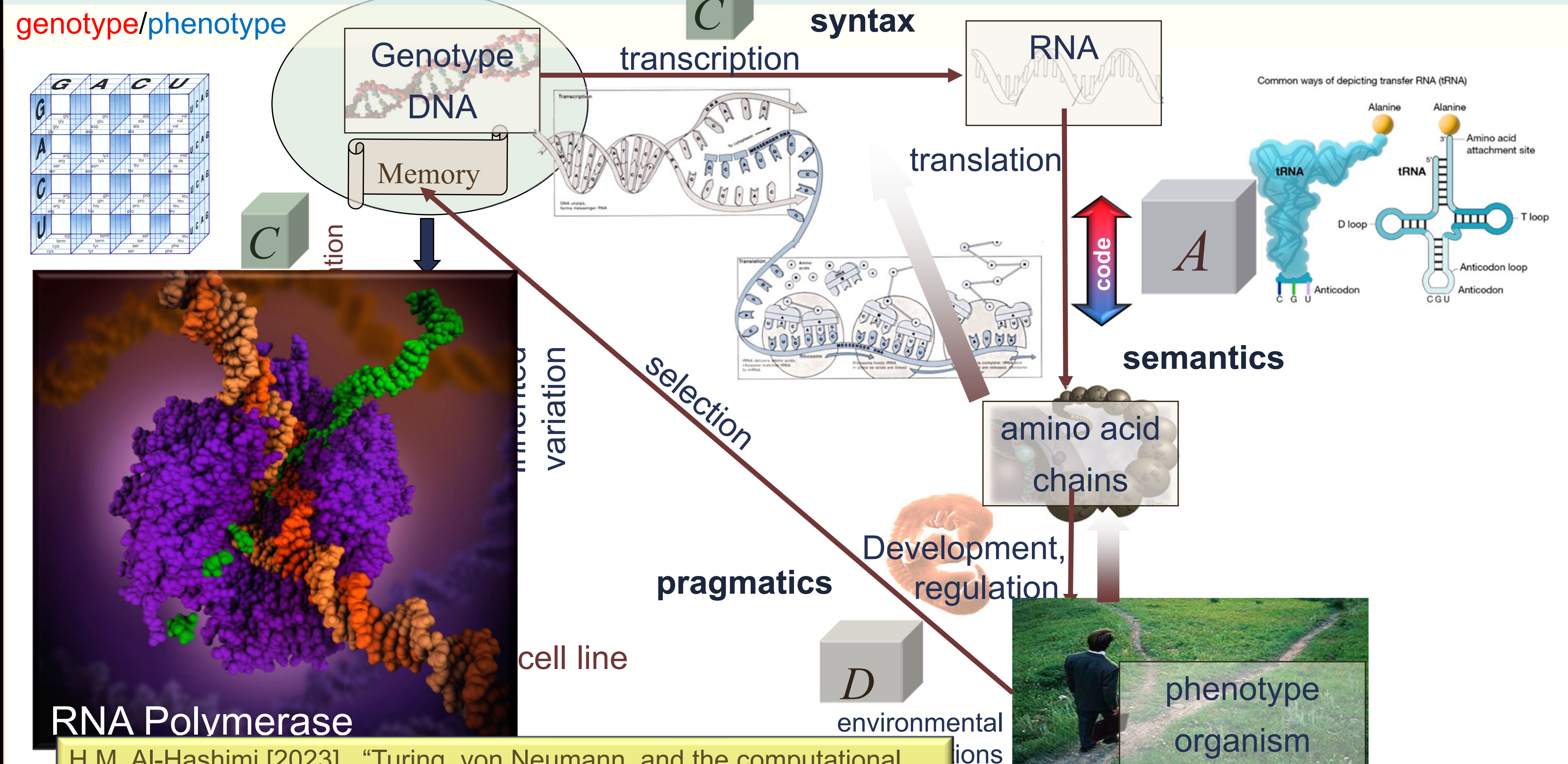
Mutations in *D* can be propagated *vertically*

Leads to **open-ended evolution**

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

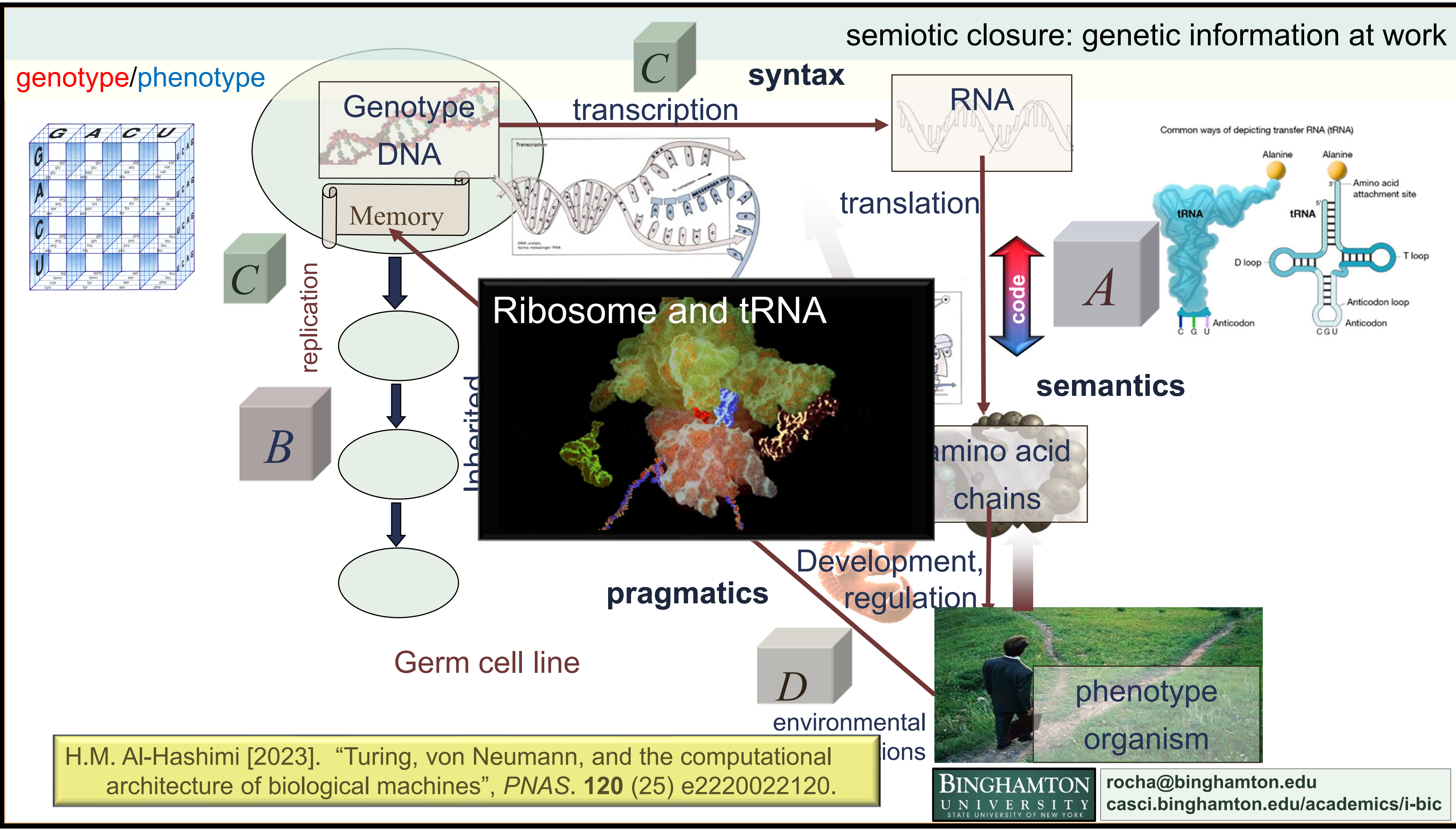

semiotic closure: genetic information at work
genotype/phenotype
Genotype
DNA
Memory
C
syntax
transcription
RNA
translation
code
A
semantics
Common ways of depicting transfer RNA (tRNA)
Alanine
Amino acid attachment site
tRNA
D loop
T loop
Anticodon loop
Anticodon
C
replication
B
Inherited variation
selection
amino acid chains
Development, regulation
pragmatics
Germ cell line
D
environmental ramifications
phenotype organism
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

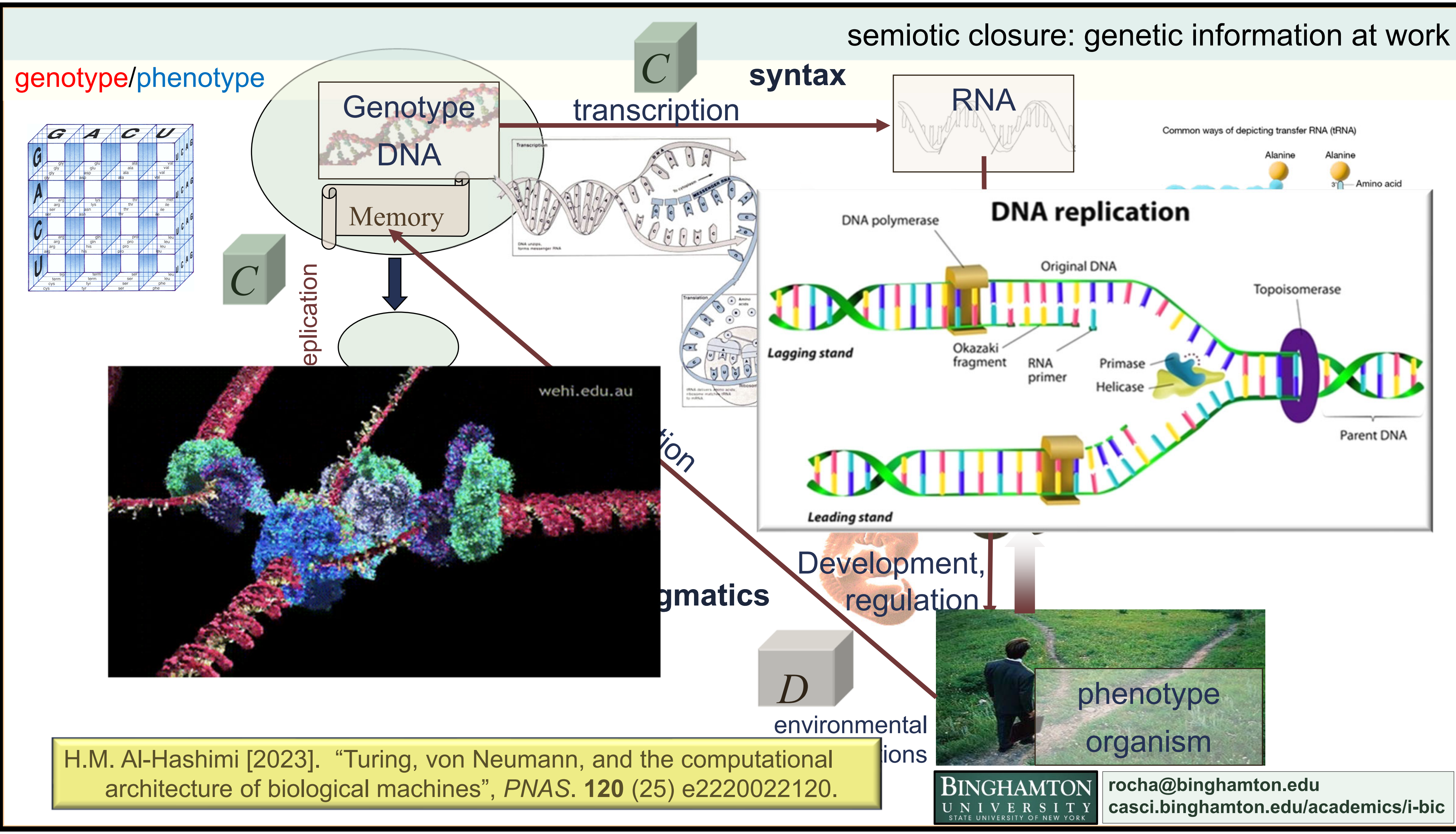
semiotic closure: genetic information at work

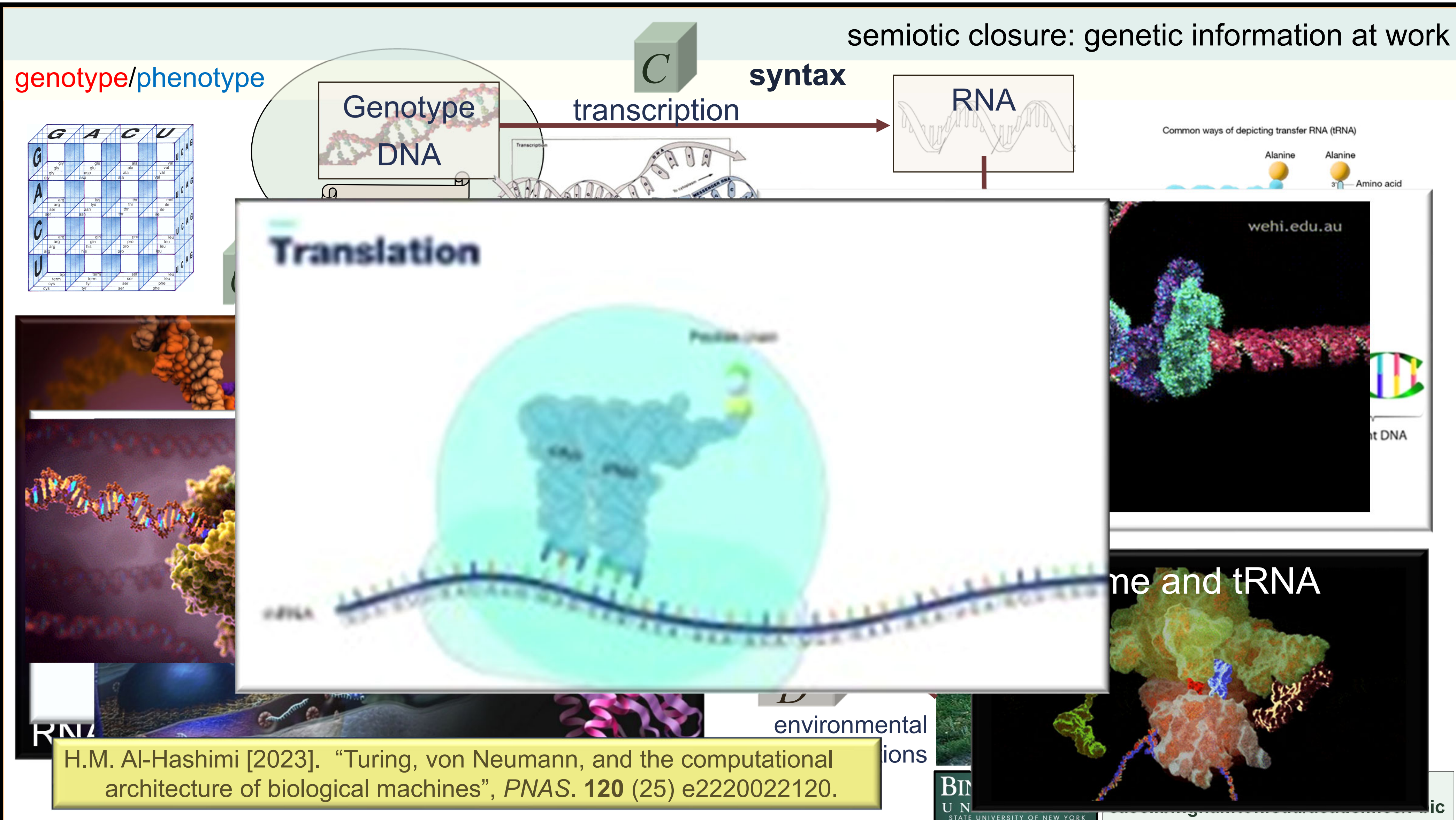


H.M. Al-Hashimi [2023]. “Turing, von Neumann, and the computational architecture of biological machines”, *PNAS*. **120** (25) e2220022120.

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic


semiotic closure: genetic information at work
genotype/phenotype
C
syntax
transcription
RNA
Genotype
DNA
Memory
translation
Common ways of depicting transfer RNA (tRNA)
Alanine
Alanine
Amino acid attachment site
tRNA
tRNA
D loop
T loop
Anticodon loop
Anticodon
Anticodon
code
A
C
replication
semantics
B
Ribosome and tRNA
chains
Development,
regulation
pragmatics
Germ cell line
D
environmental
phenotype
organism
H.M. Al-Hashimi [2023]. "Turing, von Neumann, and the computational architecture of biological machines", PNAS. 120 (25) e2220022120.
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic


semiotic closure: genetic information at work
genotype/phenotype
G A C U
G A C U
C
syntax
C
transcription
RNA
Genotype
DNA
Memory
eplication
tion
gmatics
Common ways of depicting transfer RNA (tRNA)
Alanine
Alanine
Amino acid
DNA replication
DNA polymerase
Original DNA
Topoisomerase
Lagging stand
Okazaki fragment
RNA primer
Primase
Helicase
Parent DNA
Leading stand
wehi.edu.au
Development,
regulation
D
environmental
ions
phenotype
organism
H.M. Al-Hashimi [2023]. “Turing, von Neumann, and the computational architecture of biological machines”, *PNAS*. **120** (25) e2220022120.
BINGHAMTON UNIVERSITY
STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic


semiotic closure: genetic information at work
genotype/phenotype
C
syntax
Genotype
DNA
transcription
RNA
Common ways of depicting transfer RNA (tRNA)
Alanine
Alanine
Amino acid
Translation
wehi.edu.au
environmental
H.M. Al-Hashimi [2023]. "Turing, von Neumann, and the computational architecture of biological machines", *PNAS*. **120** (25) e2220022120.

in biology

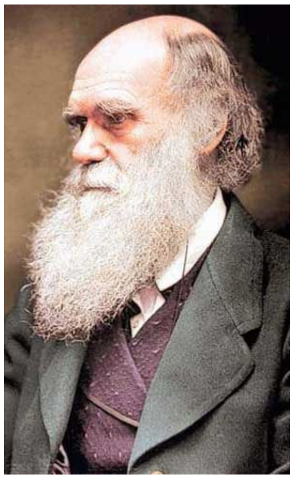
- The “information turn”
  - Unlike Schrödinger, Turing and Von Neumann had no direct effect on molecular biology
  - But the “external tape” separated from the constructor (semiotic closure) has become an unavoidable **principle of organization of biocomplexity**
  - A new synthesis?
    - In 1971 Brenner: “in the next twenty-five years we are going to have to teach biologists another language still, […] where a science like physics works in terms of laws, or a science like molecular biology, to now, is stated in terms of mechanisms, maybe now what one has to begin to think of is algorithms. Recipes. Procedures.”

