

The Role of Emergence in Open-Ended Systems

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Algorithmic Nature Group, LABORES for the Natural and Digital Sciences

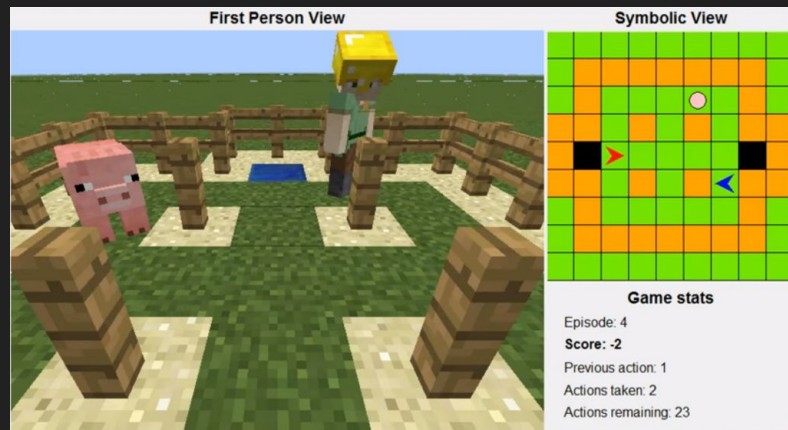
My background...

- Undergrad @ ETSU - Physics, 2013
 - I love solving problems in abstract math space
- Grad school - Origin of Life, 2017
 - Advisor: Sara I Walker
 - What is the difference between living systems and non-living ones?
 - Open-ended evolution and innovation
 - Discrete, finite, deterministic systems



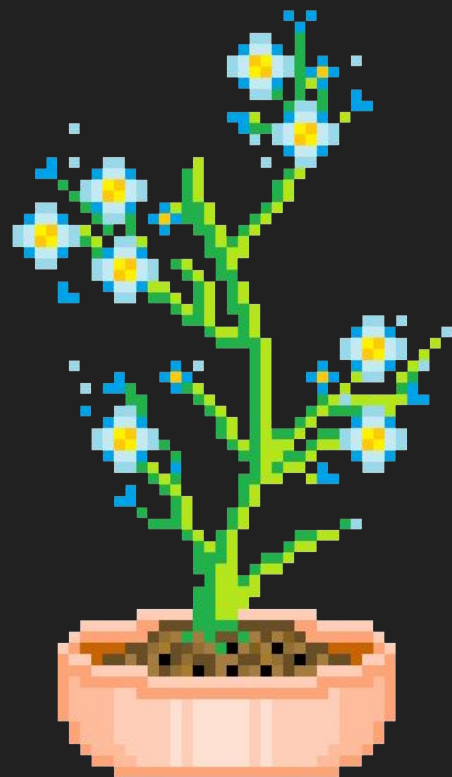
My background...

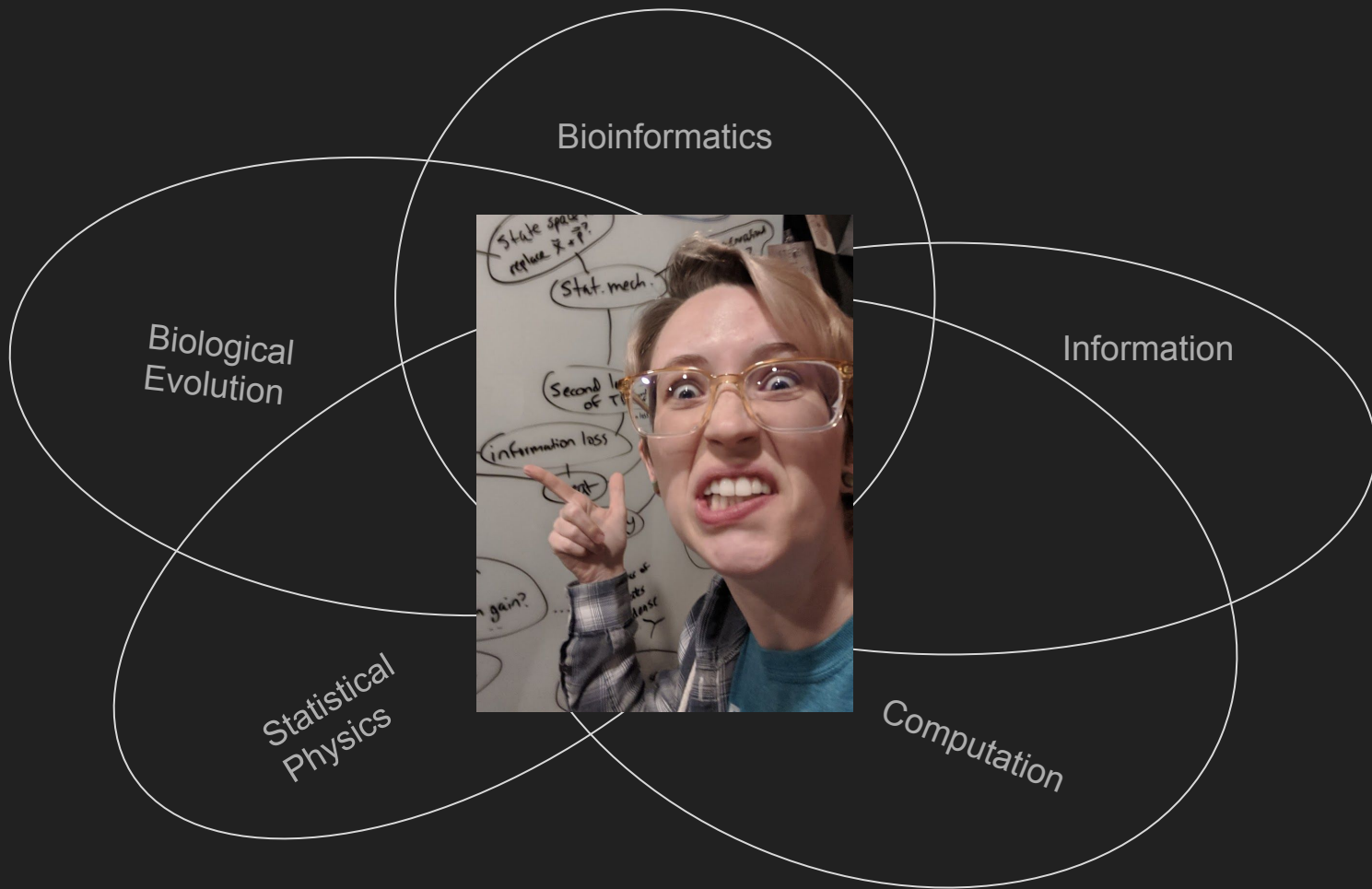
- Microsoft Research, 2017
 - Machine learning algorithms in Minecraft
- VEDA Data Solutions, 2017
 - Python software development
 - Industrial research & management
 - Problems in big data
- UW Bacteriology, Bioinformatics, 2019
 - Microbiomes, bacteria, and viruses
 - Emergence of function