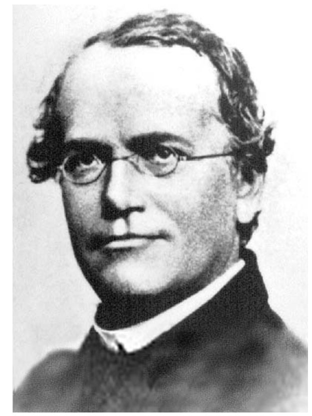
> “The concept of the gene as a symbolic representation of the organism — a ***code script*** — is a fundamental feature of the living world and must form the kernel of biological theory. […] at the core of everything are the tapes containing the descriptions to build these special Turing machines.” (Sydney Brenner)

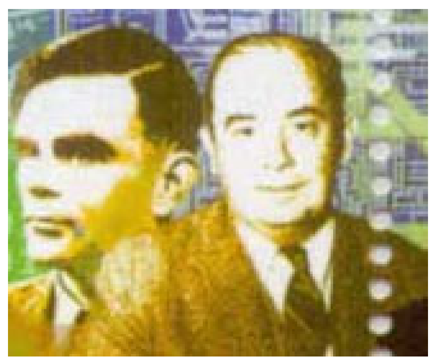
Brenner, Sydney. [2012]. “Life’s code script.” *Nature* **482** (7386): 461-461.

rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

fundamental principle of organisms as *cybernetic mechanisms*

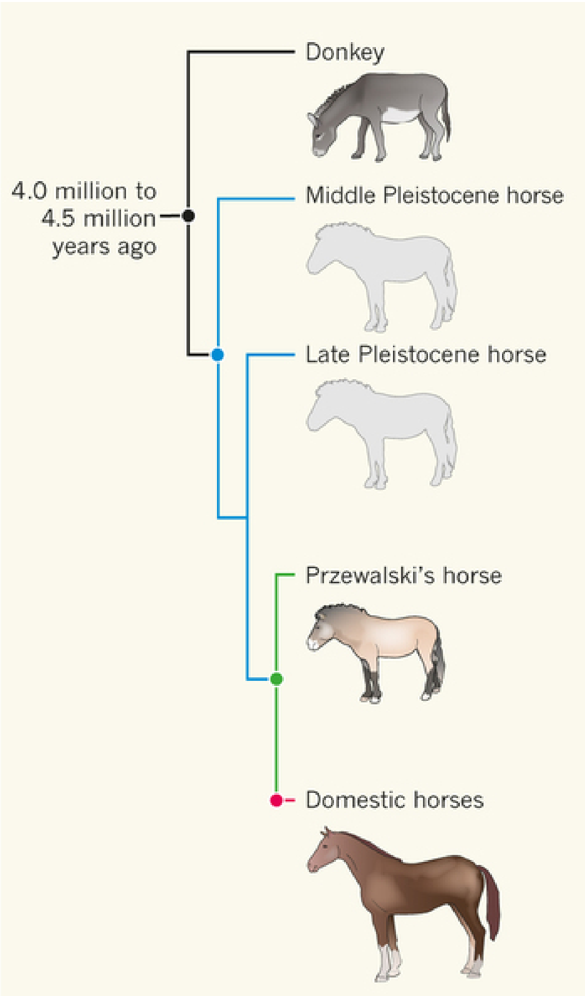






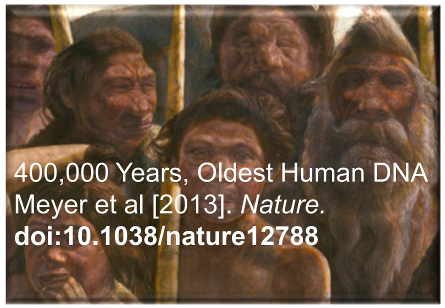
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

decoupled information



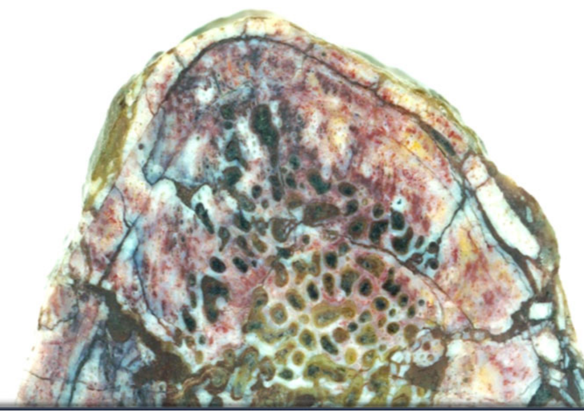
Millar & Lambert [2013]. "Ancient DNA: Towards a million-year-old genome." *Nature*. **doi:10.1038/nature12263**

Orlando, L. et al. [2013] *Nature* **doi.org/10.1038/nature12323**



What other components of life can be ***fossilized*** and ***recovered*** with biochemical reproducibility this way?

ancient (80-100 million year) fossilized protein fragments (collagen)

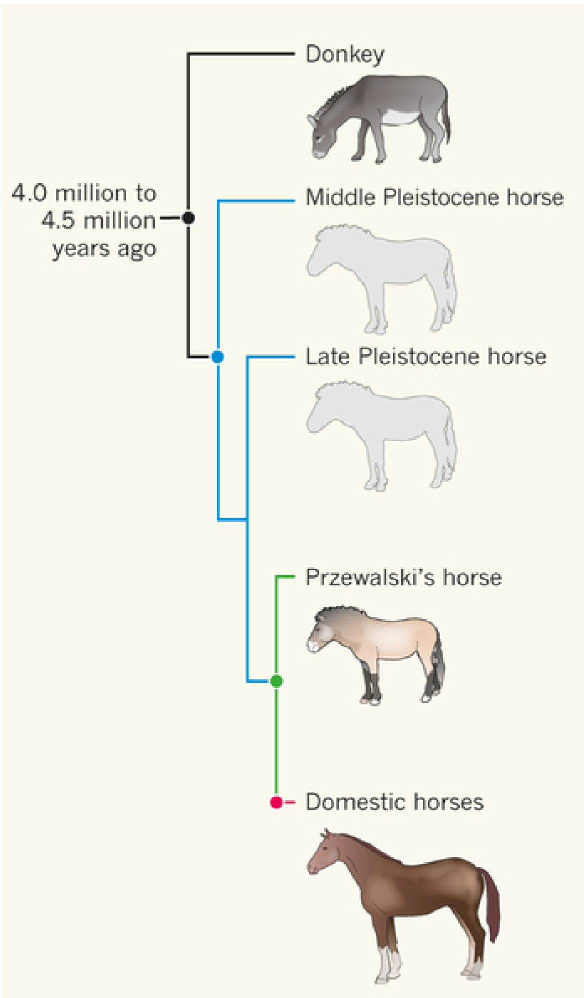


Schweitzer et al [2007] *Science*. **316** (5822): 277-280
Schweitzer et al [2009] *Science*. **324** (5927): 626-631.
Schroeter et al [2017] *J. Proteome Res.* **16** (2):920–932
Lee et al [2017] *Nature Communications* **8**: 1422.
Service, R. [2017] *Science*. DOI: 10.1126/science.aal0679

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK

rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

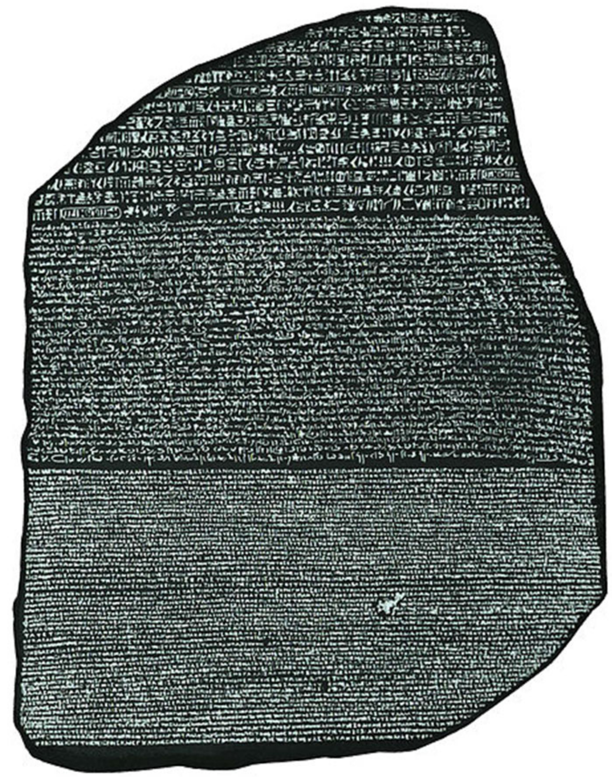
decoupled information



Millar & Lambert [2013]. "Ancient DNA: Towards a million-year-old genome." *Nature*. **doi:10.1038/nature12263**

Orlando, L. et al. [2013] *Nature* **doi.org/10.1038/nature12323**

What other components of life can be ***fossilized*** and ***recovered*** with biochemical reproducibility this way?

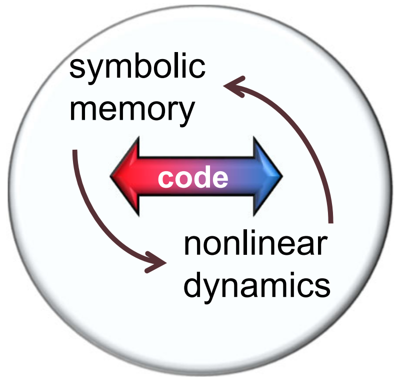


BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

the tape is not necessarily self-contained in cells, brains, or machines

decoupling and externalization enable collective behavior

semiotic closure



AUTONOMY

two roles of information
data/program (Turing)
passive/active (Von Neumann)
description/construction-function (Pattee)
genotype/phenotype (Biology)

“Let the whole outside world consist of a long paper tape”. —John von Neumann, 1948

Rocha, L.M. [2000] *Annals N.Y. Acad. Sci.* **901**(1): 207-223.
Rocha, L.M. & W. Hordijk [2005] *Artificial Life* **11**:189 - 214.

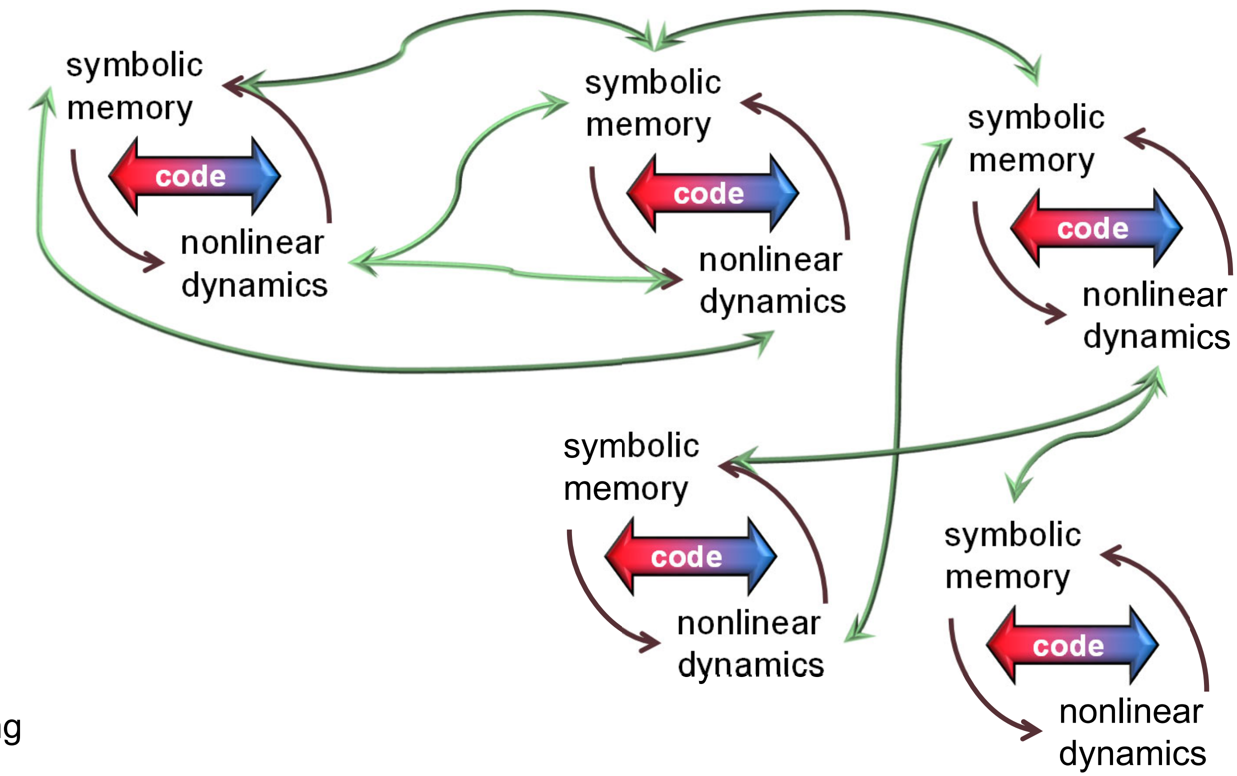
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

the tape is not necessarily self-contained in cells, brains, or machines

decoupling and externalization enable collective behavior

GENES

semiotic closure → **semiotic control networks**



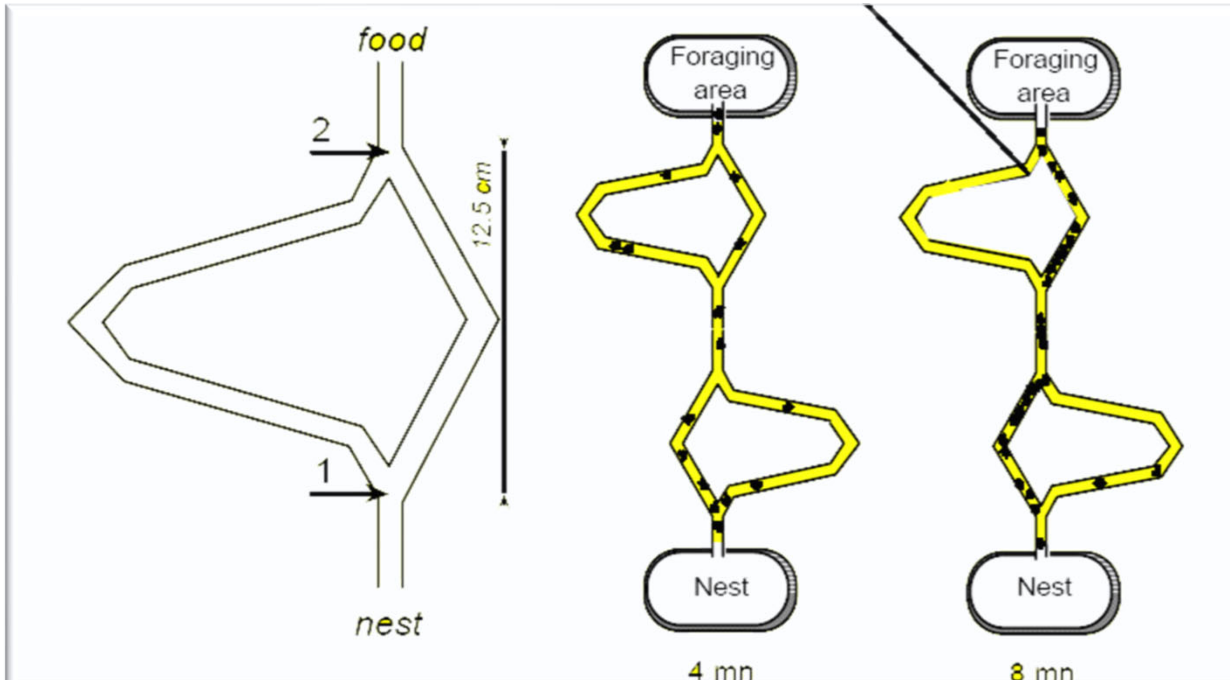
two roles of information
- data/program (Turing)
- passive/active (Von Neumann)
- description/construction-function (Pattee)
- genotype/phenotype (Biology)

“Let the whole outside world consist of a long paper tape”. —John von Neumann, 1948

Rocha, L.M. [2000] *Annals N.Y. Acad. Sci.* **901**(1): 207-223.
Rocha, L.M. & W. Hordijk [2005] *Artificial Life* **11**:189 - 214.

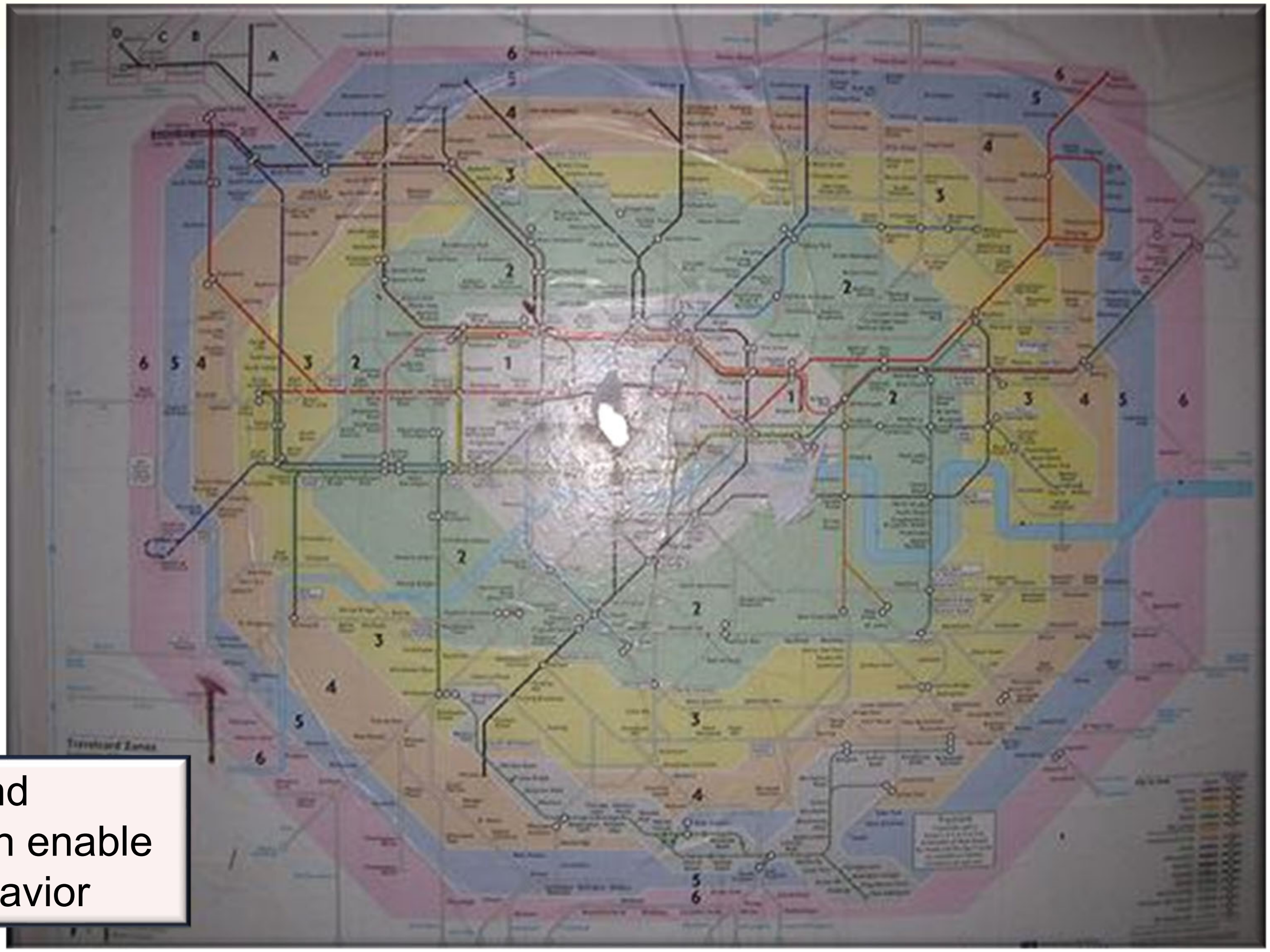
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

stigmergy



S Goss, S Aron, JL Deneubourg, JM Pasteels [1989]. “Self-organized shortcuts in the Argentine ant”. *Naturwissenschaften*, **76**: 579–581.

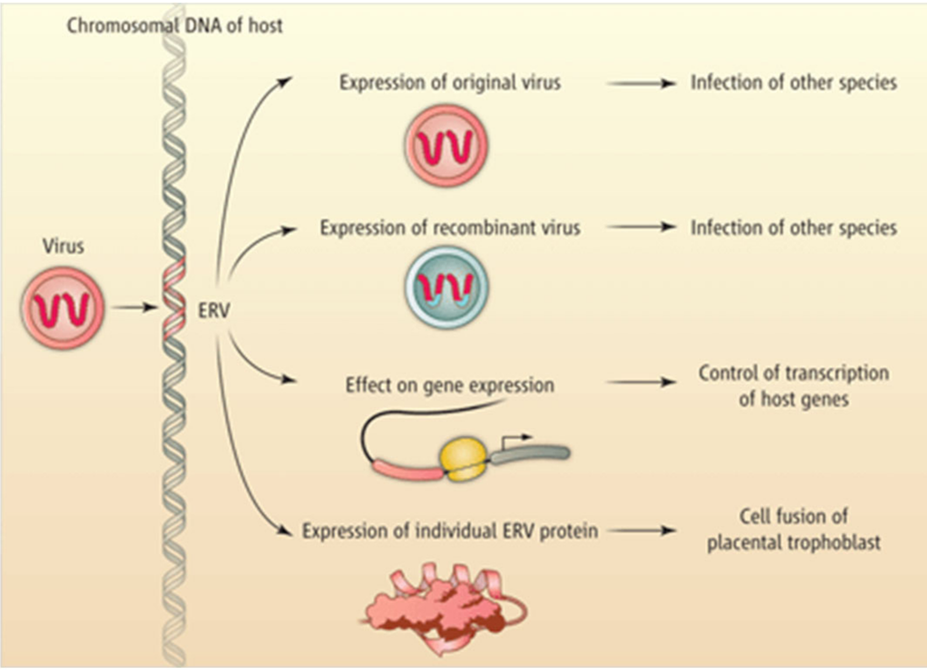
decoupling and externalization enable collective behavior stigmergy

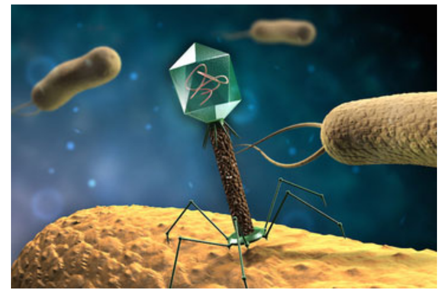


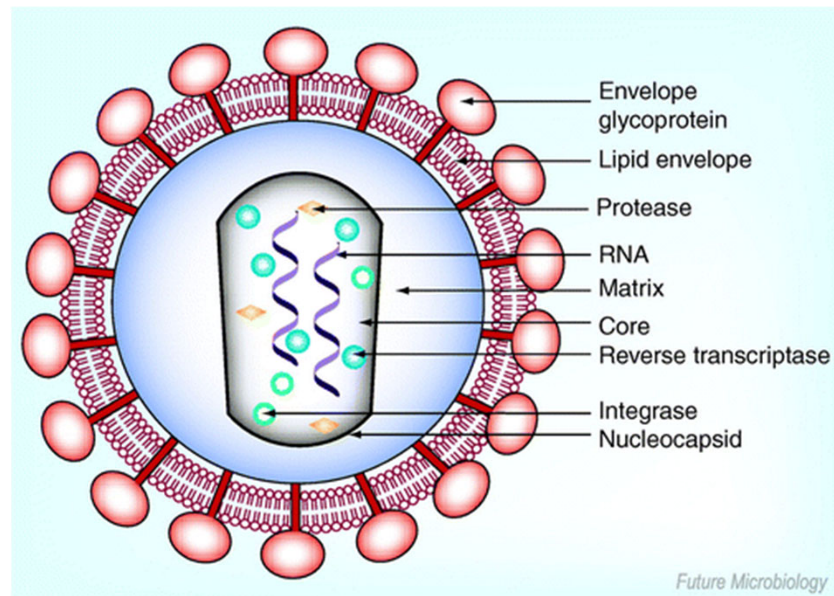
decoupling and externalization enable collective behavior

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

Turing machines written on other Turing machines (naturally)





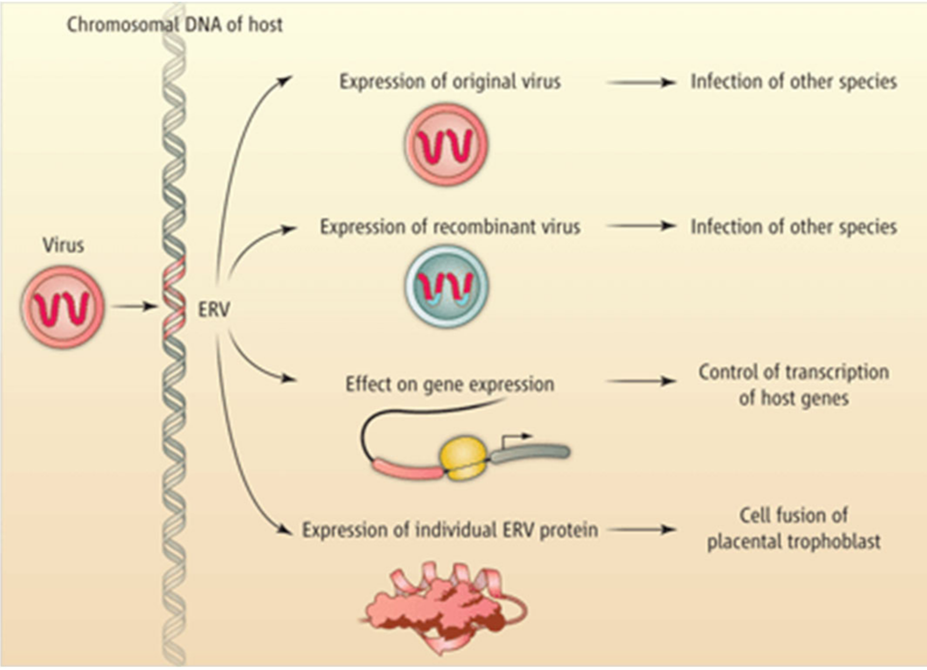


Sequences from RNA and DNA viruses found in host genomes Retroviral genomes, account **for 6 to 14% of host genomes**
~8% of human DNA.
endogenous retroviruses (ERVs) comprise more DNA than host proteome.

Weiss & Stoye [2013]. "Our Viral Inheritance." *Science*.**340** (6134): 820-821.

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

Turing machines written on other Turing machines (naturally)



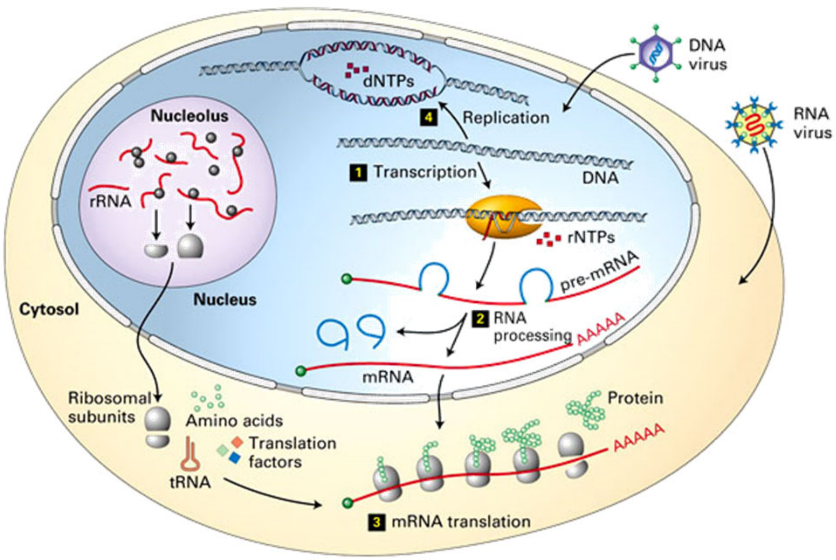
Sequences from RNA and DNA viruses found in host genomes Retroviral genomes, account **for 6 to 14% of host genomes**
~8% of human DNA.
endogenous retroviruses (ERVs) comprise more DNA than host proteome.

Weiss & Stoye [2013]. "Our Viral Inheritance." *Science*.**340** (6134): 820-821.

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

The social symbiome

semiotic control networks enable new, interacting levels of organization and selection, which take control of genes, organisms, and even societies.



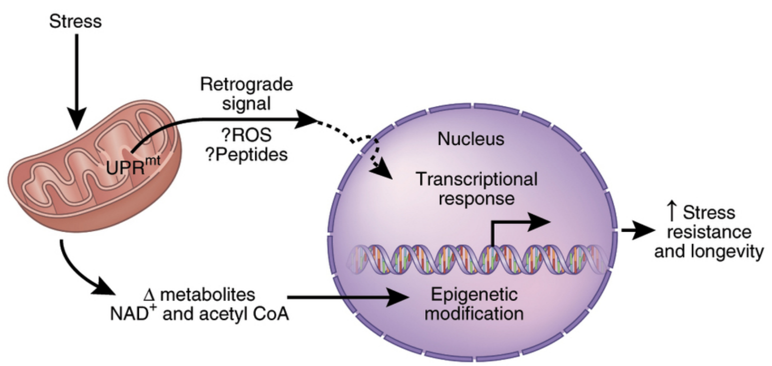
Mercer et al. [2012] Targeted RNA sequencing reveals the deep complexity of the human transcriptome. *Nat. Biotech*. **30**, 99–104.

Examples: eukaryotic RNA/DNA complexity, vertebrate immunity, eusociality, cultural constraints on reproduction, GMOs (including via CRISPR), viral pandemics, etc.

rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

The social symbiome

semiotic control networks enable new, interacting levels of organization and selection, which take control of genes, organisms, and even societies.



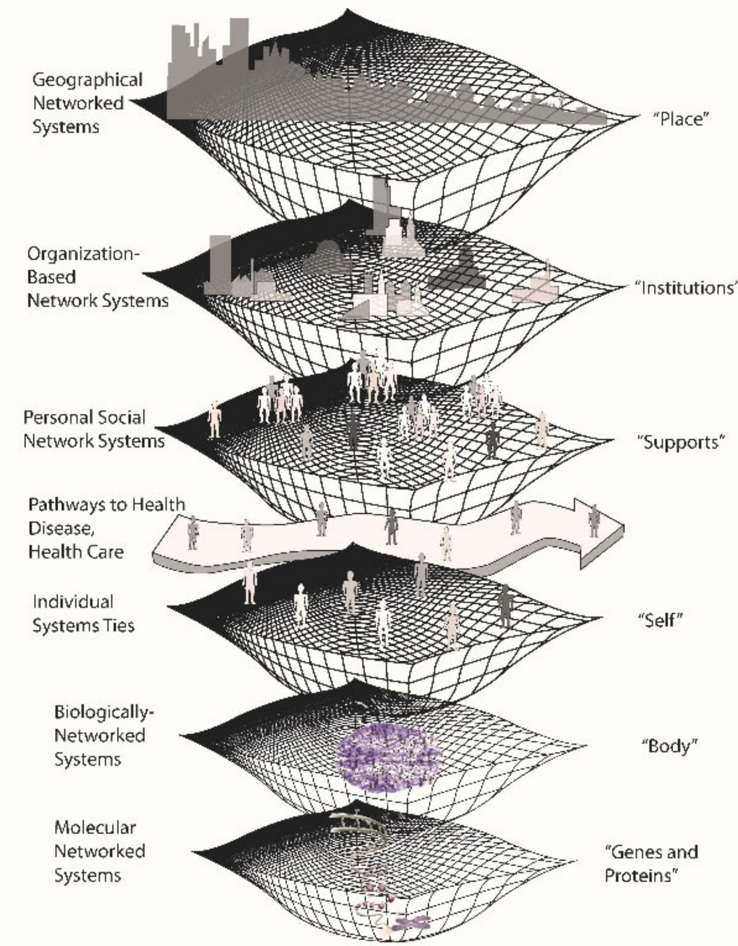
Eukaryote **complexity in regulation**: regulatory components larger than coding, genome size is secondary: 10-100K times more energy per gene than bacteria (# proteins expressed)
Lane & Martin [2010] *Nature* **467**(7318):929–934.

Examples: eukaryotic RNA/DNA complexity, vertebrate immunity, eusociality, cultural constraints on reproduction, GMOs (including via CRISPR), viral pandemics, etc.

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

The social symbiome

semiotic control networks enable new, interacting levels of organization and selection, which take control of genes, organisms, and even societies.

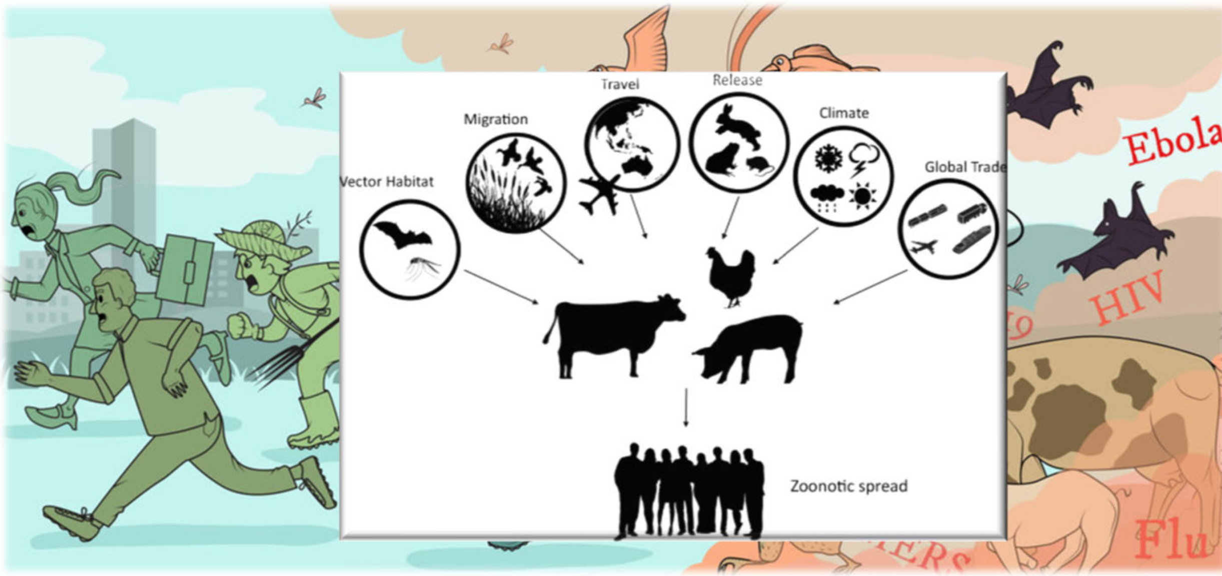


Examples: eukaryotic RNA/DNA complexity, vertebrate immunity, eusociality, cultural constraints on reproduction, GMOs (including via CRISPR), viral pandemics, etc.

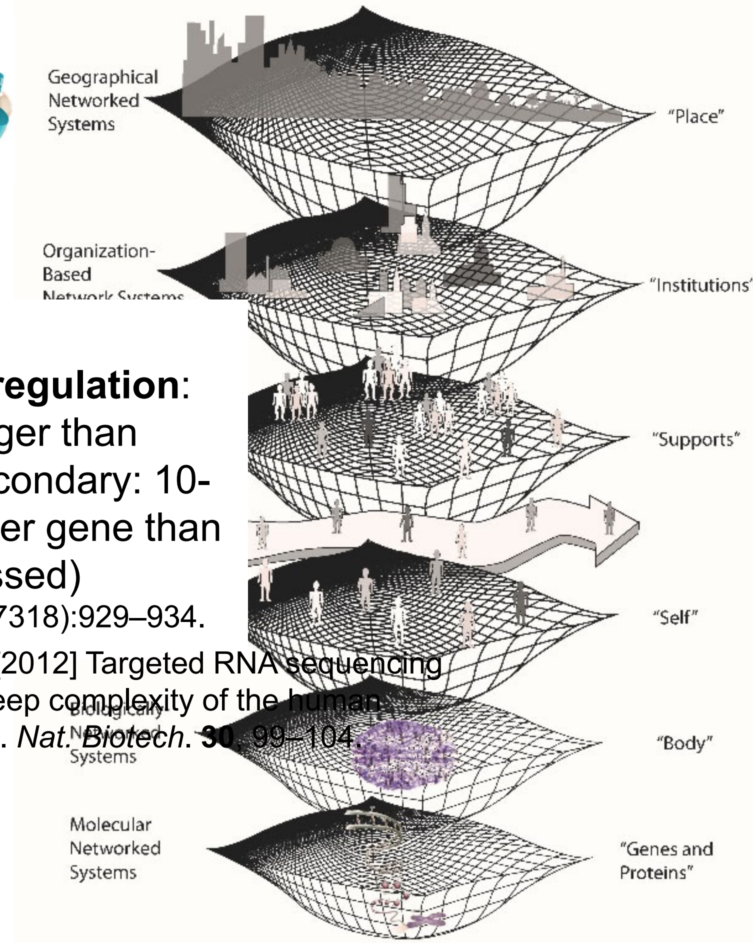
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

The social symbiome

semiotic control networks enable new, interacting levels of organization and selection, which take control of genes, organisms, and even societies.

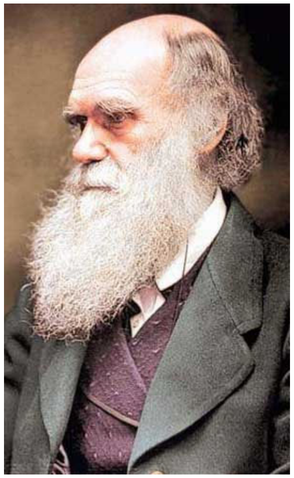


in regulation:
larger than
secondary: 10-
y per gene than
ressed)
67(7318):929–934.
al. [2012] Targeted RNA sequencing
e deep complexity of the human
ome. *Nat. Biotech*. **30**, 99–104.



Examples: eukaryotic RNA/DNA complexity, vertebrate immunity, eusociality, cultural constraints on reproduction, GMOs (including via CRISPR), viral pandemics, etc.

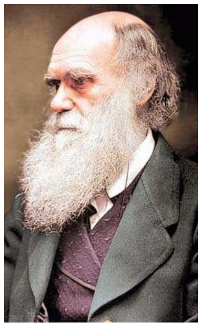
fundamental principle of organisms as *cybernetic mechanisms*

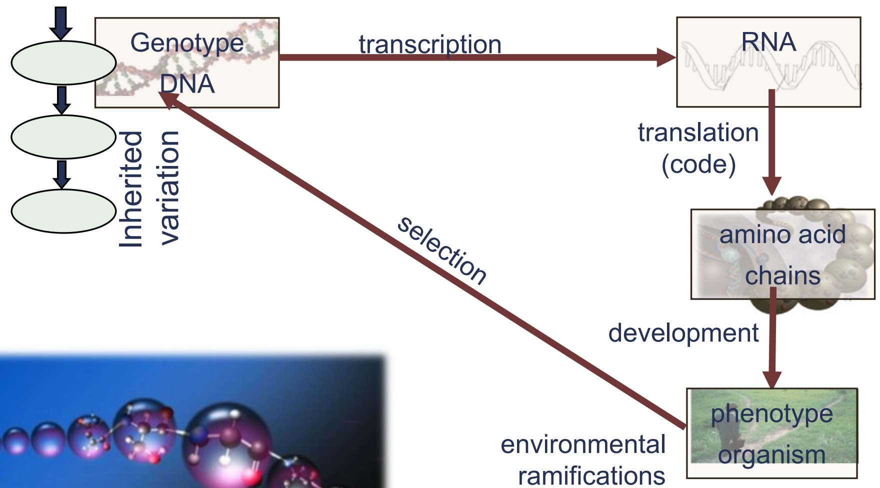


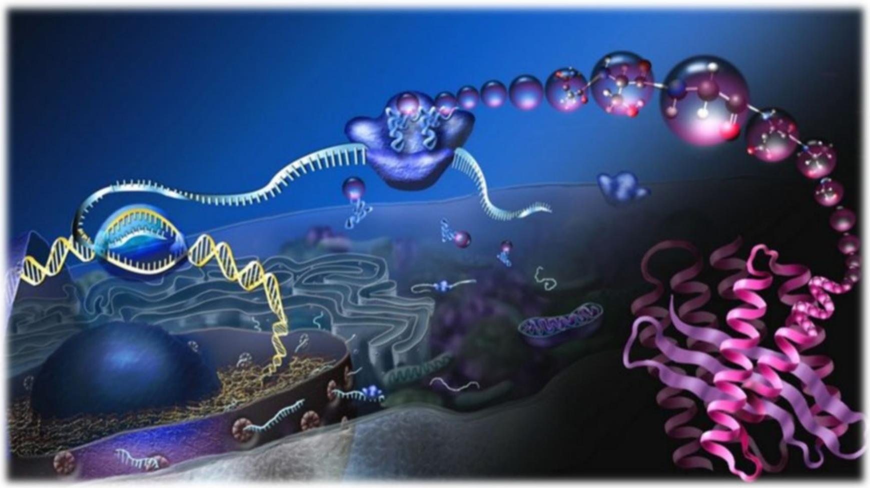
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