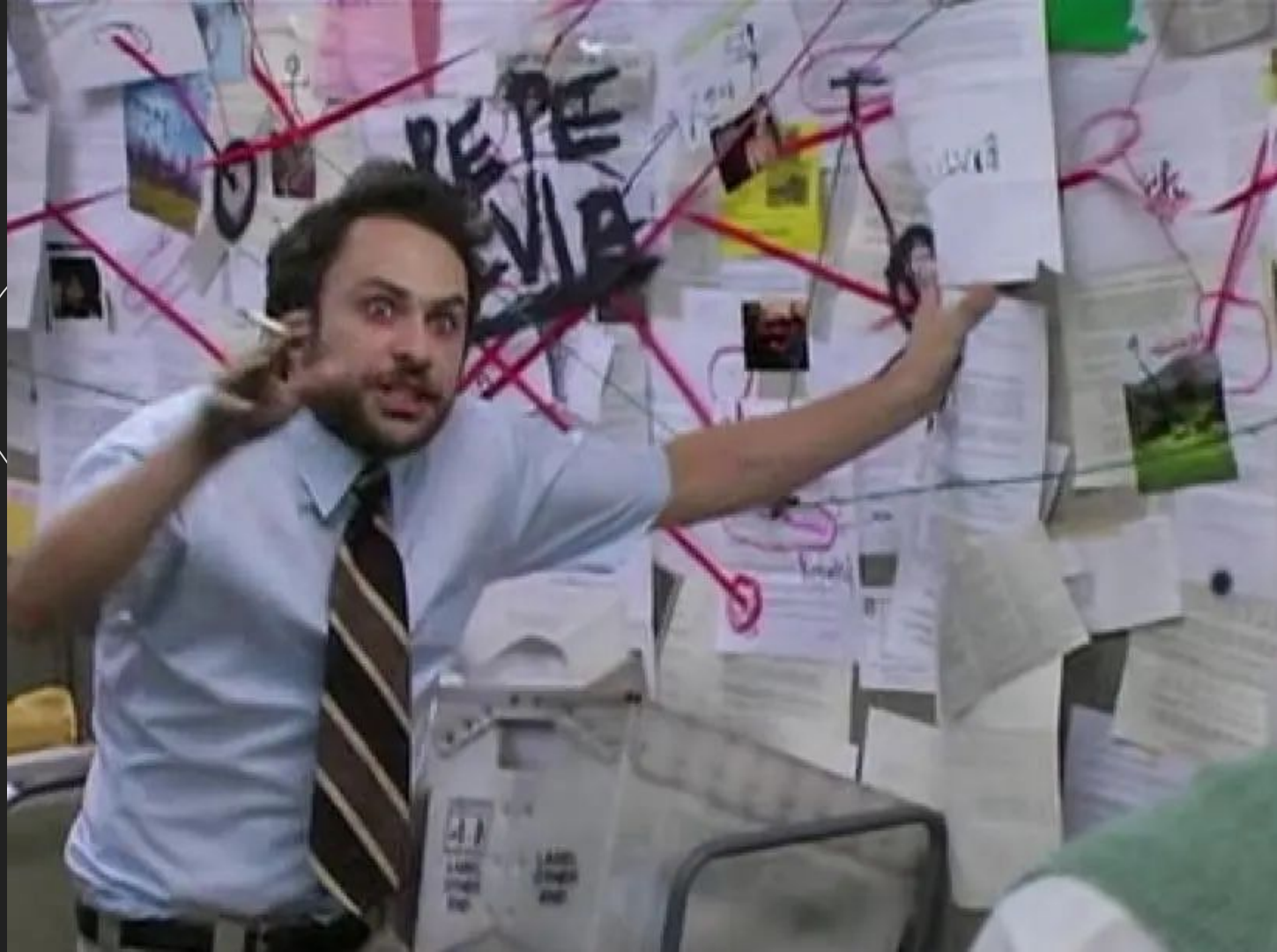


Questions I Study

- How are living systems different than non-living ones?
 - What are the unique mechanisms of living *systems*?
- Can statistical mechanics be useful for biology?
 - Relationships between different levels of organization
 - Emergent functions
- How does life arrange itself in physical space to perform computation?
 - Structure = Function
- What can biological data tell us?
 - Viruses, bacteria, human social systems, data on the internet







Time for Three Stories

Once upon a time...

30,000 base pairs are arranged in some particular order...

- Earth's humans stay inside small structures more frequently.

Elon Musk posts an arrangement of letters on Twitter...

- The stock market takes a hit.

A butterfly flaps its wings in the Amazon...

- Tornadoes in Texas.

More realistic scenarios...

30,000 base pairs are arranged in some particular order...

- The virus is malformed and does nothing.

I post an arrangement of letters on Twitter...

- I get two likes.

A butterfly flaps its wings in the Amazon...

- Its neighbor is graced with a refreshing breeze.

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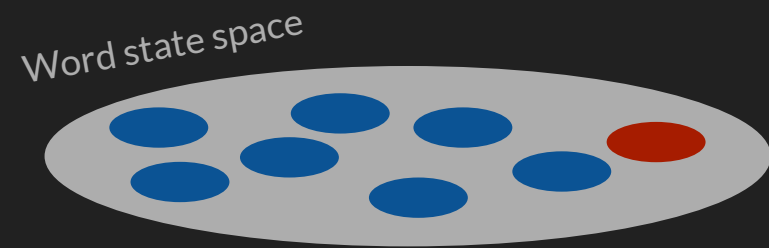
*Can we make predictions about which
“perturbations” will result in a particular
change?*

“The whole is *different* than the sum of its parts.”

Emergence

Weak

- “The cat emerged from under the bed”
- “Ebola emerged once again”
- The appearance of something *new* from a *known* possibility space
- Expanding a state space

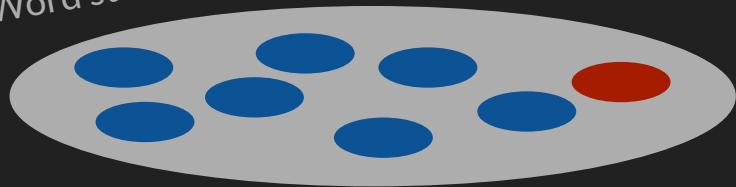


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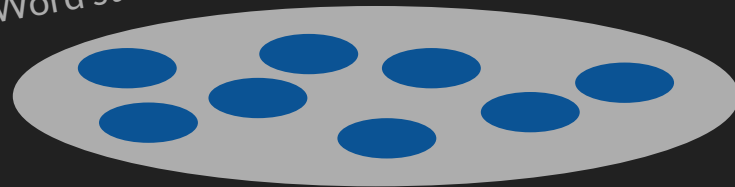
Word state space



Strong

- “The emergence of multicellularity”
- “The emergence of language”
- The appearance of an *entirely new* possibility space

Word state space



Story state space



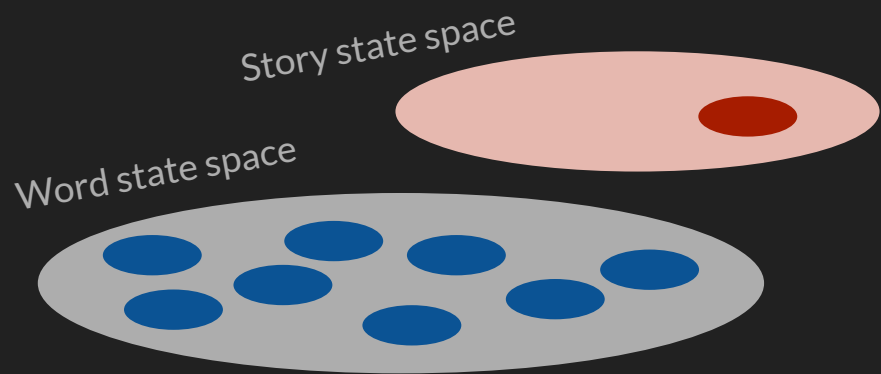
Emergence

Coarse-graining: Condensing a state space into a smaller one.

- One-to-many maps
- Loss of information
- Decreases complexity in CA
 - Israeli, N.; Goldenfeld, N. *Coarse-graining of cellular automata, emergence, and the predictability of complex systems*. Phys. Rev. E 2006, 73, 026203.
- Does biology use this to make solving problems easier?

Strong

- “The emergence of multicellularity”
- “The emergence of language”
- The appearance of an *entirely new* possibility space



Open-endedness: The last grand challenge you've never heard of

While open-endedness could be a force for discovering intelligence, it could also be a component of AI itself.

By Kenneth O. Stanley, Joel Lehman, and Lisa Soros. December 19, 2017

“Novelty search ... only really address finding new solutions to existing challenges open-endedly, but they don't inherently generate new kinds of challenges to be solved. The most powerful open-ended system would generate both.”

Definitions of OEE

1. On-going innovation and generation of novelty
2. Unbounded evolution
3. On-going production of complexity
4. A defining feature of life

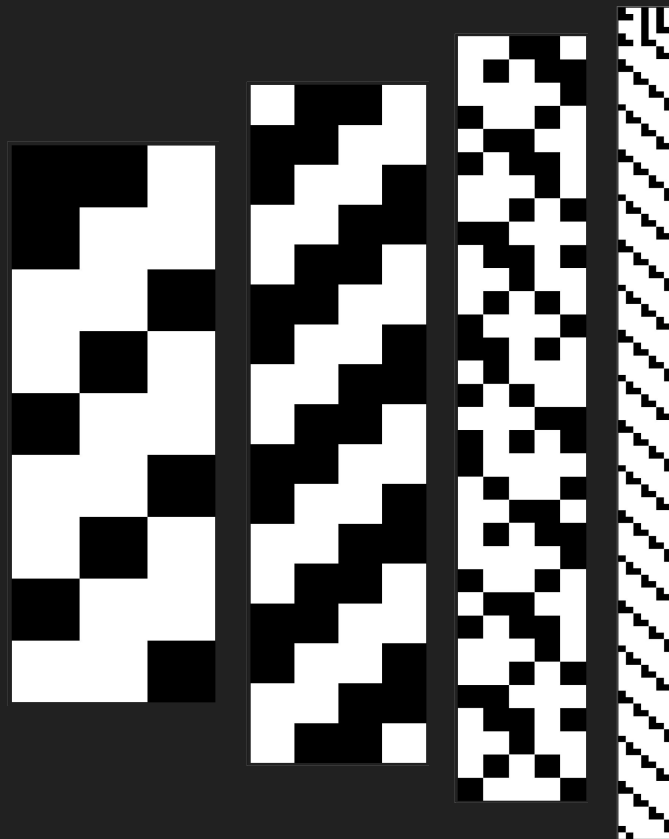
In finite, deterministic, bounded systems?