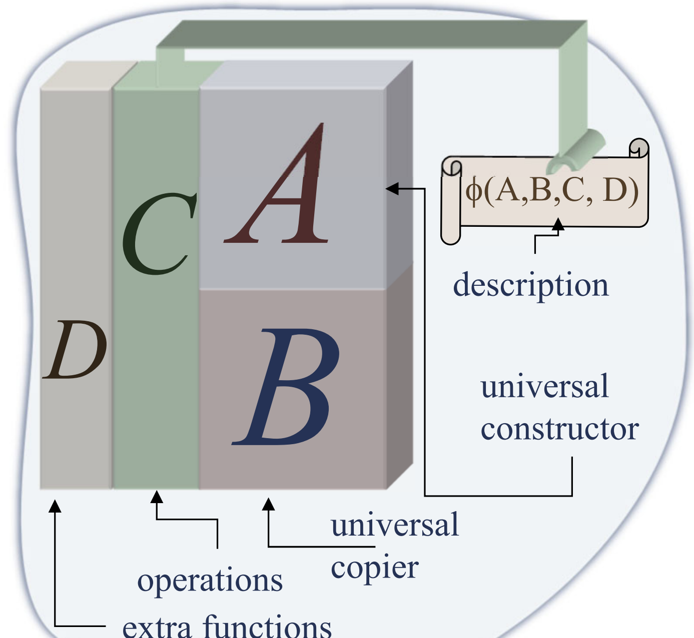
Turing’s tape

from cybernetic mechanisms to bio-inspired algorithms





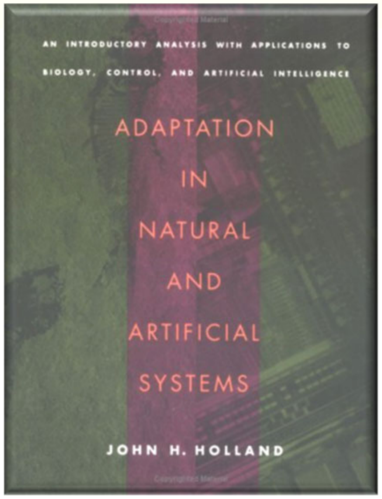


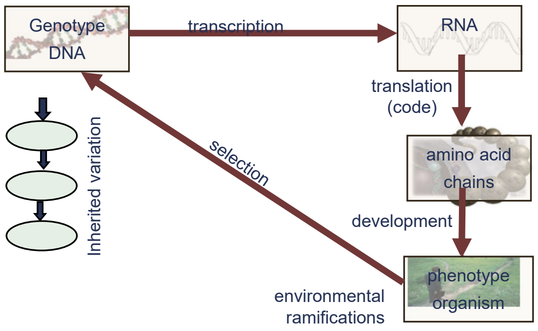


BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

History of evolutionary computation

- Evolutionary Operation
  - Box (1957)
    - Perturbations to continuous variables followed by selection to improve industrial productivity
- Evolution Strategies
  - Rechenberg (1960's), Schweffel (1970's)
    - To optimize real-valued parameters in wind-tunnel experiments
    - Real-valued genotypes under variation and selection
- Evolutionary Programming
  - Fogel, Owens, and Walsh (1966)
    - Evolution of tables of state-transition functions (diagrams) under mutation and selection
- Artificial ecosystems
  - Conrad and Pattee (1970)
    - Population of artificial cells evolving with genotype and phenotype
- Other early evolution-inspired algorithms and models
  - Barricelli CA-like model(1957), game-strategy model (1963)
    - Symbiogenetic evolution
  - Friedman (1957, 1959), Bledsoe (1961), Bremmermann (1962)
- Genetic Algorithms
  - John Holland (1960's and 1970's)
    - *Adaptation in Natural and Artificial Systems*, University of Michigan Press, 1975. (MIT Press, second edition 1992)





BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

via genetic algorithms

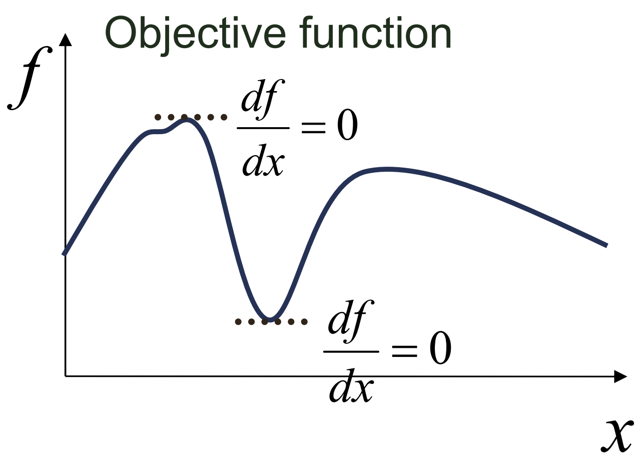
- Search algorithms based on the mechanics of Natural Selection
  - Holland, Conrad, Fogel
  - Based on distinction between a machine and a description of a machine
    - Solution alternatives for optimization problems

Direct analysis depends on

Knowing the function

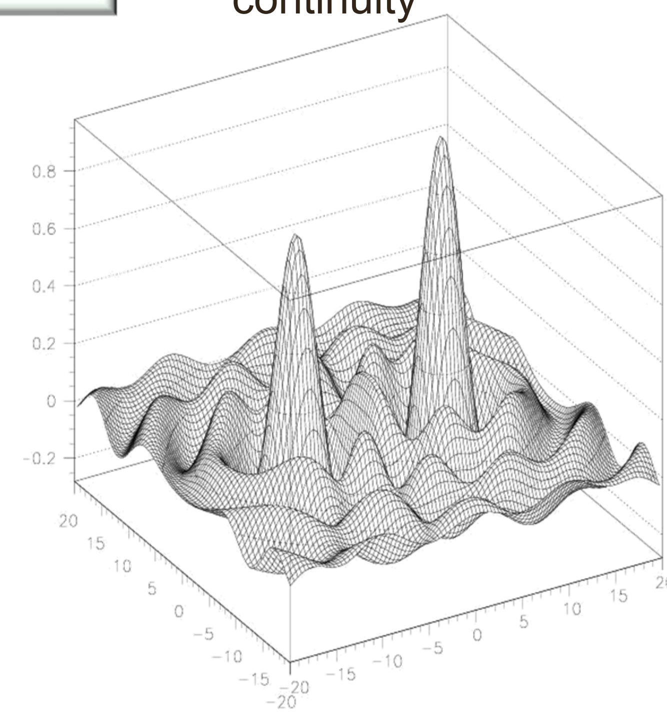
Existence of derivatives

continuity



"hill-climbing"

"hop" on the function and move along the steepest direction until a local extrema is found



Random Search

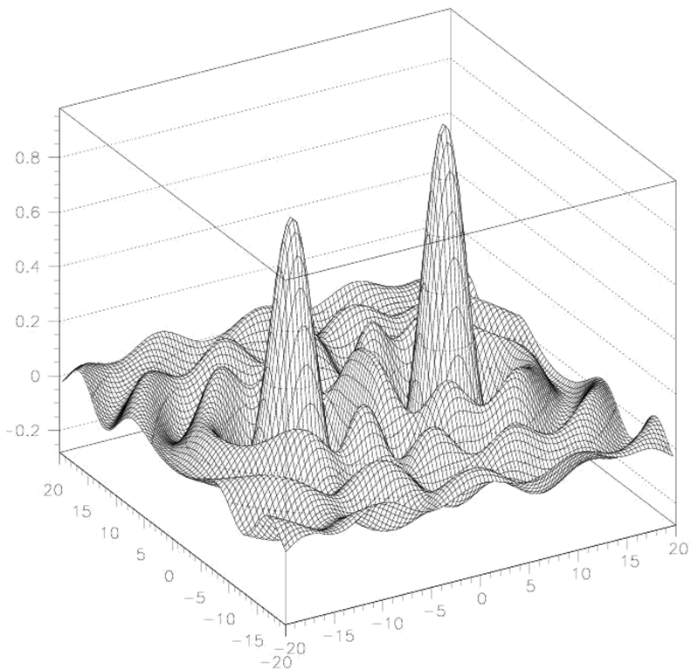
directionless

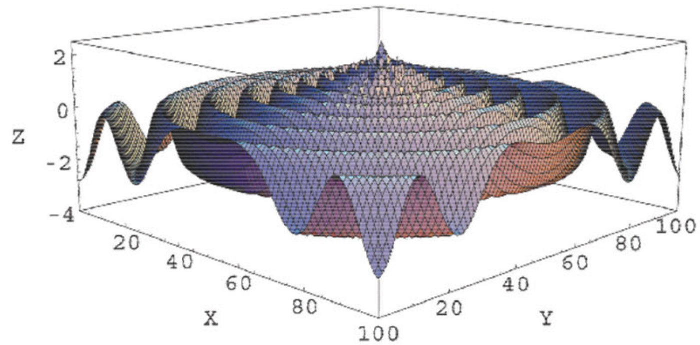
Enumerative Search

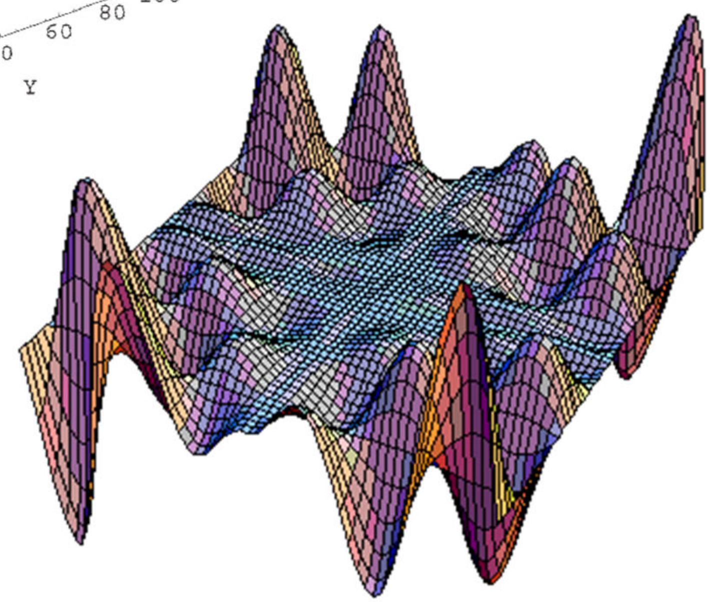
Search point by point

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

examples

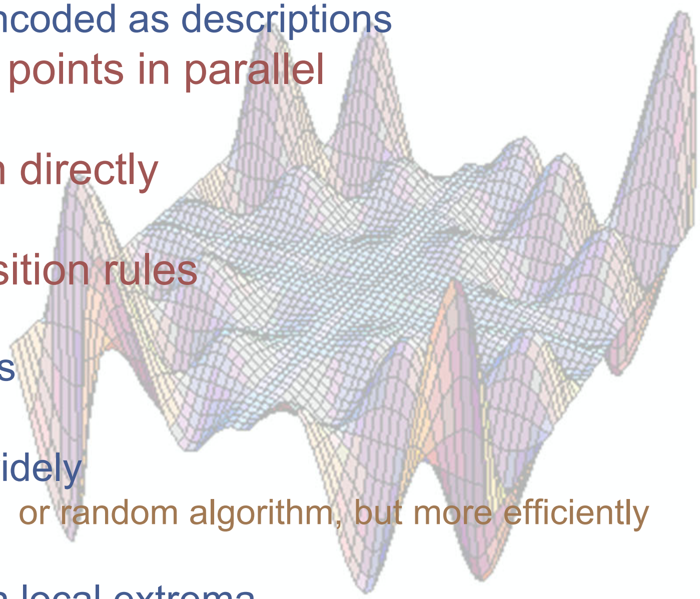






BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

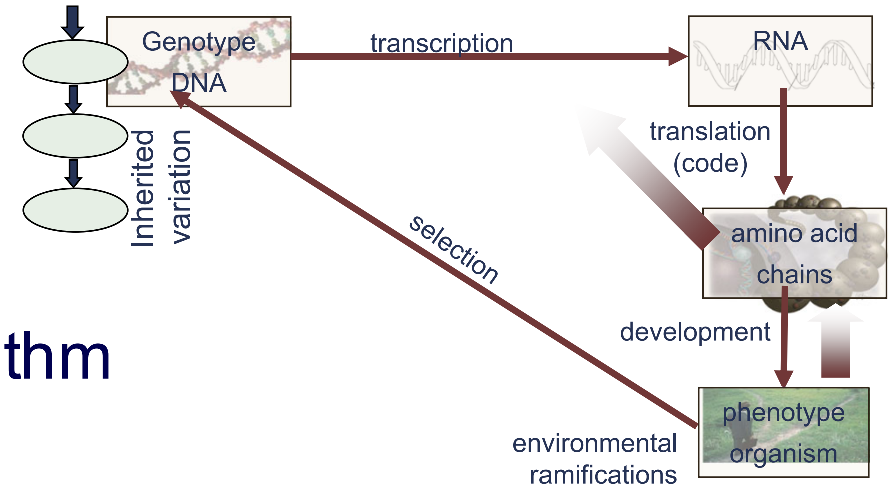
- Work with an encoding of the parameter set, not the parameters themselves
  - solution alternative encoded as descriptions
- Search a population of points in parallel
  - Not a single point
- Uses objective function directly
  - Not derivatives
- Uses probabilistic transition rules
  - Statistical bias
  - Not deterministic rules
- Advantages
  - Samples the space widely
    - like an enumerative or random algorithm, but more efficiently
    - Directed search
  - Not so easily stuck on local extrema
    - Population search
    - Variation mechanisms to search new points



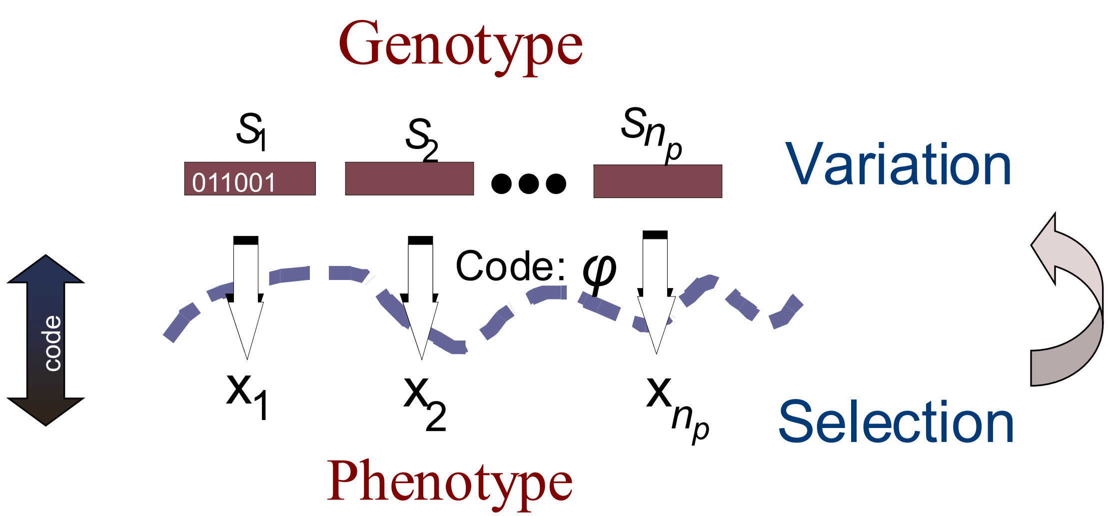
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

artificial genotype/phenotype mapping

Search algorithms based on the mechanics of Natural Selection
- Based on distinction between a machine and a description of a machine
- Solution alternatives for optimization problems



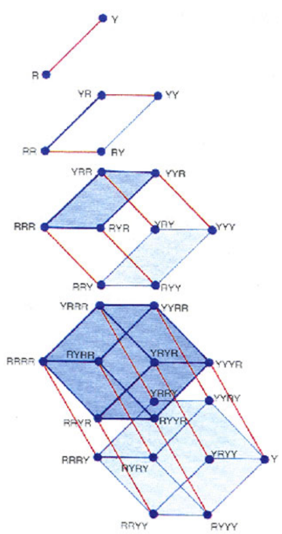
Traditional Genetic Algorithm



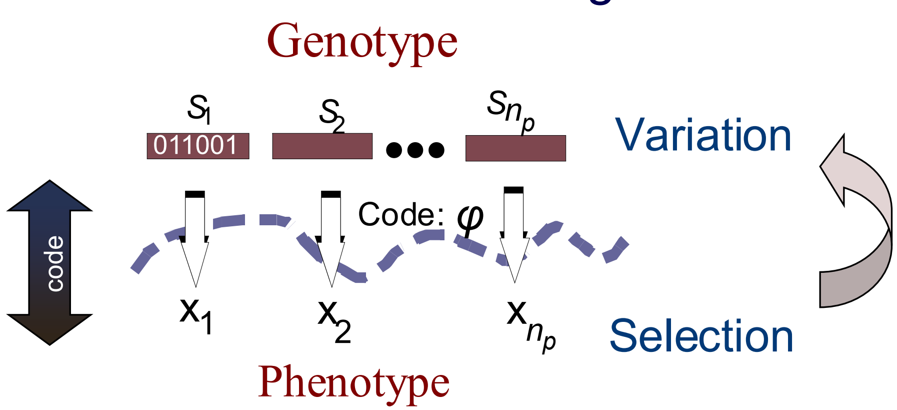
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

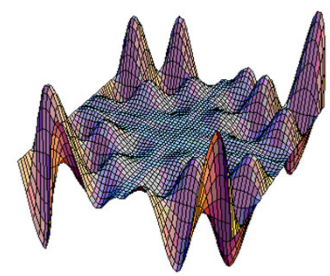
in genetic algorithms

- Solution space encoded as finite-length string over a finite alphabet
  - E.g. {0, 1}
- GA's exploit coding similarities
  - Searches the code space, not the solution space



Traditional Genetic Algorithm

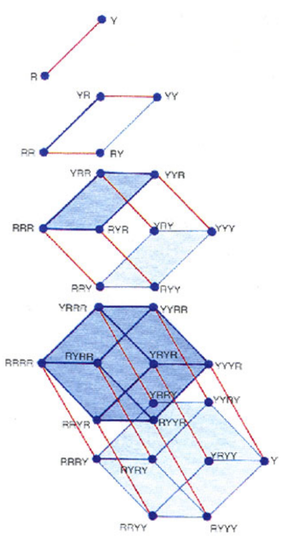


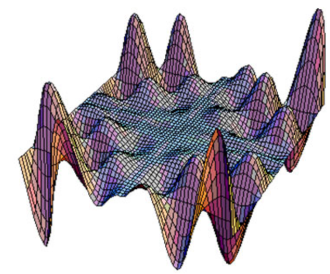


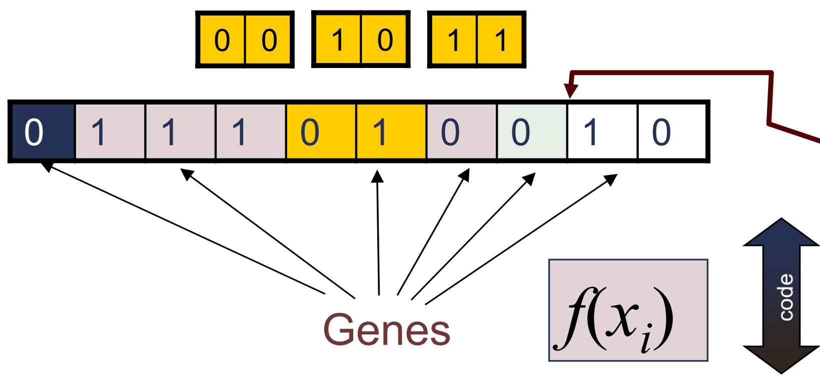
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