Banzhaf W et al. (2016) Defining and simulating open-ended novelty: requirements, guidelines, and challenges. Theory in Biosciences pp. 1–31.

Poincaré Recurrence Theorem

The state of every *finite* deterministic system approaches the initial condition within a sufficient amount of time

- Natural bound on complexity
- Natural bound on number of possible states
- Natural bound on open-endedness



OEE = Innovation + Unbounded Evolution

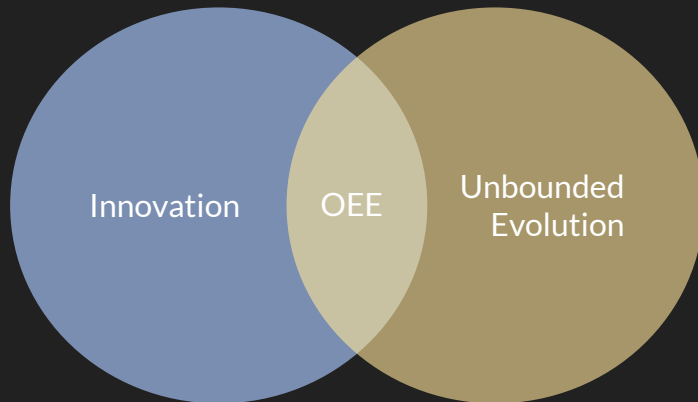
Innovation

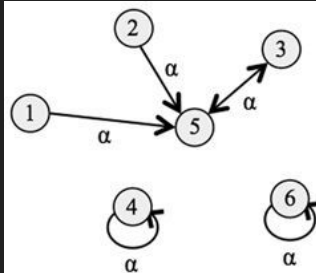
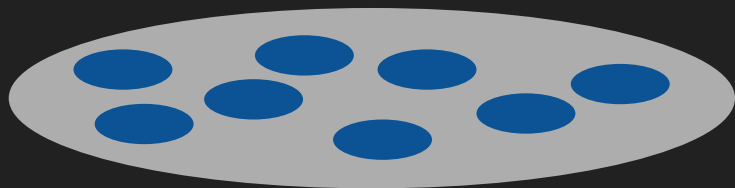
A unique path through state space *not* observed when the system is in isolation.

Definition is based on counterfactual paths through **ONE** state space.

Unbounded Evolution

The path through state space takes longer than the Poincare Recurrence time to reach an attractor state/cycle.



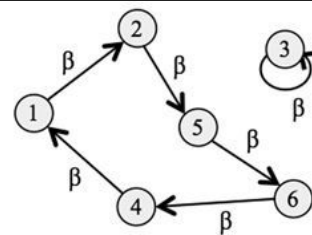


Fixed Rule α

$s = \{3, 5, 3, 5, 3, \dots\}$

$r = \{\alpha, \alpha, \alpha, \alpha, \alpha, \dots\}$

(a)

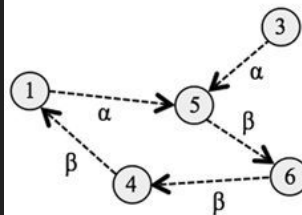


Fixed Rule β

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(b)

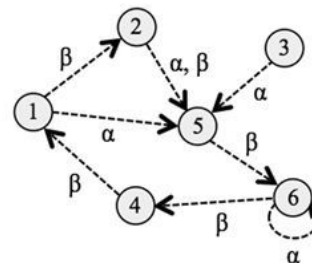


INN

$s = \{3, 5, 6, 4, 1, 5, 6, 4, 1, \dots\}$

$r = \{\alpha, \beta, \beta, \beta, \alpha, \beta, \beta, \beta, \alpha, \dots\}$

(c)



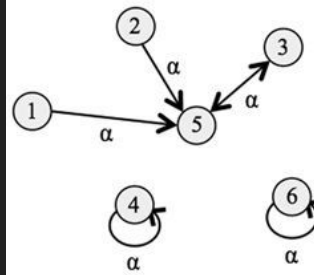
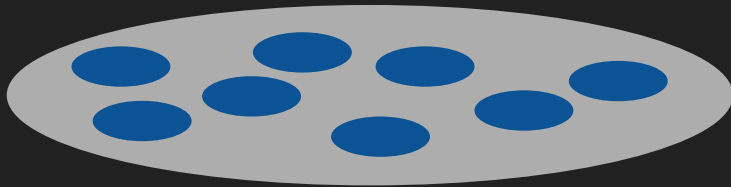
UE

$s = \{3, 5, 6, 6, 4, 1, 2, 5, 6, 4, 1, 5, 6, 4, 1, \dots\}$

$r = \{\alpha, \beta, \alpha, \beta, \beta, \beta, \alpha, \beta, \beta, \beta, \beta, \beta, \beta, \alpha, \dots\}$

(d)

- All impossible for regular ECA
- Requires the ability to change rules
- Coupled CA system
- (Checking for innovation or unbounded evolution requires knowing all counterfactual trajectories from regular non-coupled ECA)

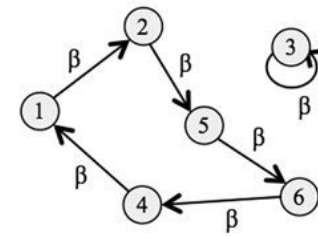


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(a)

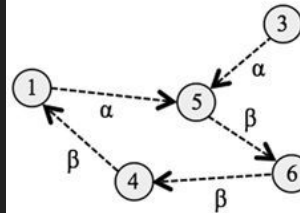


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$r = \{\beta, \beta, \beta, \beta, \beta, \dots\}$

(b)

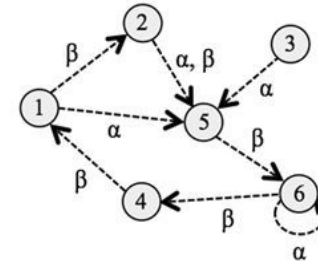


INN

$s = \{3, 5, 6, 4, 1, 5, 6, 4, 1, \dots\}$

$r = \{\alpha, \beta, \beta, \beta, \alpha, \beta, \beta, \beta, \alpha, \dots\}$

(c)



UE

$s = \{3, 5, 6, 6, 4, 1, 2, 5, 6, 4, 1, 5, 6, 4, 1, \dots\}$

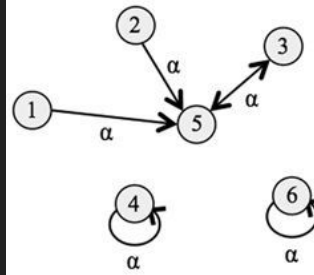
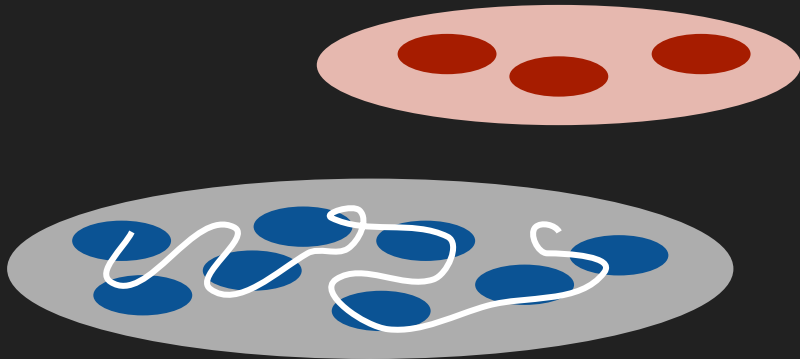
$r = \{\alpha, \beta, \alpha, \beta, \beta, \beta, \alpha, \beta, \beta, \beta, \beta, \beta, \beta, \alpha, \dots\}$

(d)

Open-ended evolution is how a system moves within a *single state space*.

In an ensemble of systems with different state spaces, open-ended evolution is a property of a single state space.

For bounded, discrete, deterministic systems like CA, OEE is only possible in an ensemble of systems.

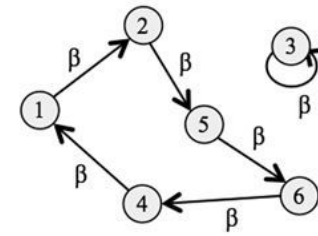


Fixed Rule α

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(a)

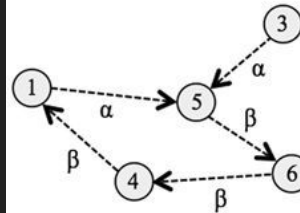


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(b)

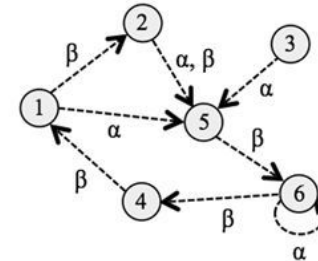


INN

$s = \{3, 5, 6, 4, 1, 5, 6, 4, 1, \dots\}$

$r = \{\alpha, \beta, \beta, \beta, \alpha, \beta, \beta, \beta, \alpha, \dots\}$

(c)



UE

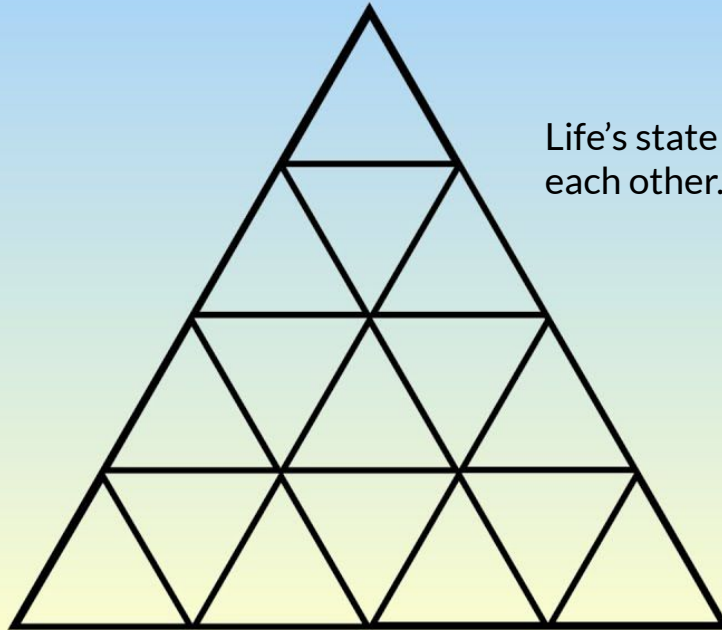
$s = \{3, 5, 6, 6, 4, 1, 2, 5, 6, 4, 1, 5, 6, 4, 1, \dots\}$

$r = \{\alpha, \beta, \alpha, \beta, \beta, \beta, \alpha, \beta, \beta, \beta, \beta, \beta, \beta, \alpha, \dots\}$

(d)

Biological state spaces do ***not*** exist in isolation!

HOW MANY TRIANGLES DO YOU SEE?



Life's state spaces overlap with each other.

Biological state spaces do **not** exist in isolation!



@echo_adventure_photography

Life's state spaces overlap with each other.

Life also employs self-reference.

We pick state spaces that allow us to make predictions:

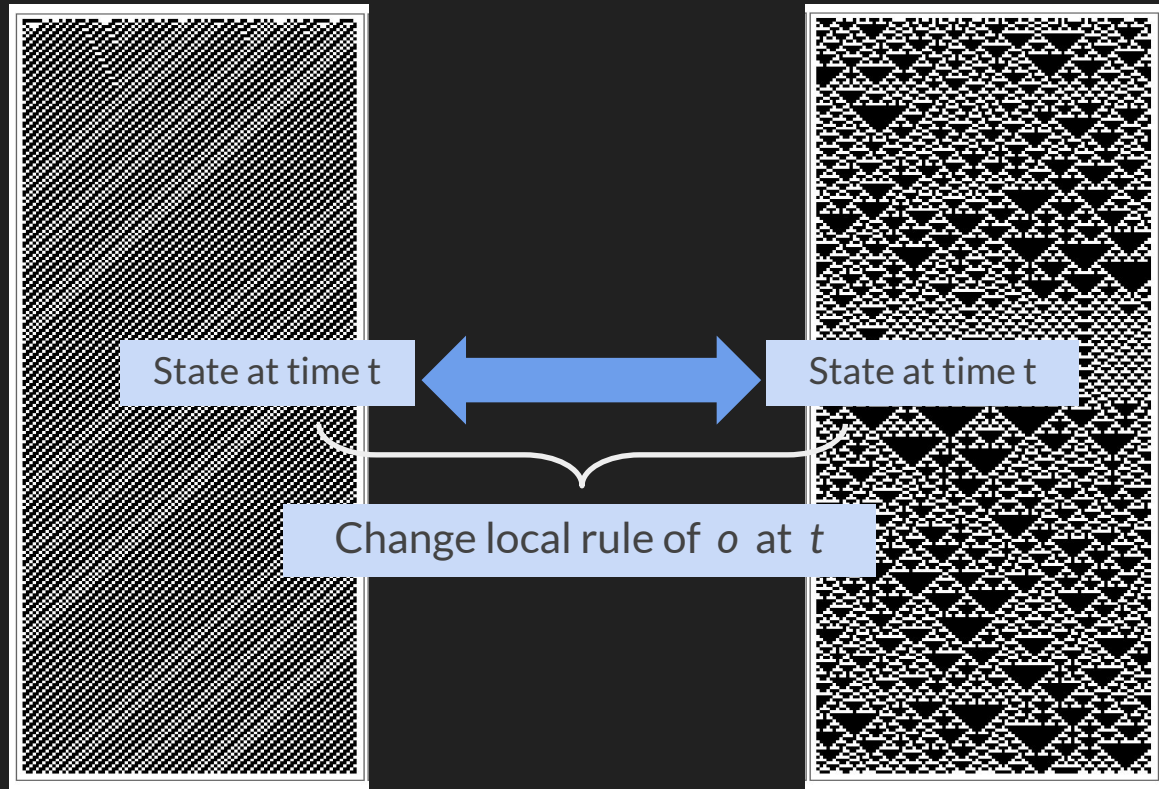
- Temperature
- pH
- Taxonomy
- Population

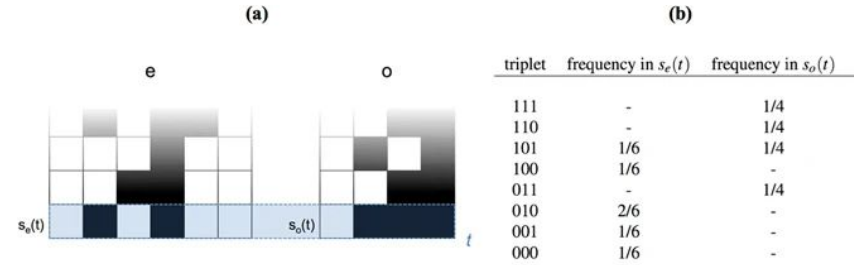
Coupled CA that employ self-reference.