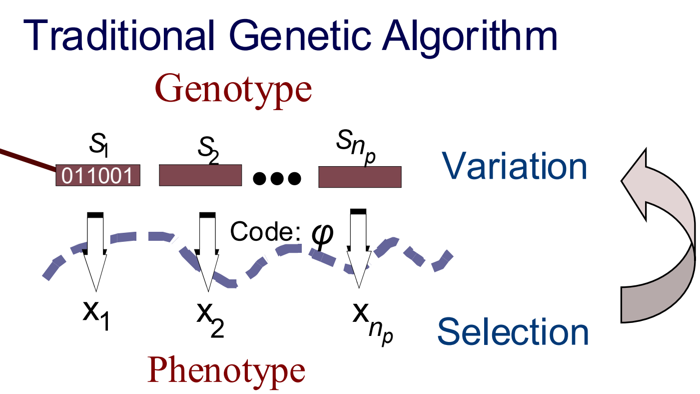
The workings

1) Generate Random population of bit-strings
   - Chromosomes/Genotypes
     - A candidate solution to a problem
   - Genes
     - Single or short blocks of adjacent bits
   - Allele
     - Actual value of a gene
2) Evaluate Fitness Function for each decoded solution
3) Reproduce next generation
   - Genotypes of solutions with higher fitness value reproduce with higher probability
4) Go back to 2)



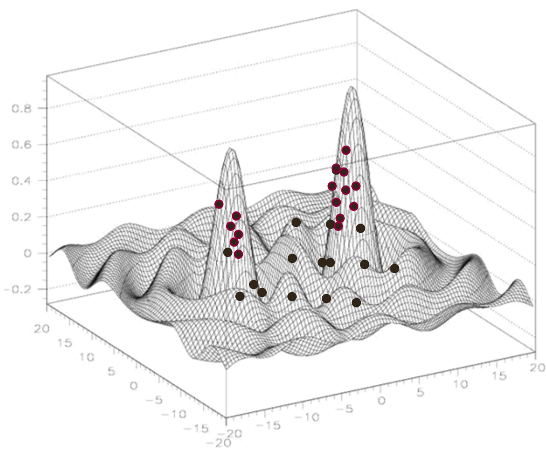


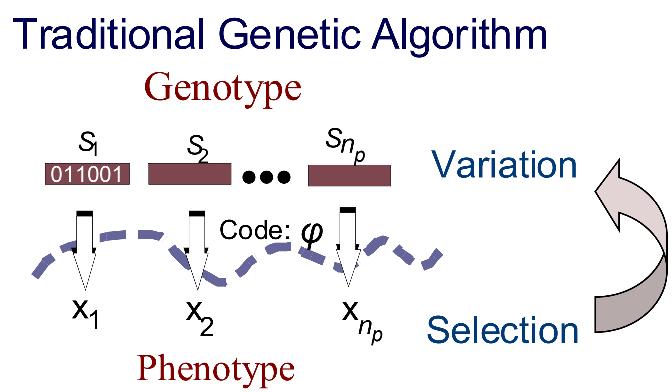




biased population generation

- Solution space encoded as finite-length string over a finite alphabet
  - E.g. {0, 1}
- GA's exploit coding similarities
  - Searches the code space, not the solution space
- Searches the space with many alternatives in parallel
  - Avoids getting trapped in local optima
  - Higher probability of finding better solutions
- Not random search
  - Search towards regions with likely improvement
  - Better solutions reproduce more often
    - Does not work in very rugged, chaotic, uncorrelated landscapes

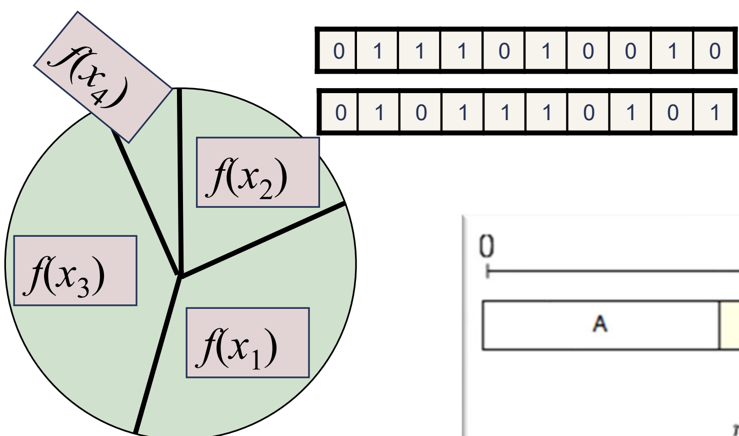


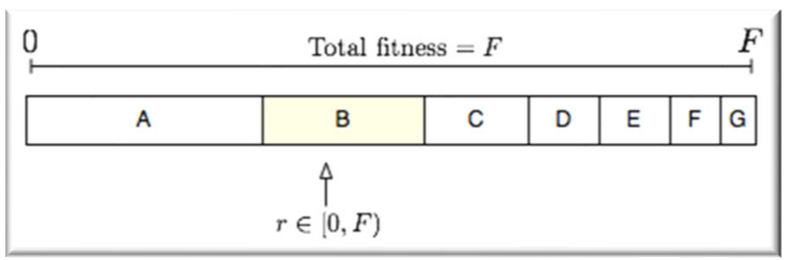


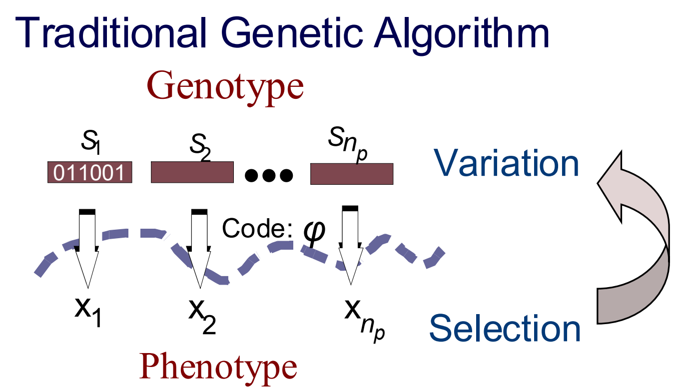
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

Modeling fitness selection

1) Reproduction: New population is generated
   a) Selection
      - Select two parent chromosomes from a population according to their fitness
        - Biased roulette wheel according to fitness of solution
        - Elite group
        - Tournament

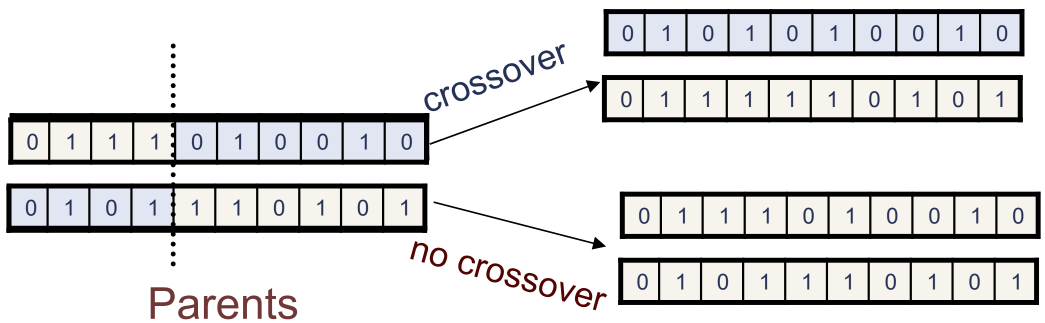






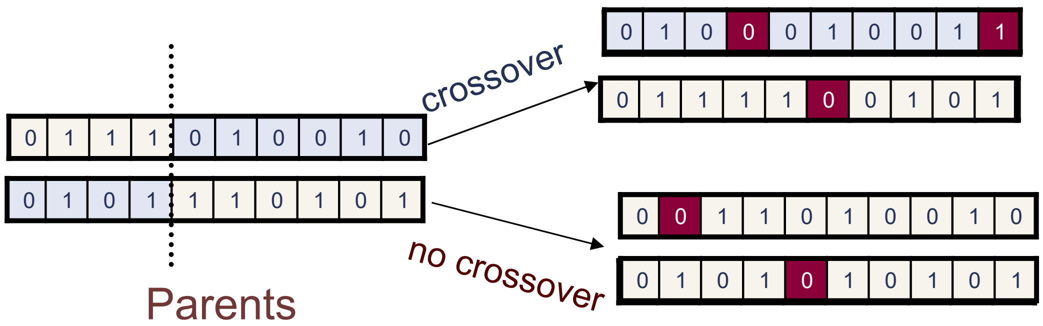
Variation: crossover

1) Reproduction: New population is generated
   a) Selection
      - Select two parent chromosomes from a population according to their fitness
   b) Variation: Crossover
      - With a ***crossover probability*** produce offspring pair by recombining parents.



Variation: mutation

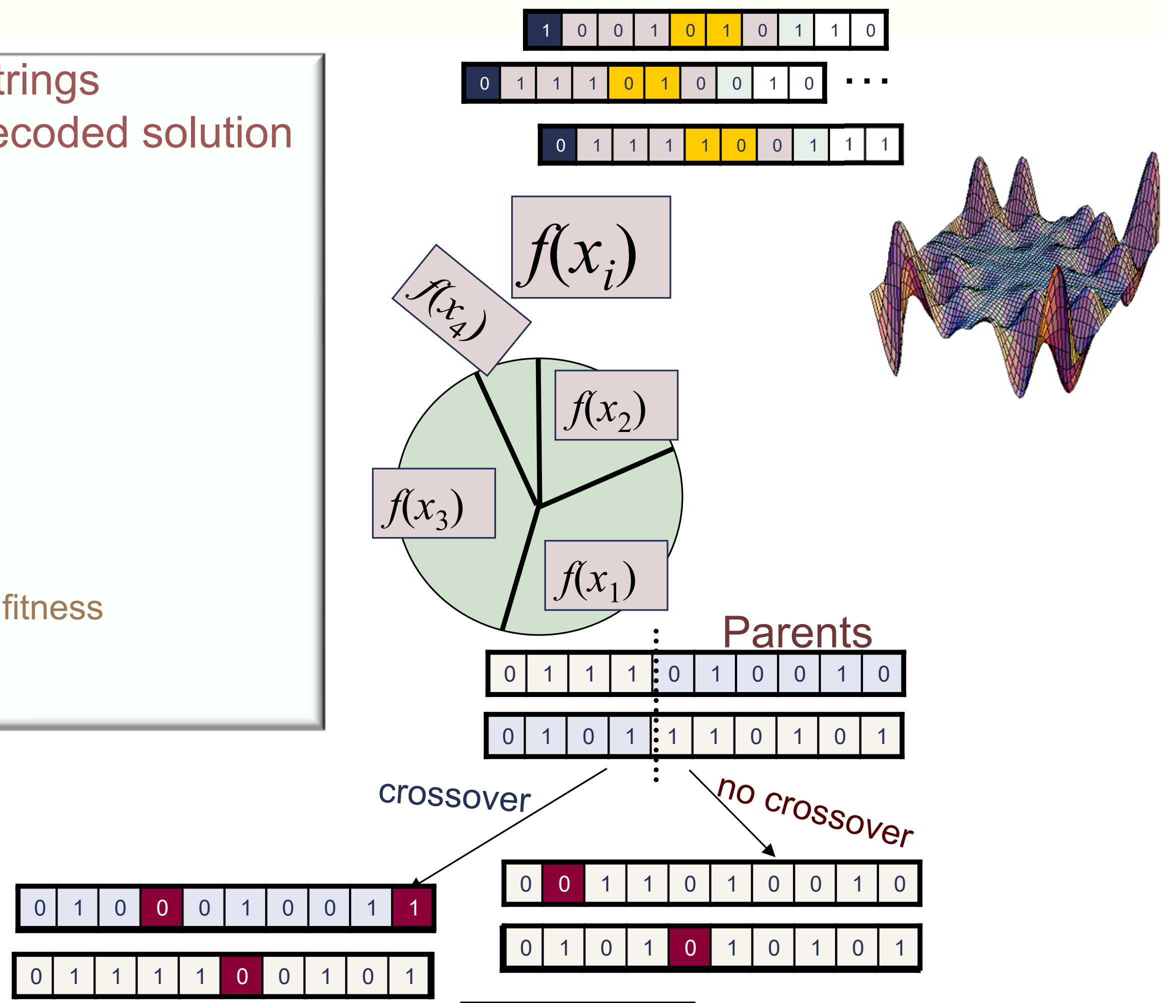
1) Reproduction: New population is generated
   a) Selection
      - Select two parent chromosomes from a population according to their fitness
   b) Variation: Crossover
      - With a ***crossover probability*** produce offspring pair by recombining parents.
   c) Variation: Mutation
      - With a ***mutation probability*** mutate (bit flip) new offspring at each bit position



BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

The workings

1) Generate Random population of bit-strings
2) Evaluate Fitness Function for each decoded solution
3) Reproduce next generation
    - Selection by fitness
    - Variation
        - crossover and mutation
    - Fill new population
4) Go back to 2) until stop criteria is met
    - Desired fitness
    - Specified number of generations
    - Convergence
        - Lack of variability in population and/or fitness
            - Tends to a peak

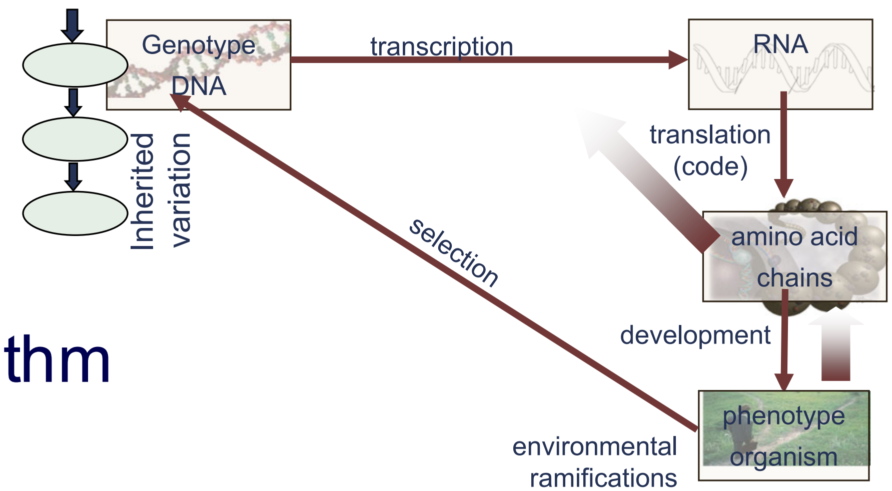


BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

artificial genotype/phenotype mapping

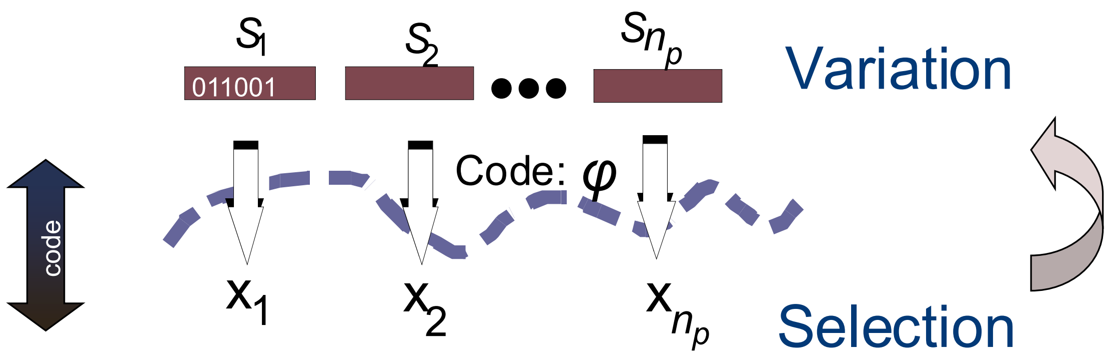
Search algorithms based on the mechanics of Natural Selection

- Based on distinction between a machine and a description of a machine
- Solution alternatives for optimization problems



Traditional Genetic Algorithm

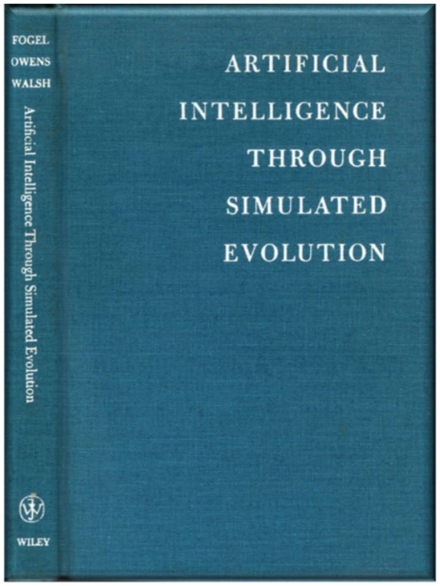
Genotype

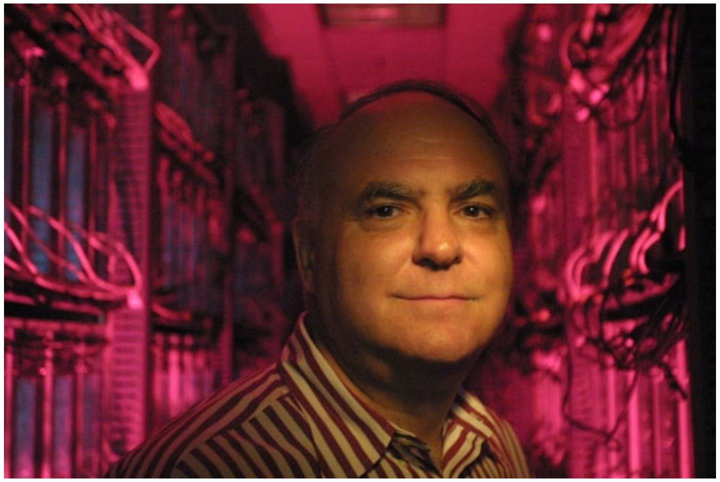


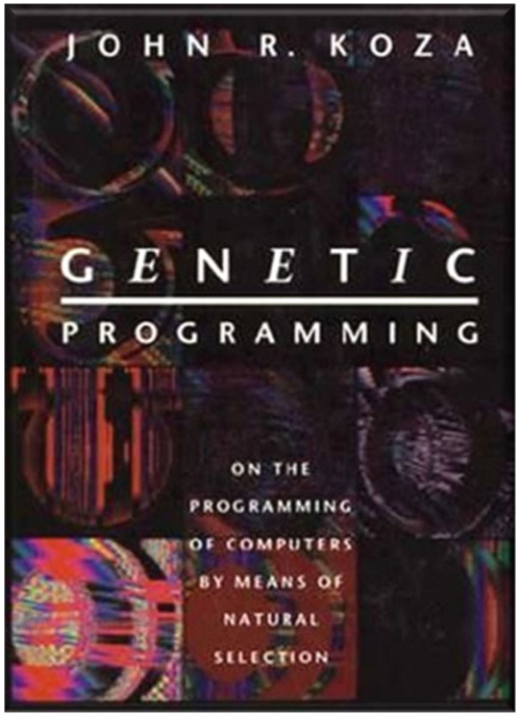
Phenotype

rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

- Fogel, Owens and Walsh (1966)
  - *Artificial Intelligence through simulated evolution*. Wiley.
    - Evolution of finite-state machines
- John Koza (1992) at Stanford University
  - *Genetic Programming: On the programming of computers by means of Natural Selection*. MIT Press.

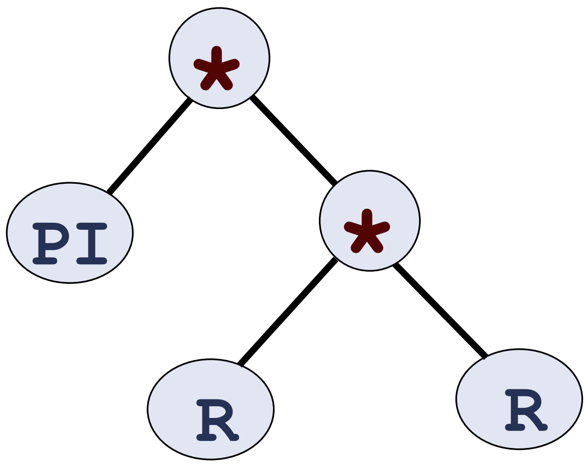






tree encodings

- Evolving computer programs to perform a task
  - No strict genotype-phenotype mapping
  - LISP programs
    - Can be expressed in the form of parse trees




```
(DEFUN AREA-OF-CIRCLE ()
  (SETF R 45)
  (SETF PI 3.1415)
  (* PI (* R R)))
```

functions terminals

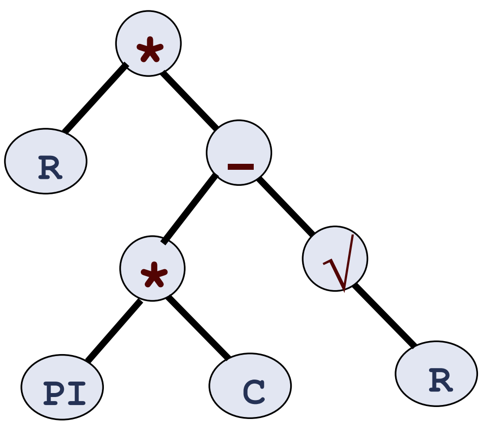
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

the workings

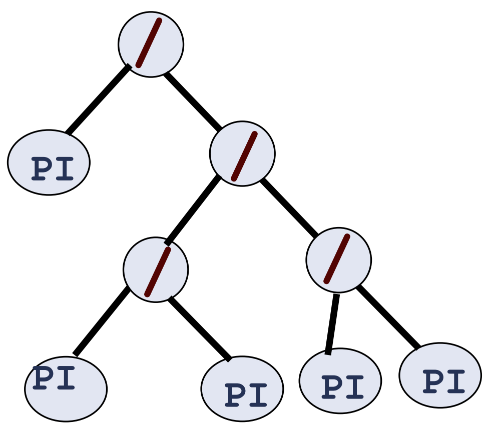
1) Choose a pool of possible functions and terminals
   - Setting up a language of description
2) Generate Random population of trees (programs)
   - Must be syntactically correct (parsing)
   - Size is usually restricted
3) Evaluate Fitness Function for each tree
   - Desired I/O
   - Simplicity, speed
4) Reproduce next generation with variation
   - Trees with higher fitness value reproduce with higher probability
5) Go back to 3)

- / + == √ ABS …

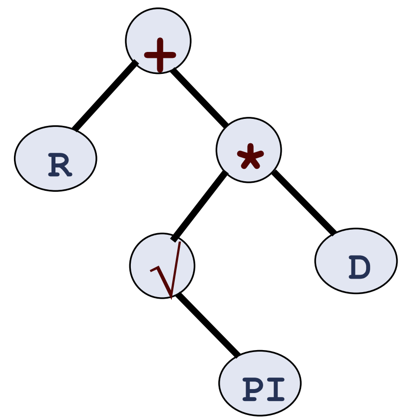
PI C R B …



R*[(PI*C)–√R]



PI/{[(PI/PI)/(PI/PI)]}

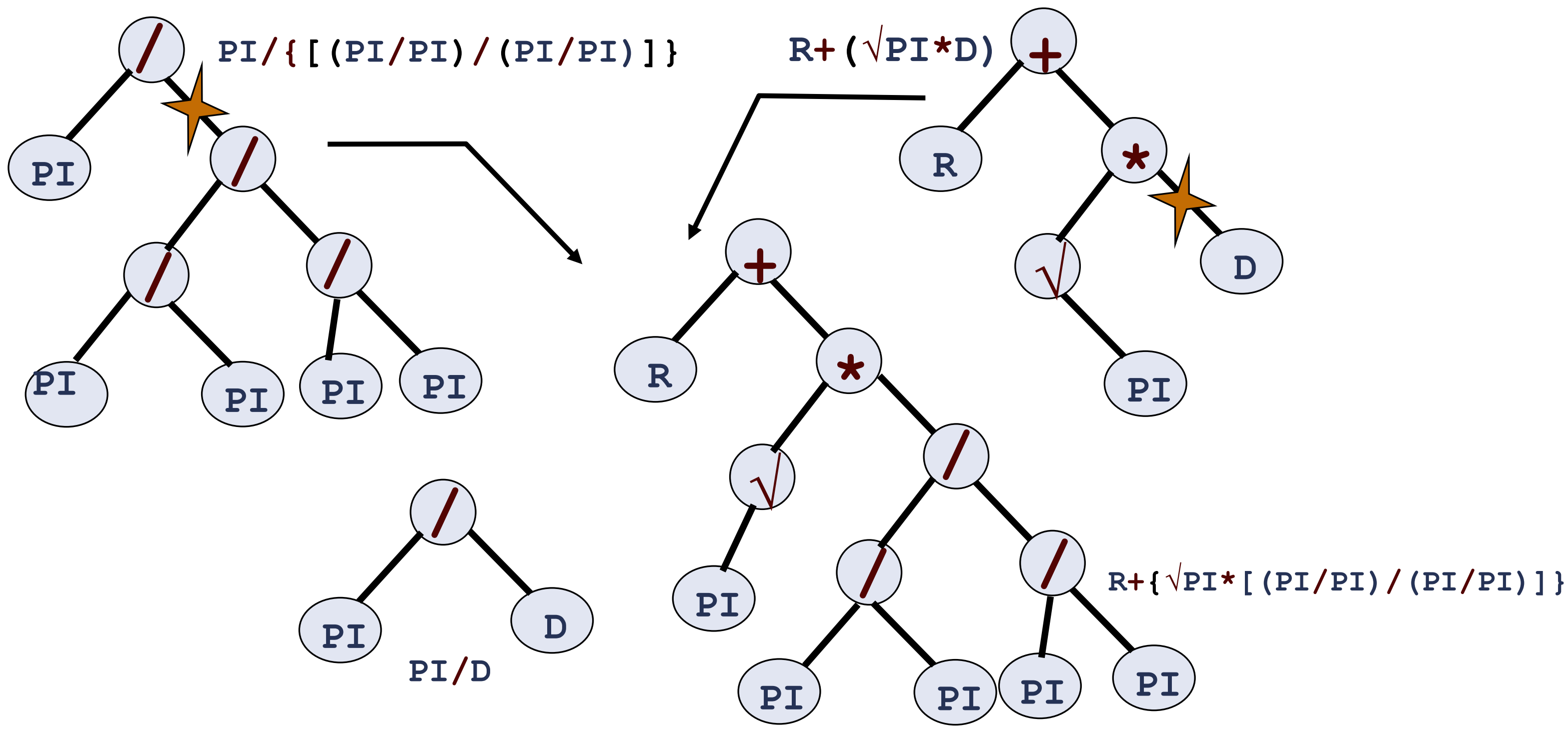


R+(√PI*D)

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

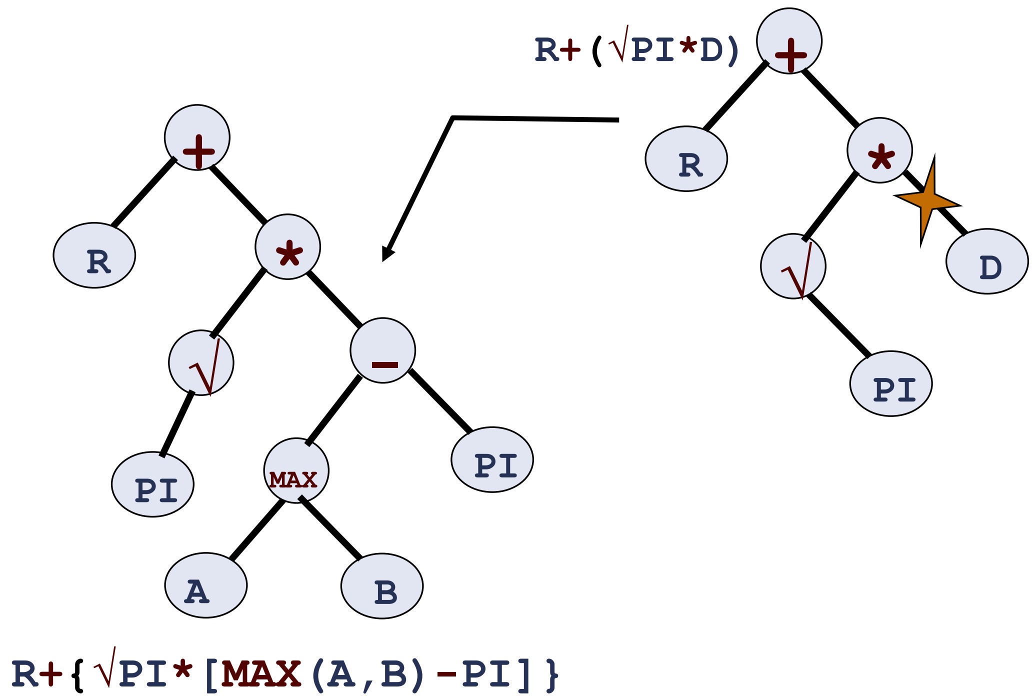
crossover

- Choose random point in each parent's tree
- Exchange subtrees beneath to produce offspring
  - Allows size of program to increase or decrease



mutation

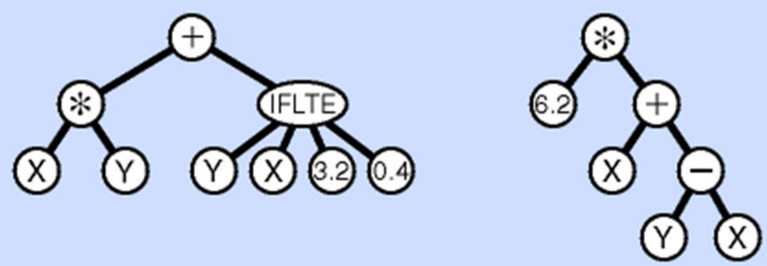
- Choose random point in a tree
- Replace subtree beneath with random tree



Creation demo

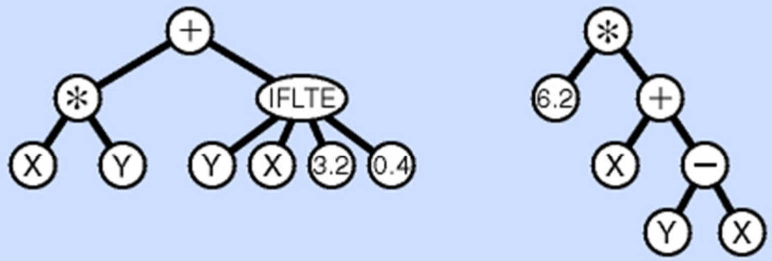
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

crossover demo



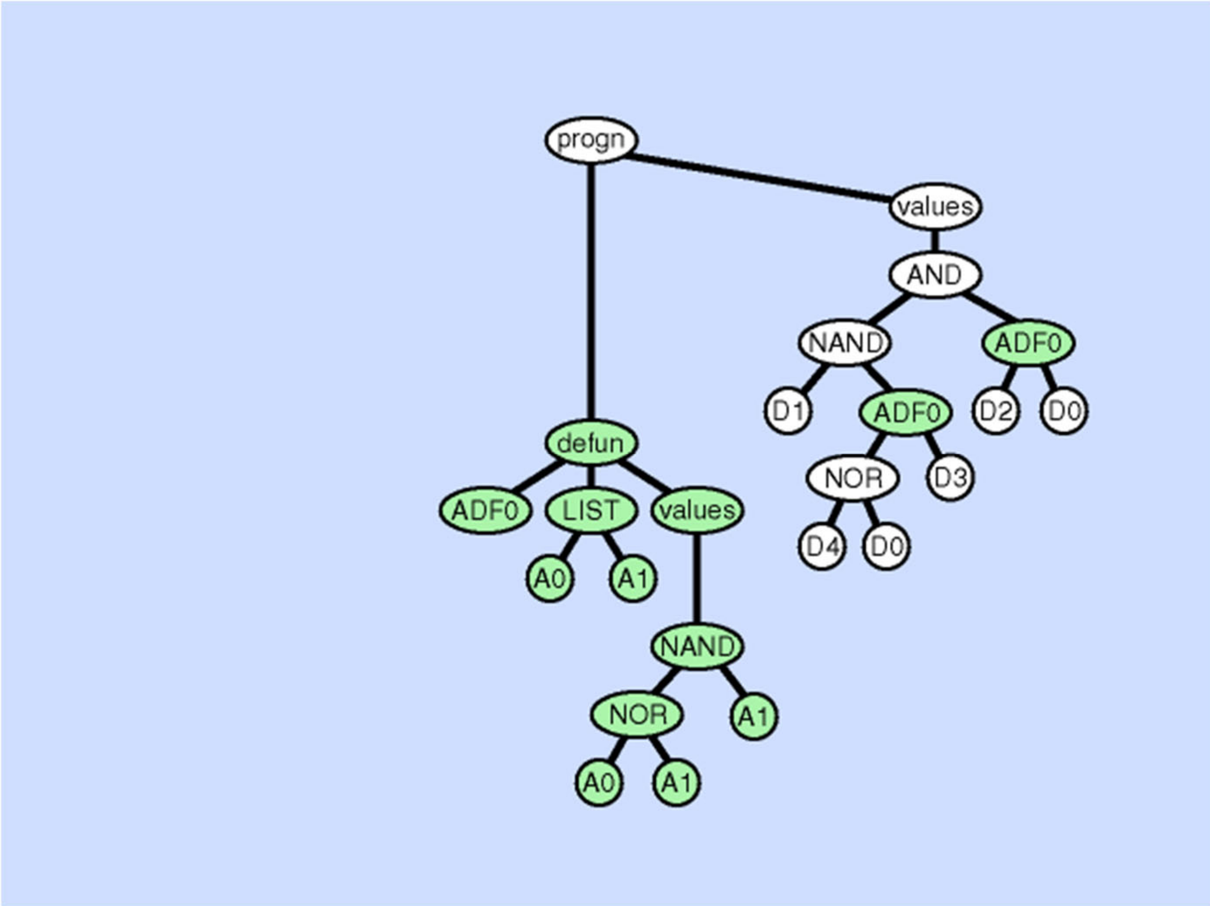
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

Mutation demo



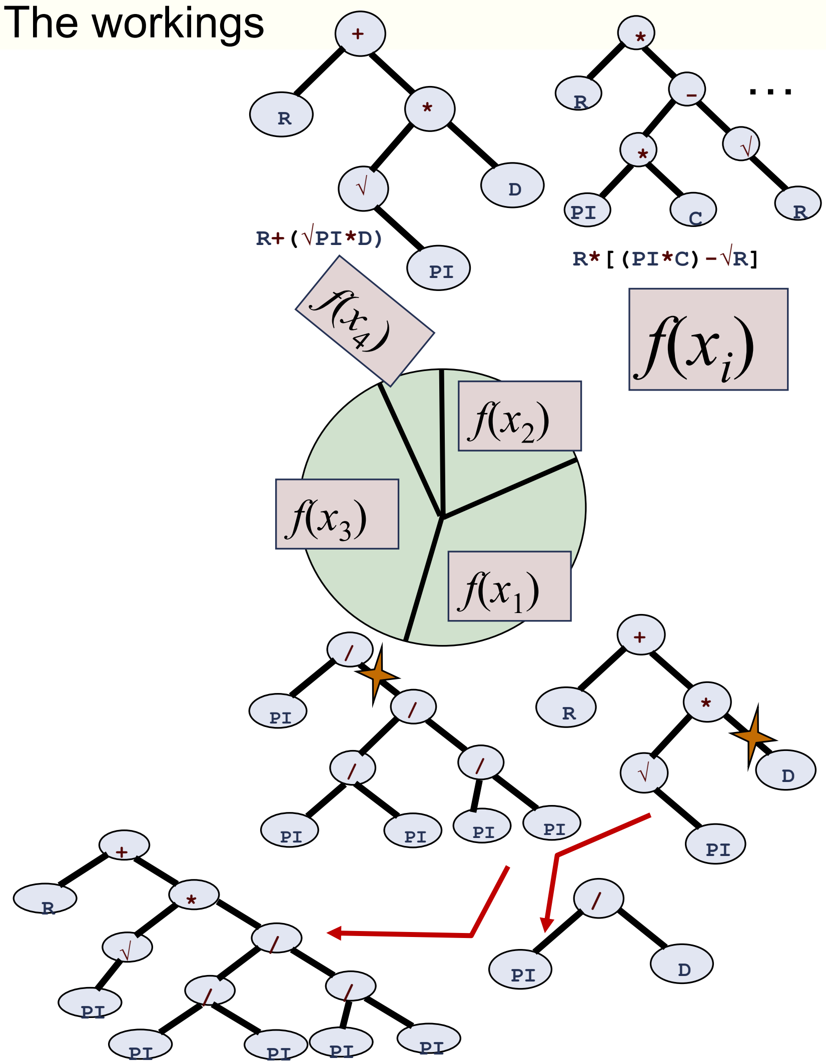
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

Architecture-altering operations



rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

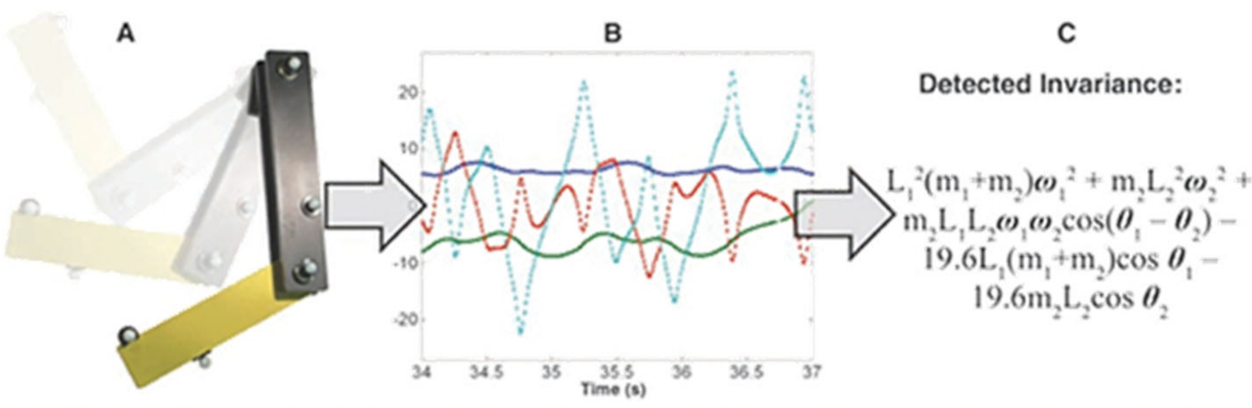
The workings



1) Generate Random population of trees/programs
2) Evaluate Fitness Function for each program
   - Desired I/O, simplicity, speed
3) Reproduce next generation
   - Selection by fitness
   - Variation
     - crossover and mutation
   - Fill new population
4) Go back to 2) until stop criteria is met
   - Desired fitness
   - Specified number of generations
   - Convergence

applications

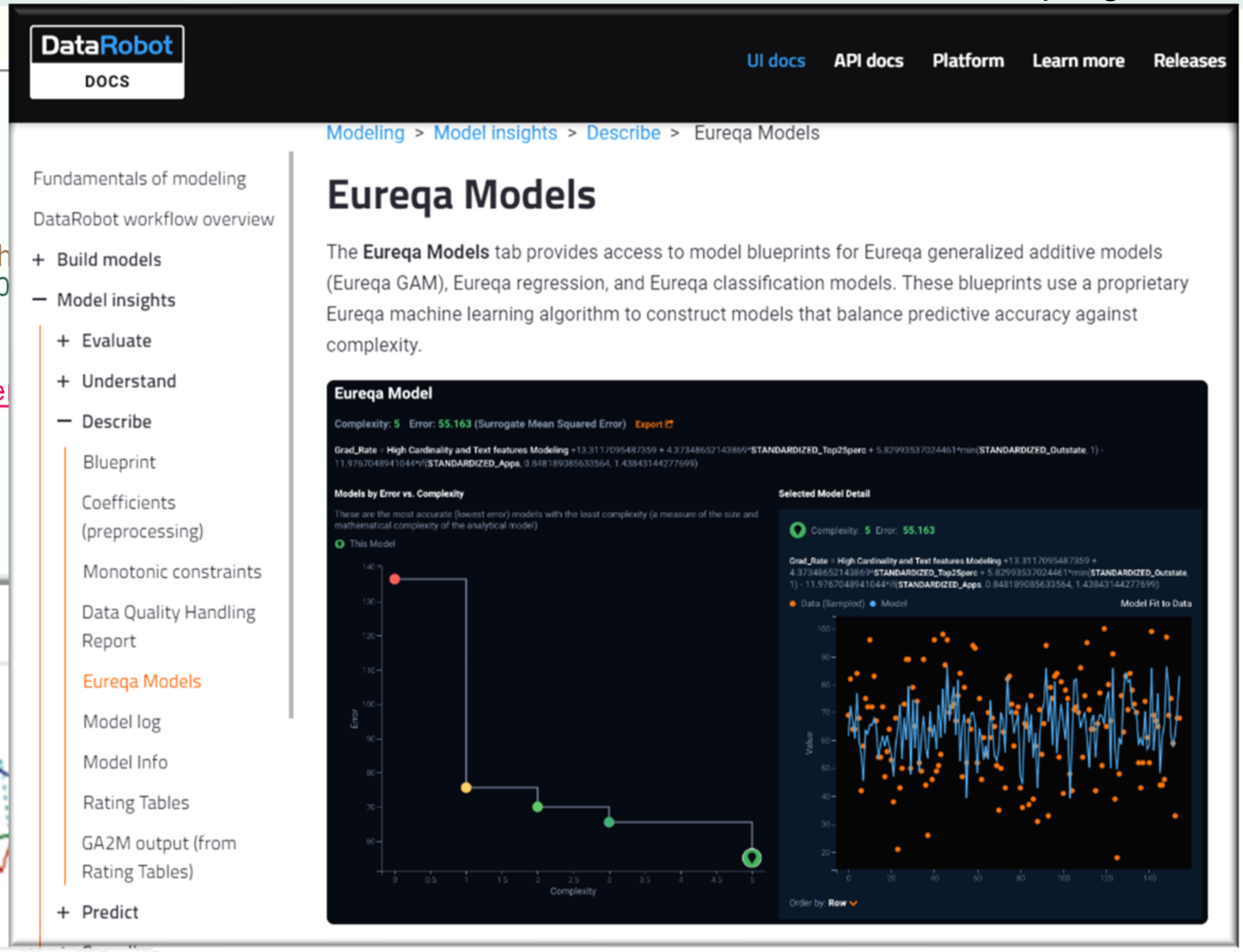
- Optimal control
- Planning
- Symbolic regression
  - Fit real data
    - Example: Uncover laws of physics
      - Schmidt M., Lipson H. (2009) "Distilling Free-Form Natural Laws from Experimental Data," *Science*, **324** (5923): 81 - 85.
    - Binary Classification
  - Software Tool
    - Eureqa: https://www.creativemachineslab.com/eureqa.html
- Robot strategies
  - Robocup
- Evolvable hardware