System u

“Environment” e

“Organism” o





(c)

$0 \cdot 2^7 + 0 \cdot 2^6 + 0 \cdot 2^5 + 1 \cdot 2^4 + 1 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 30$

$0 \cdot 2^7 + 0 \cdot 2^6 + 1 \cdot 2^5 + 1 \cdot 2^4 + 1 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 62$

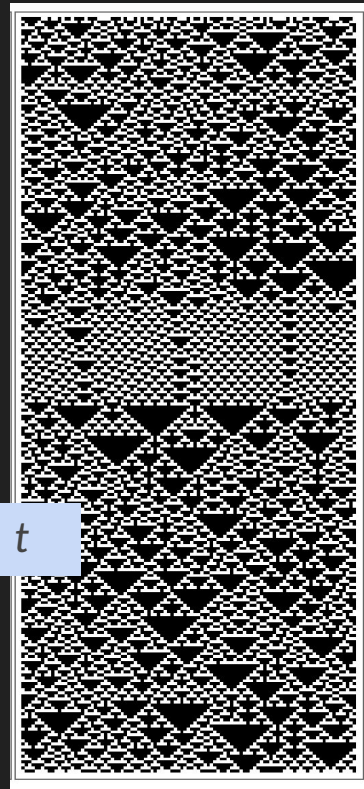
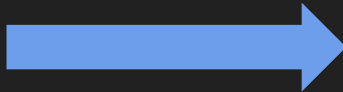
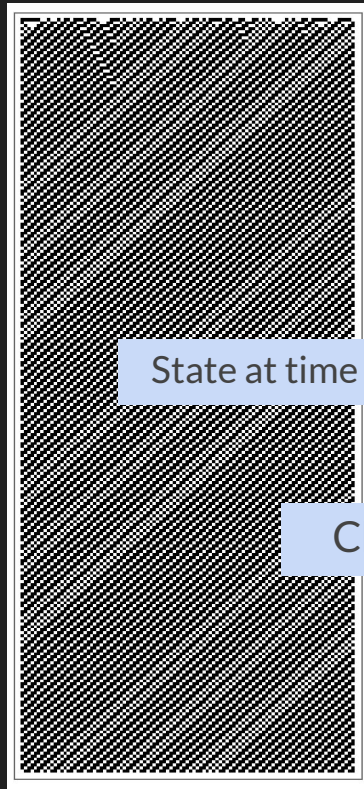
System u

“Environment” e

“Organism” o

State at time t

Change local rule of o at t



System u

“Organism” o

Change local rule randomly at t

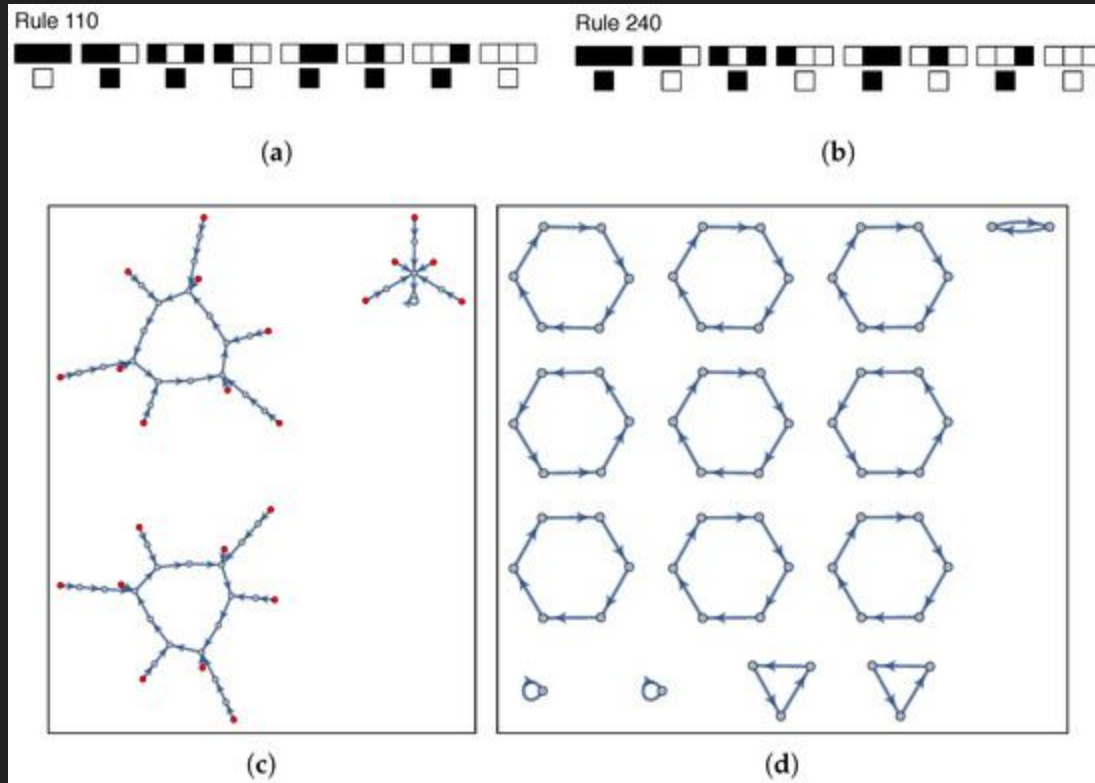
State at time t



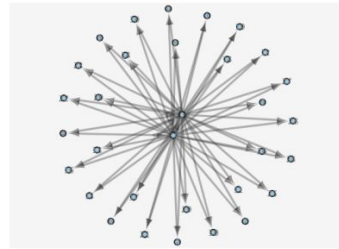
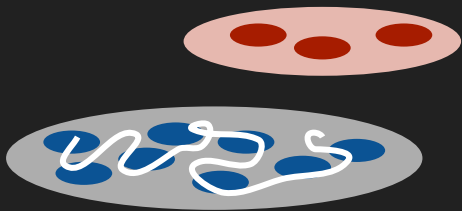
% Open-Ended o Trajectories

w_o	$\frac{1}{2} w_o$	w_o	$\frac{3}{2} w_o$	$2 w_o$	$\frac{5}{2} w_o$
3	0	0.02	6.52	10.81	28.14
4	0	0.38	2.28	2.94	9.65
5	0	3.41	7.04	7.5	8.64
6	0	0.03	2.15	2.64	5.82
7	0	1.06	2.95	4.39	5.34

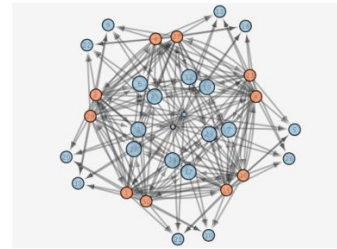
Adams, A., Zenil, H., Davies, P.C.W. *et al.* Formal Definitions of Unbounded Evolution and Innovation Reveal Universal Mechanisms for Open-Ended Evolution in Dynamical Systems. *Sci Rep* 7, 997 (2017). <https://doi.org/10.1038/s41598-017-00810-8>



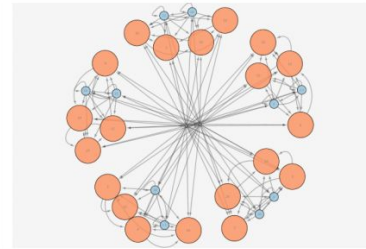
Adams, A.M.; Berner, A.; Davies, P.C.W.; Walker, S.I. Physical Universality, State-Dependent Dynamical Laws and Open-Ended Novelty. *Entropy* **2017**, *19*, 461.



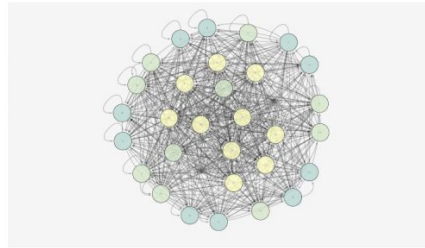
(a) $R_p = 0$



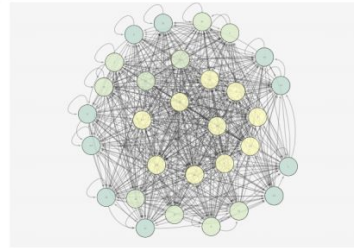
(b) $R_p = 0.2$



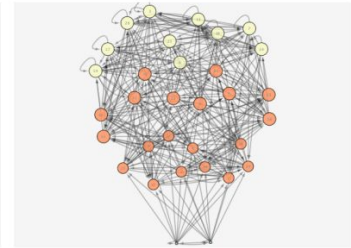
(c) $R_p = 0.4$



(d) $R_p = 0.5$

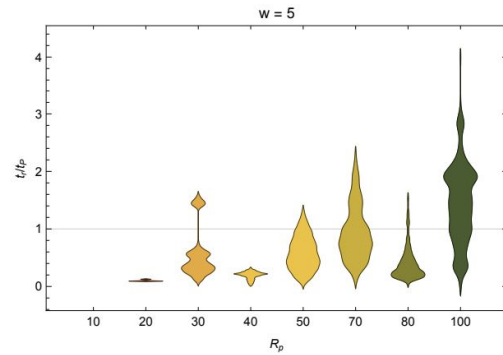
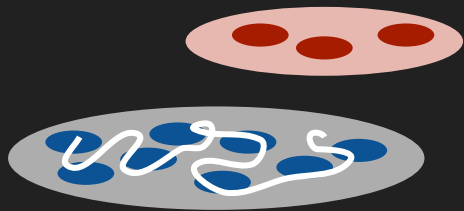


(e) $R_p = 0.7$

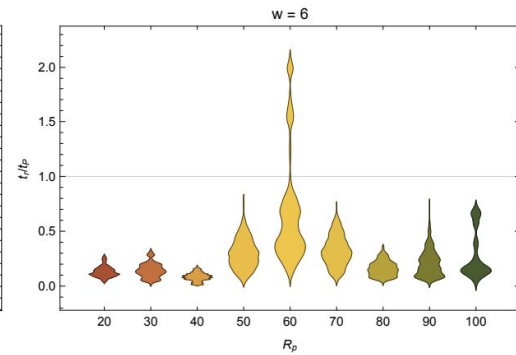


(f) $R_p = 0.8$

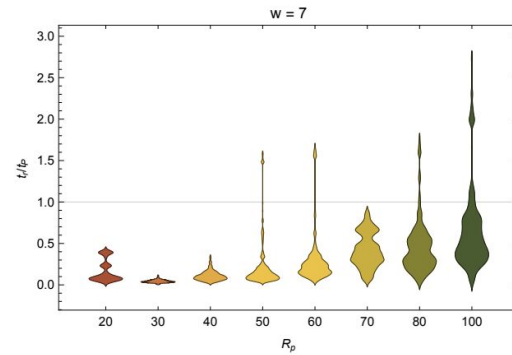
Figure 5. State transition diagrams for with $w = 5$ with varying R_p . Node size is weighted by out-degree and colors indicate betweenness centrality (high values are warm, low values cool tones).



(c)



(d)

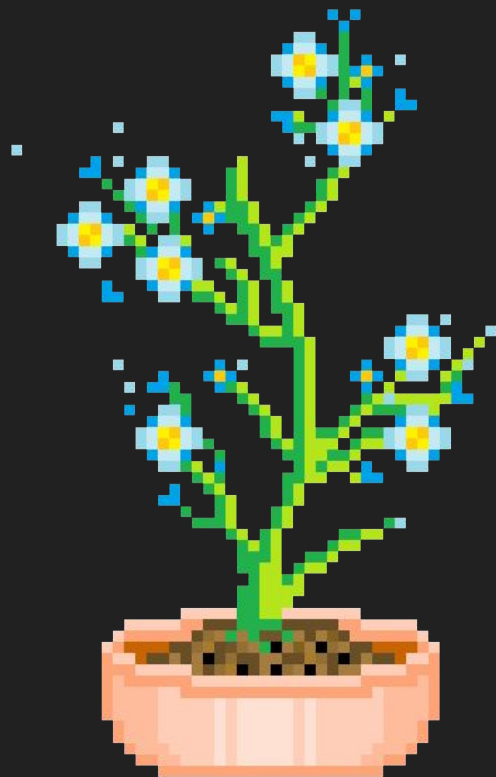


(e)

Adams, A.M.; Berner, A.; Davies, P.C.W.; Walker, S.I. Physical Universality, State-Dependent Dynamical Laws and Open-Ended Novelty. *Entropy* **2017**, *19*, 461.

(More specific) Questions I study

- How does biology create new state spaces?
 - (What are the mechanisms of strong emergence?)
- How does biology discover new states?
 - (What are the mechanisms of weak emergence?)
- How do state spaces interact with each other?
- What gives a state more predictive power than other states, according to an observer?
- Does this have a relationship with complexity?
- How can we use real biological data to inform models?



If we have...

The current positions and velocities of each bird...

The neural activity of a brain...

What every person is talking about in 1788...

A chemical soup...

The genetic code for a virus...

Can we predict...

The shape of the flock in 5 minutes?

How a person is feeling?

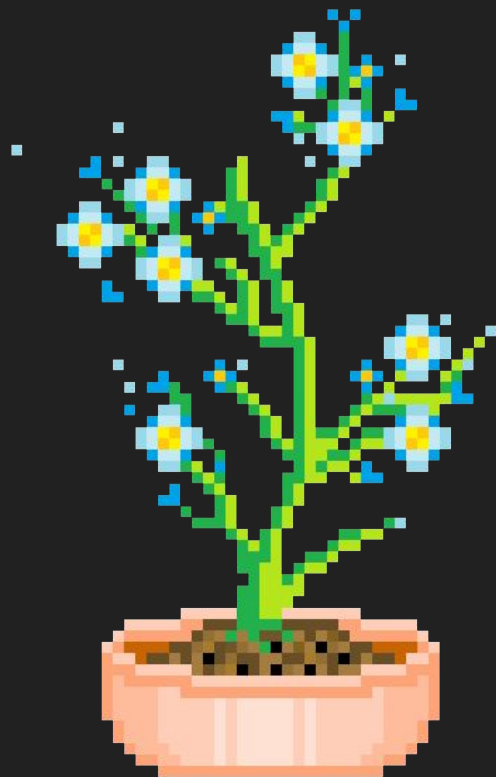
The exact day the French Revolution starts in 1789?

If (and when) life will emerge?

How it will evolve over the next few years?

(More specific) Questions I study

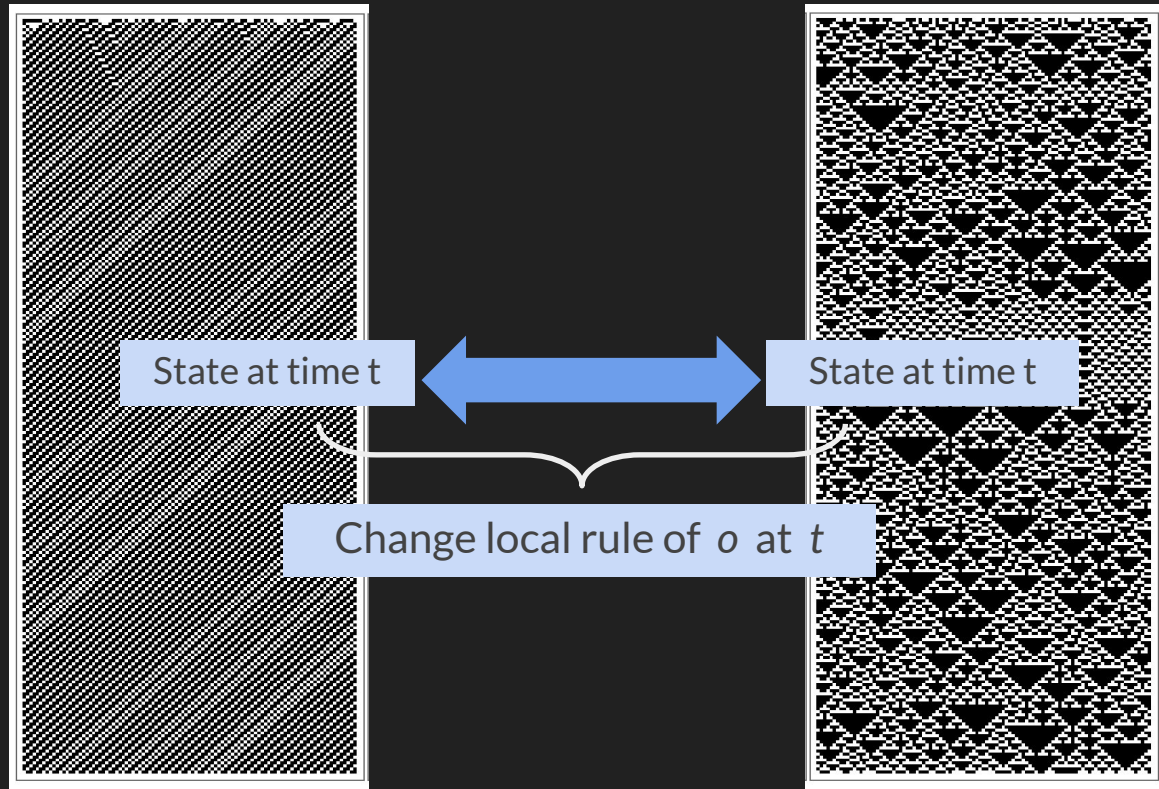
- How does biology create new state spaces?
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- *How do state spaces interact with each other?*
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System u