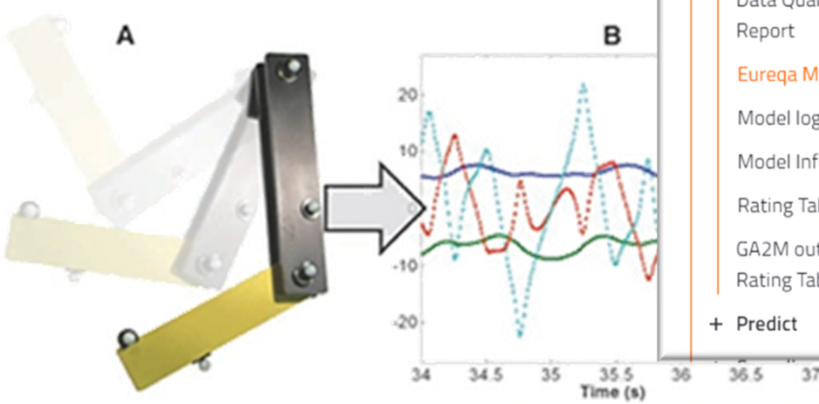


BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

applications

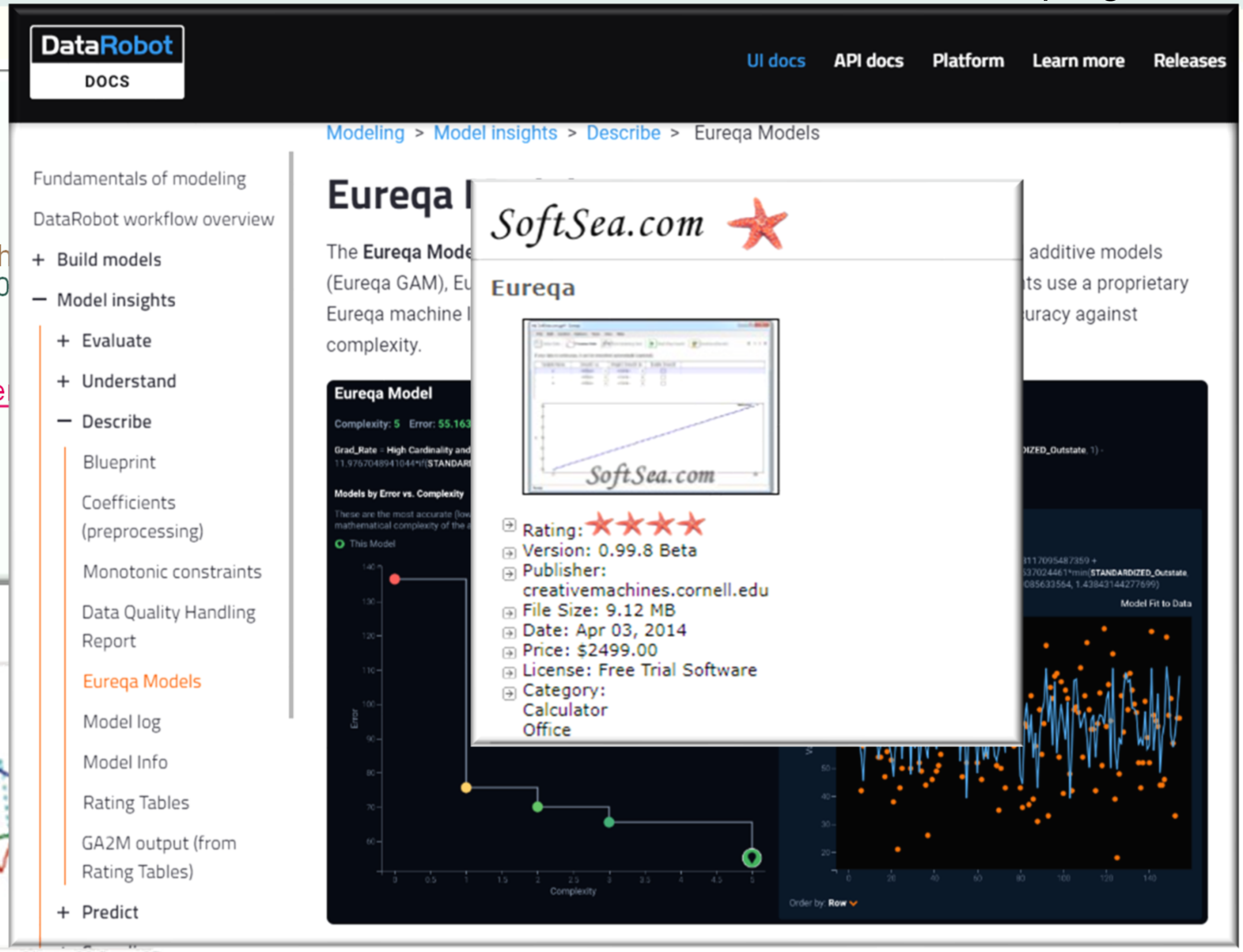
- Optimal control
- Planning
- Symbolic regression
  - Fit real data
    - Example: Uncover laws of ph
      - Schmidt M., Lipson H. (200
    - Binary Classification
  - Software Tool
    - Eureqa: https://www.creative
- Robot strategies
  - Robocup
- Evolvable hardware

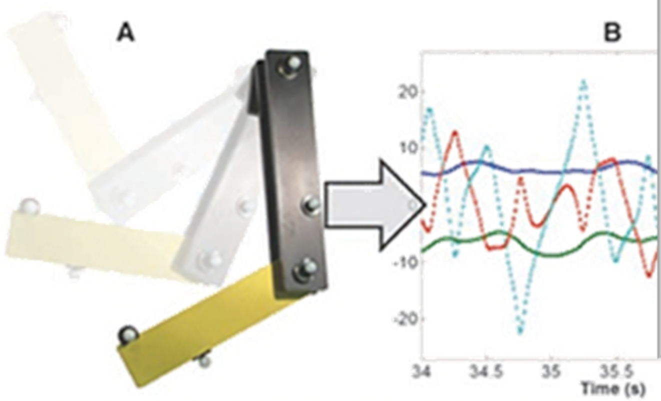




applications

- Optimal control
- Planning
- Symbolic regression
  - Fit real data
    - Example: Uncover laws of ph
      - Schmidt M., Lipson H. (200
    - Binary Classification
  - Software Tool
    - Eureqa: https://www.creative
- Robot strategies
  - Robocup
- Evolvable hardware

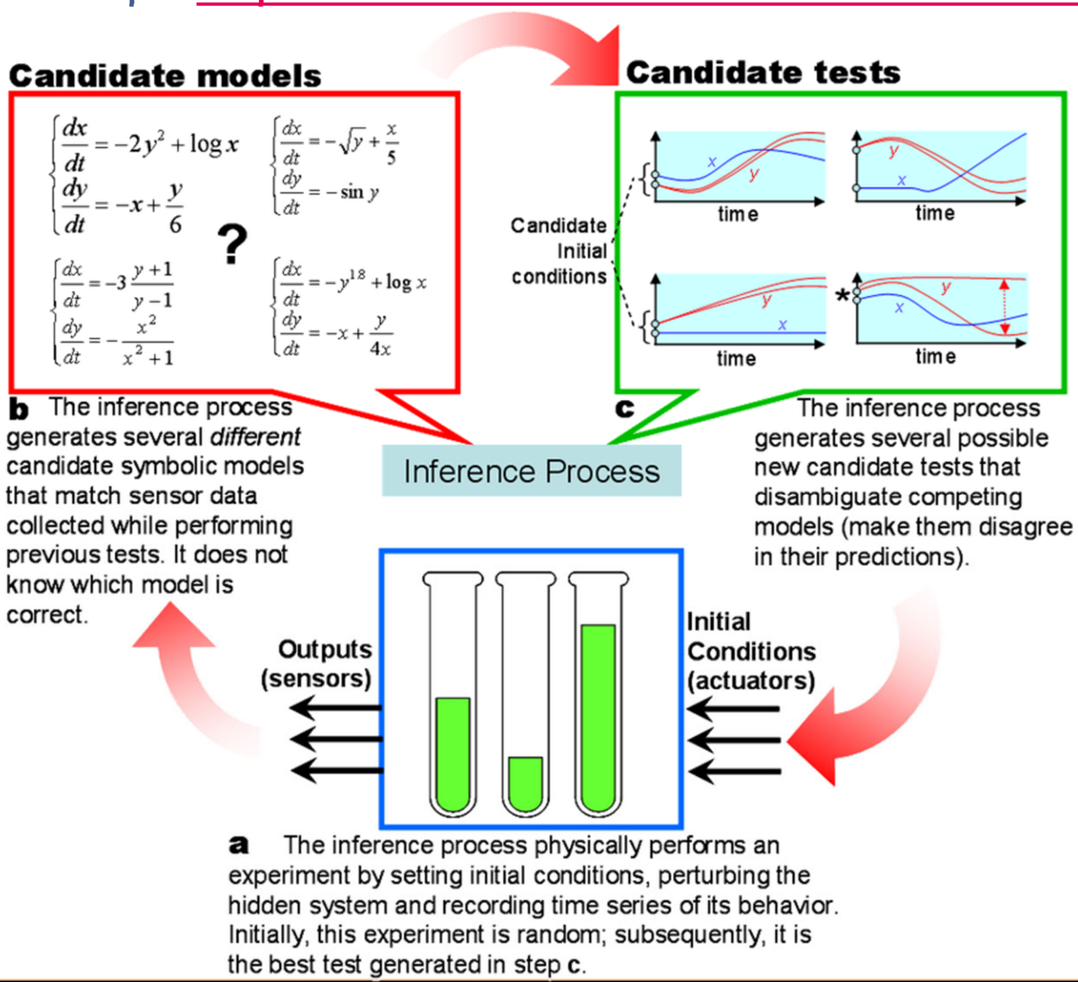


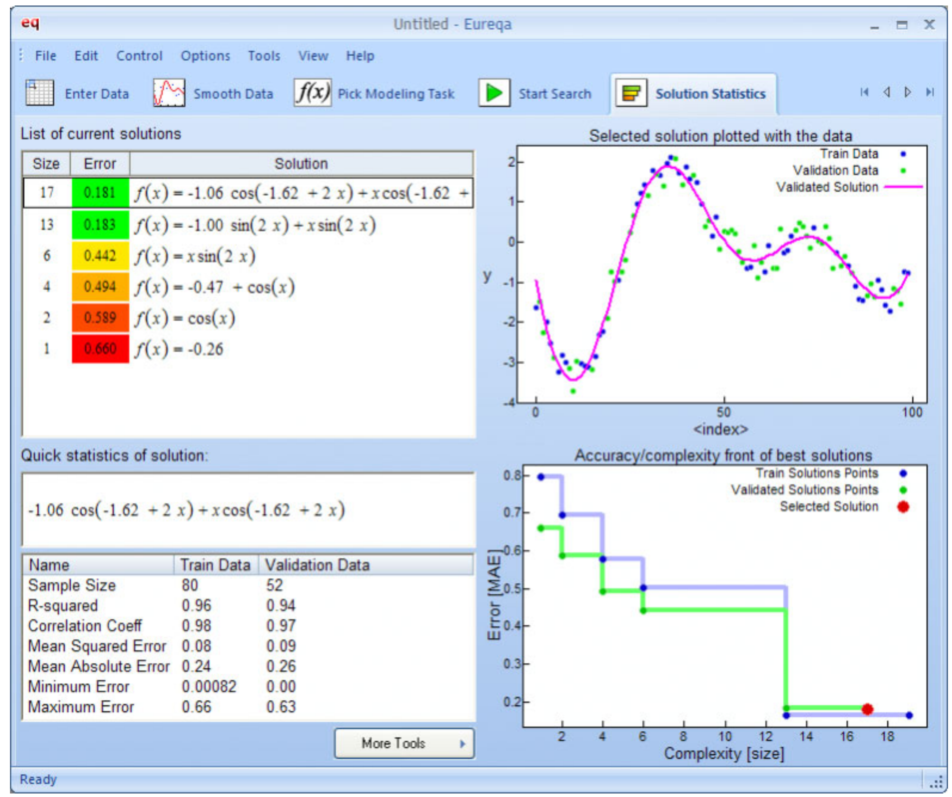


BINGHAMTON UNIVERSITY
STATE UNIVERSITY OF NEW YORK
rocha@indiana.edu
casci.binghamton.edu/academics/i-bic

A symbolic regression tool

Eureqa: https://www.creativemachineslab.com/eureqa.html

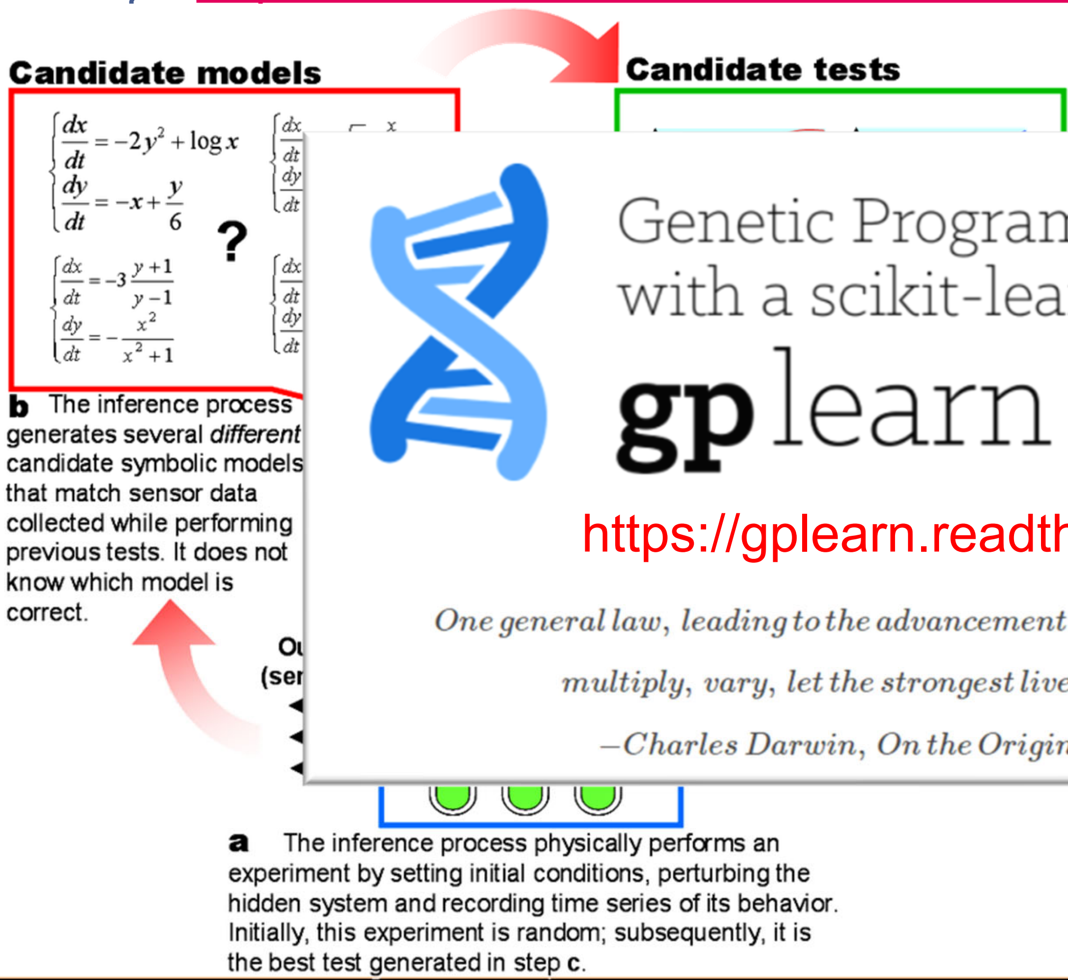


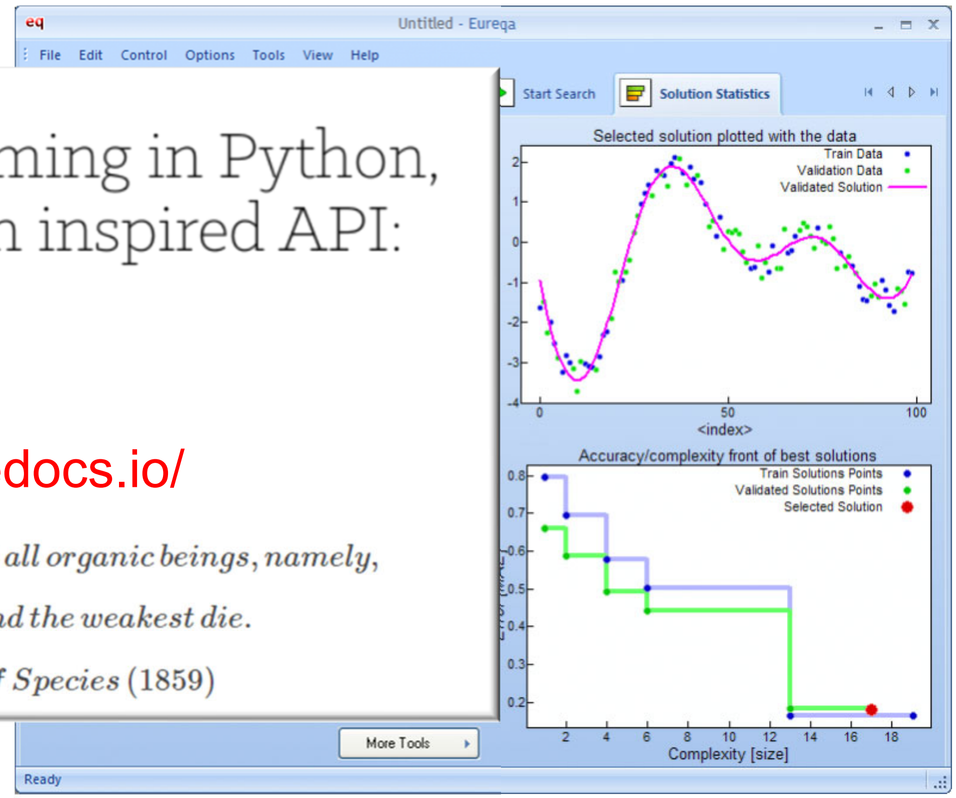


BINGHAMTON UNIVERSITY
STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

A symbolic regression tool

Eureqa: https://www.creativemachineslab.com/eureqa.html



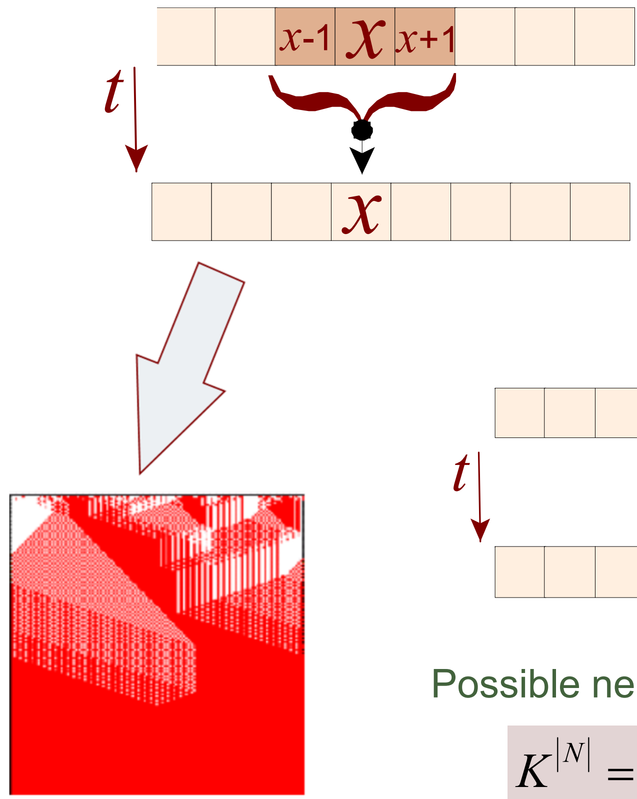


BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

- Binary encodings
  - Typically fixed-length
- Many-letter encoding
  - Larger alphabet (e.g. graph-generation grammars)
- Real-valued encodings
  - Genes take real values
- Tree Encodings
  - Genetic programming
- Indirect Encodings
  - Modeling Phenotype **development** or **post-transcription** processes
    - L-Systems, Dynamical systems, evolutionary robotics