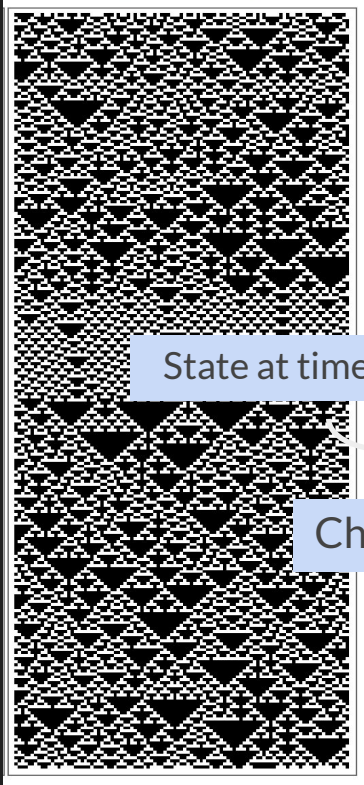
“Environment” e

“Organism” o

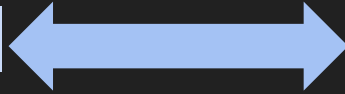


System u

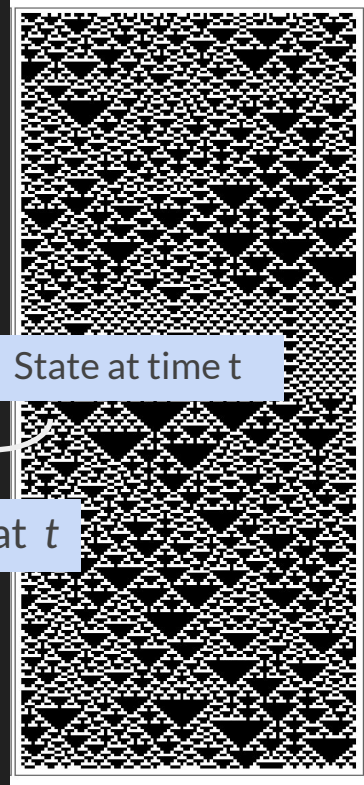
“Organism” o



State at time t



“Organism” o



State at time t

Change local rule of *both* at t

System u

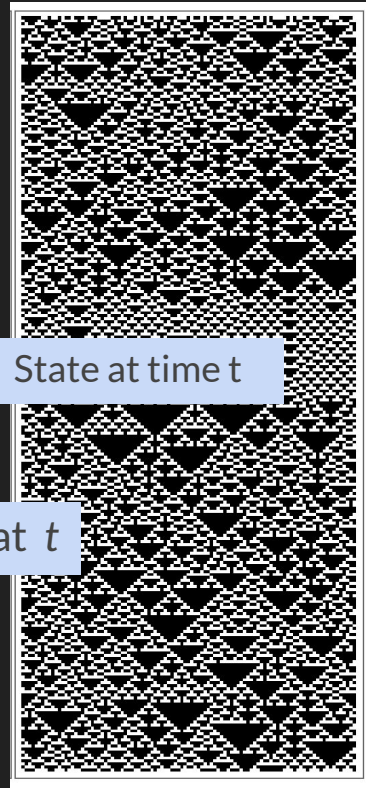
“Organism” o

“Organism” o

State at time t

State at time t

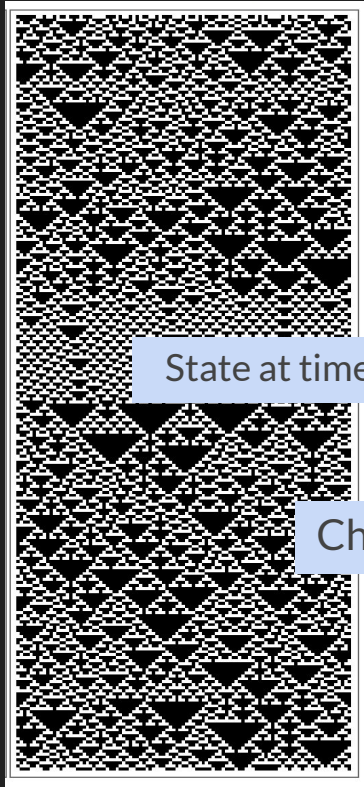
Change local rule of *both* at t



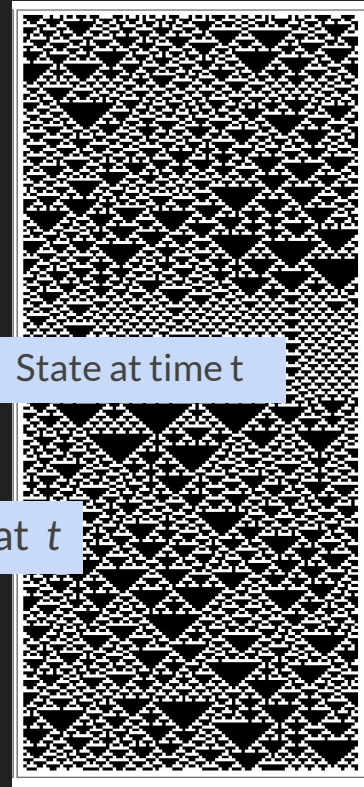
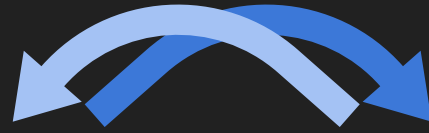
System u

“Organism” o

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State at time t

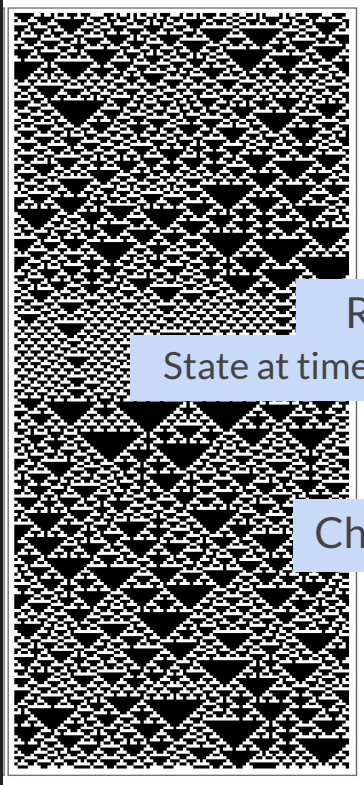


State at time t

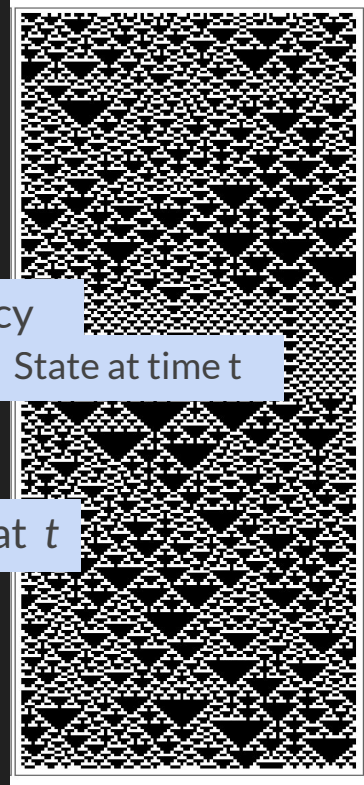
Change local rule of *both* at t

System u

“Organism” o



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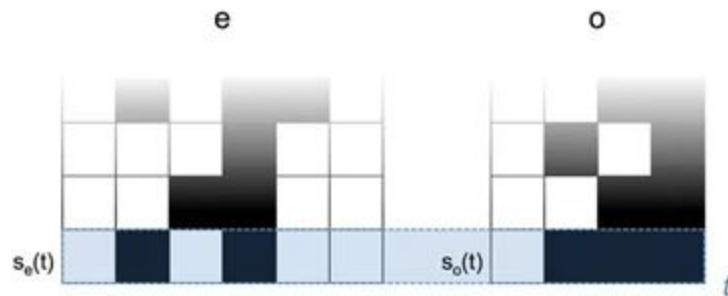
Random state dependency

State at time t

State at time t

Change local rule of *both* at t

(a)



(b)

triplet	frequency in $s_e(t)$	frequency in $s_o(t)$
111	-	1/4
110	-	1/4
101	1/6	1/4
100	1/6	-
011	-	1/4
010	2/6	-
001	1/6	-
000	1/6	-