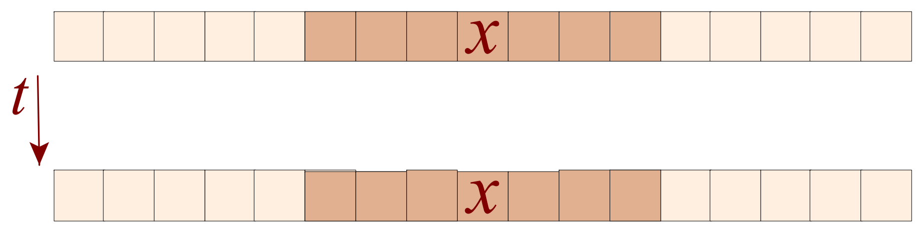
homogenous lattice of state-determined systems

Cellular Automata



Density Task
(a.k.a majority classification problem)

- Lattices of 149 Binary Cells (599, 999)
- Rules of Radius 3 (7 Cells in Neighborhood)
- Task: Organize to
  - All 1's if Initial Configuration (IC) has more 1 Cells
  - All 0's if IC has more 0 Cells



Possible neighborhood states

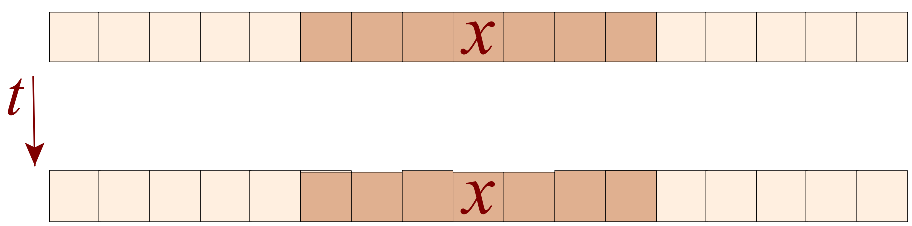
$$K^{|N|} = 2^7 = 128$$

Possible CA transition functions

$$K^{K^{|N|}} = 2^{128} \approx 3.4 \times 10^{38}$$

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

encoding in GA with binary encoding



Possible neighborhood states $K^{|N|} = 2^7 = 128$

0	0	0	0	0	0	0	0
0	0	0	0	0	0	1	0
0	0	0	0	0	1	0	1
0	0	0	0	0	1	1	0
0	0	0	0	1	0	0	1
0	0	0	0	1	0	1	0
0	0	0	0	1	1	0	0
0	0	0	0	1	1	1	0
0	0	0	1	0	0	0	1
0	0	0	1	0	0	1	0
0	0	0	1	0	1	0	1
0	0	0	1	0	1	1	1
0	0	0	1	1	0	0	0
0	0	0	1	1	0	1	0

Pop of rules

010010101100100

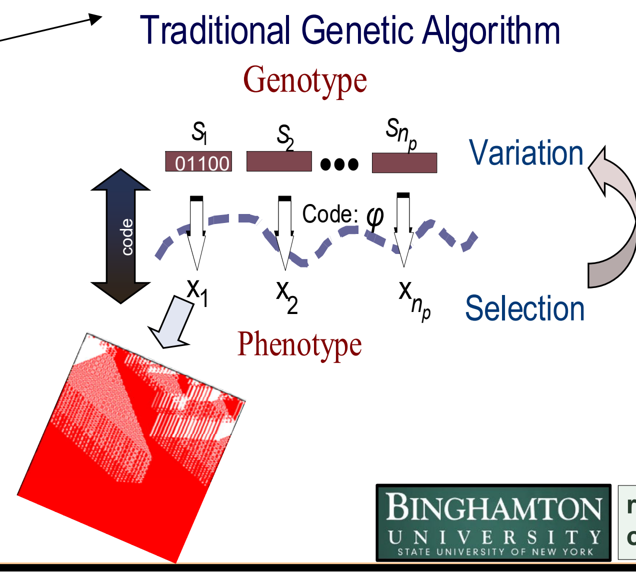
010010101100100

010010101100100

010010101100100

010010101100100

Used in the evolutionary search by GA (elite selection)

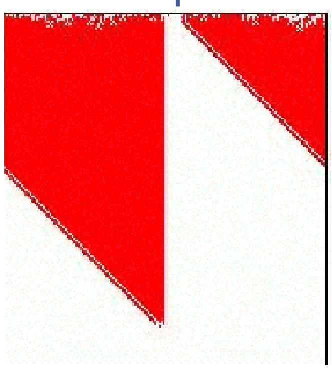


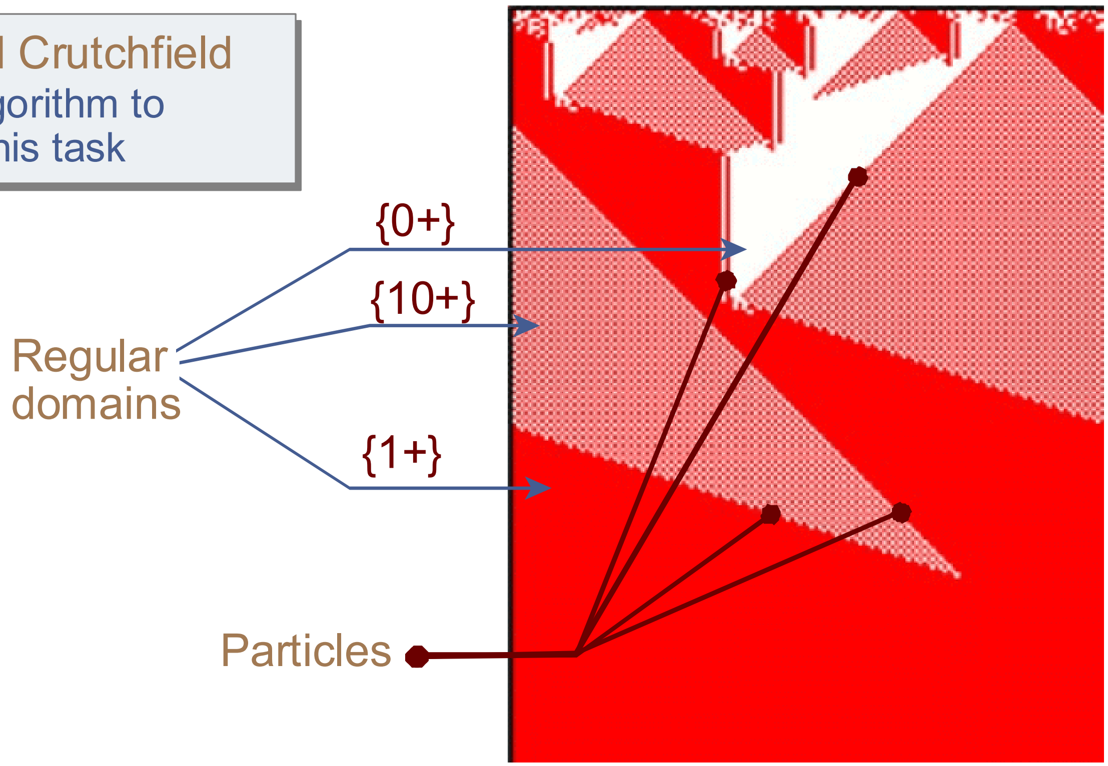
BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

With genetic algorithms

- Das, Mitchell and Crutchfield
  - Used Genetic Algorithm to evolve rules for this task

Typical Result:
Block Expansion

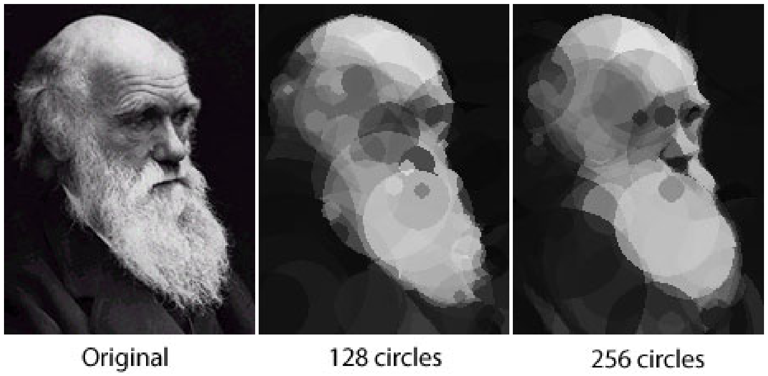


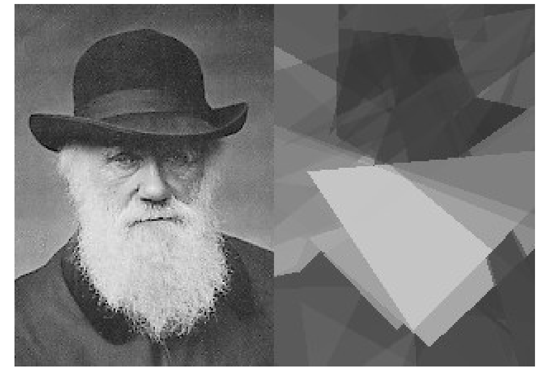


Das,R., Mitchell,M., Crutchfield,J.P., [1994]. "A genetic algorithm discovers particle-based computation in cellular automata". In: *Parallel Problem Solving from Nature - PPSN III*. Davidor,Y., Schwefel,H.-P., Manner,R. (Eds.), Springer-Verlag, pp. 344-353.

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

to evolve photos with numerical encodings





rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

In genetic algorithms

1) Genotypes contain real or integer values
   1) Crossover is performed in the same way
   2) Mutation assigns a random number in a given interval
2) More computationally demanding for Reals
3) Attention to crossover points
   1) Conversion to binary avoids crossover issues, but longer genotypes

0.3	1.7	3.8	1.7	6	1.2	3.2	6.4	2.8	0

0.3	1.7	3.8	1.7	2.9	1.2	3.2	6.4	2.8	0

n circles

x	y	r	R	G	B							...						
54	108	25	201	11	192	254	18	100	1	141	12	...	254	18	100	1	141	12

n Genes

Agent Chromosome/Genotype (Population of p agents)

Evolutionary algorithms to optimize neural networks

- Capabilities (not in gradient-based ANN)
  - Generation of ANN building blocks
    - Activation functions
  - Hyperparameter optimization
  - Architecture and learning algorithm search and optimization
- Massive Paralellism
  - Population of solutions

nature machine intelligence

Explore content About the journal Publish with us Subscribe

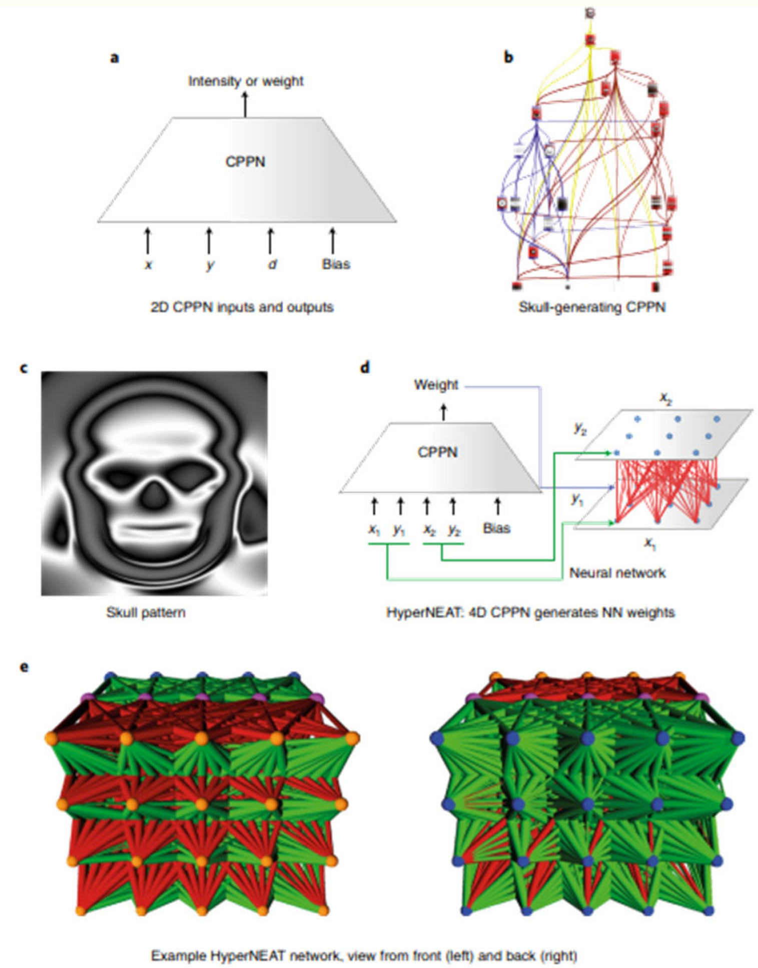
nature > nature machine intelligence > review articles > article

Review Article | Published: 07 January 2019

Designing neural networks through neuroevolution

Kenneth O. Stanley, Jeff Clune, Joel Lehman & Risto Miikkulainen

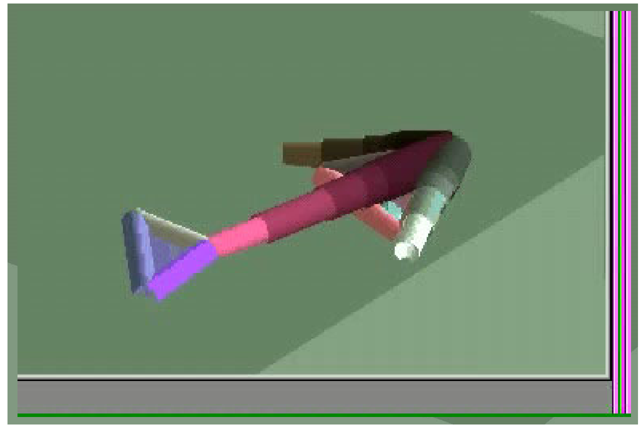
Nature Machine Intelligence **1**, 24–35 (2019) | Cite this article

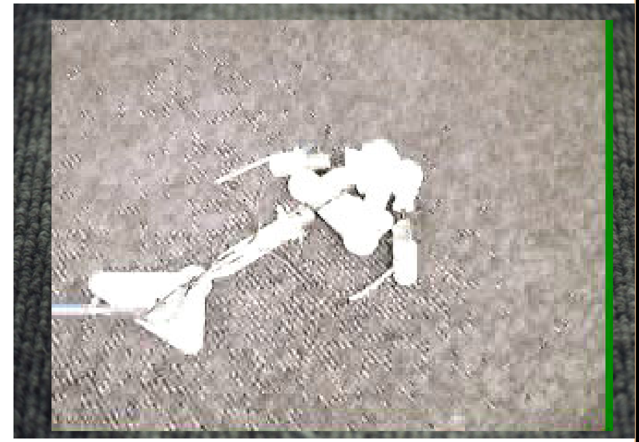


Stanley, K.O., Clune, J., Lehman, J. et al (2019). Designing neural networks through neuroevolution. *Nat Mach Intell*, 24–35.

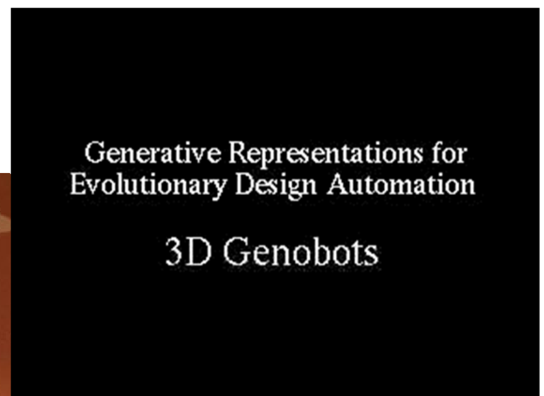
Karl Sim´s simulations, Genobots, and the Golem project

Sims, Karl. "Evolving virtual creatures."
In *Seminal Graphics Papers: Pushing the Boundaries, Volume 2*, pp. 699-706. 2023.





http://demo.cs.brandeis.edu/golem/



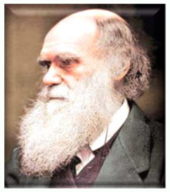
https://www.karlsims.com/evolved-virtual-creatures.html

http://www.demo.cs.brandeis.edu/pr/evo_design/evo_design.html

BINGHAMTON UNIVERSITY STATE UNIVERSITY OF NEW YORK
rocha@binghamton.edu
casci.binghamton.edu/academics/i-bic

readings

- Class Book
  - Floreano, D. and C. Mattiussi [2008]. *Bio-Inspired Artificial Intelligence: Theories, Methods, and Technologies*. MIT Press.
    - **Chapter 7**
- Lecture notes
  - Chapter 1: What is Life?
  - Chapter 2: The logical Mechanisms of Life
  - Chapter 3: Formalizing and Modeling the World
  - Chapter 4: Self-Organization and Emergent Complex Behavior
  - Chapter 5: Reality is Stranger than Fiction
  - Chapter 6: Von Neumann and Natural Selection
    - posted online @ casci.binghamton.edu/academics/i-bic
- Papers and other materials
  - Optional
    - Nunes de Castro, Leandro [2006]. *Fundamentals of Natural Computing: Basic Concepts, Algorithms, and Applications*. Chapman & Hall.
      - Chapter 5, 7.7, 8.3.1, 8.3.6,



rocha@indiana.edu
casci.binghamton.edu/academics/i-bic