(c)

$$0 \cdot 2^7 + 0 \cdot 2^6 + 0 \cdot 2^5 + 1 \cdot 2^4 + 1 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 30$$

$$0 \cdot 2^7 + 0 \cdot 2^6 + 1 \cdot 2^5 + 1 \cdot 2^4 + 1 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 62$$

(a)

(b)

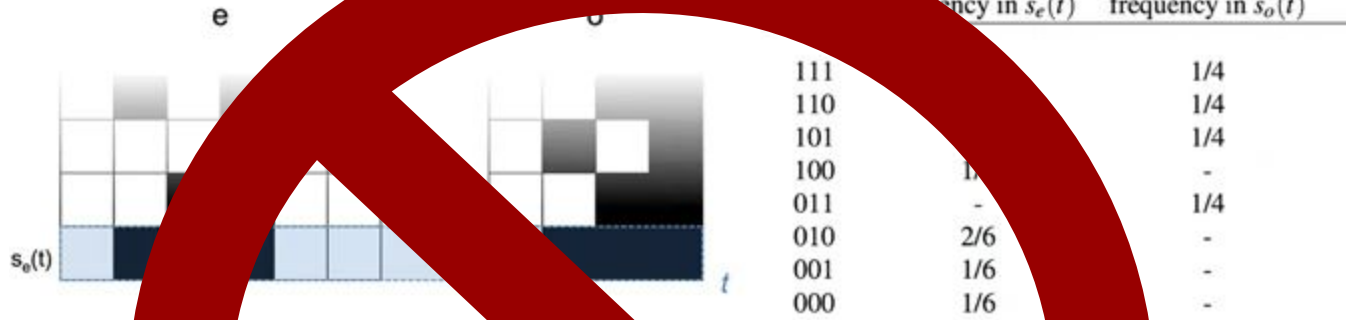


Figure (c) shows a sequence of binary strings and their corresponding decimal values:

1111111, 111111, 11111, 1111, 111, 11, 1, 0

These strings are represented by a sequence of black and white squares. Below the squares, the corresponding decimal values are listed:

$2^7 + 0 \cdot 2^6 + 0 \cdot 2^5 + 1 \cdot 2^4 + 1 \cdot 2^3 + 1 \cdot 2^2 + 1 \cdot 2^1 + 0 \cdot 2^0 = 62$

Generate random, static mappings

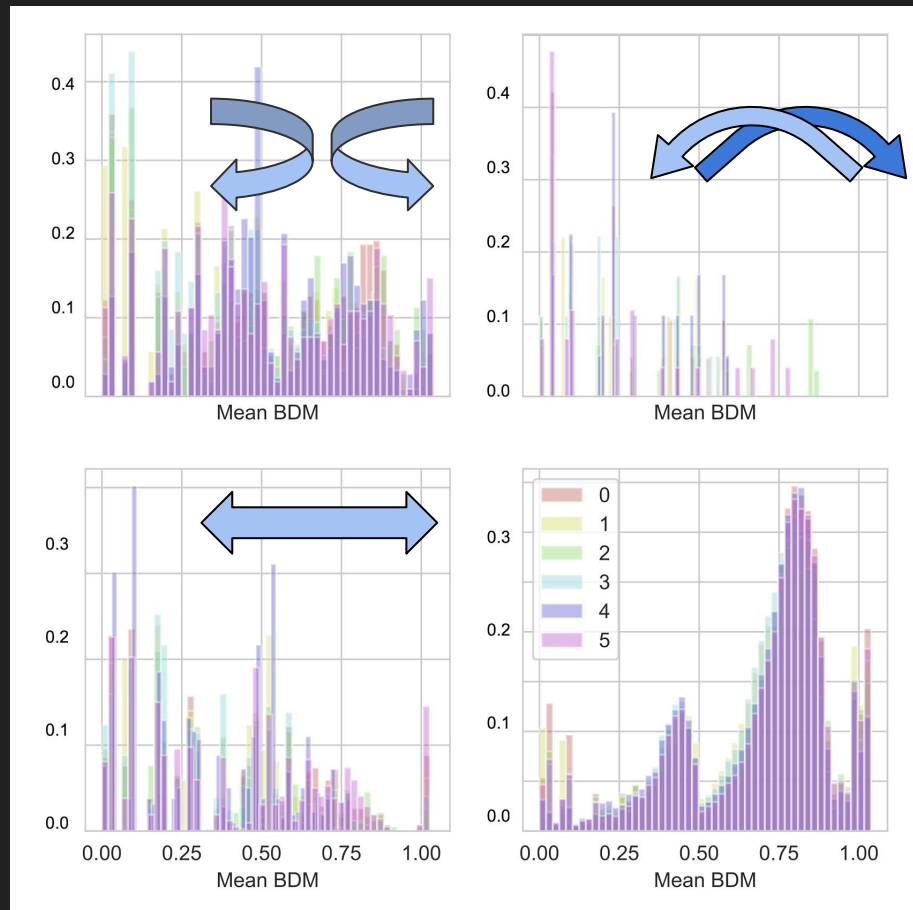
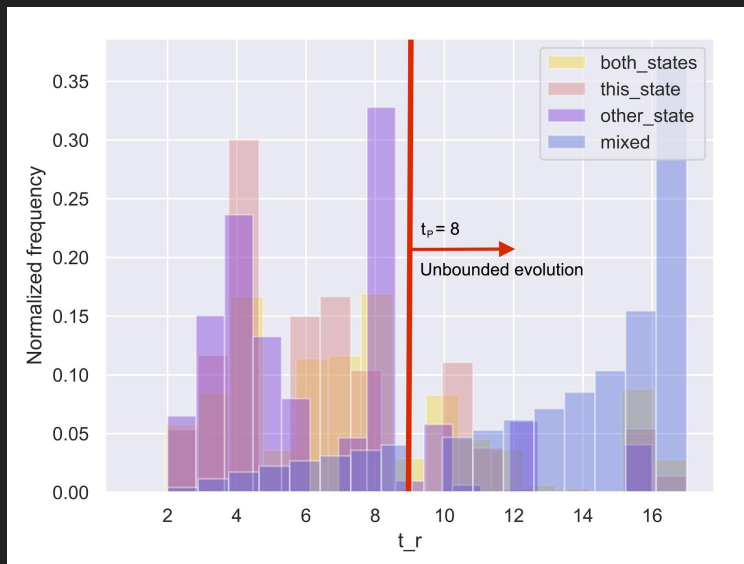
Do more complex state-rule mappings lead to:

- Complex state-space trajectories?
- Open-ended evolution? (Innovation + Unbound Evolution)

Methods:

- Generated 5000 random mappings between states and rules
- Turn into a graph → Adjacency matrix
- Measure the BDM for each
 - Generated randomly, so inherently going to have about the same value
- Pick the mappings with the highest and lowest BDM values

$w=3$ CA only!



Generate random, static mappings

Do more complex state-rule mappings lead to:

- Complex state-space trajectories? No!
- Open-ended evolution? (Innovation + Unbound Evolution) No!

But:

- Randomly changing the mapping type between rules and states (rule is determined by a random choice between its own state, the state of the other CA, or both CA together) = More % OEE cases, complex states, and complex rule trajectories

Follow-up Questions

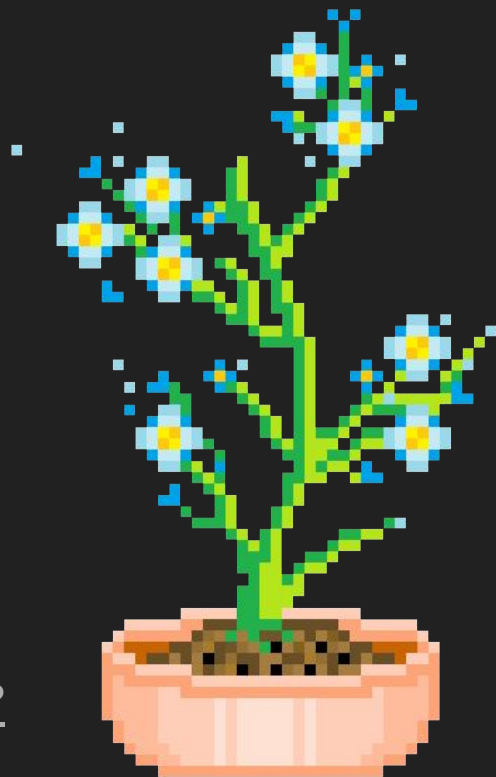
Same experiment, but with:

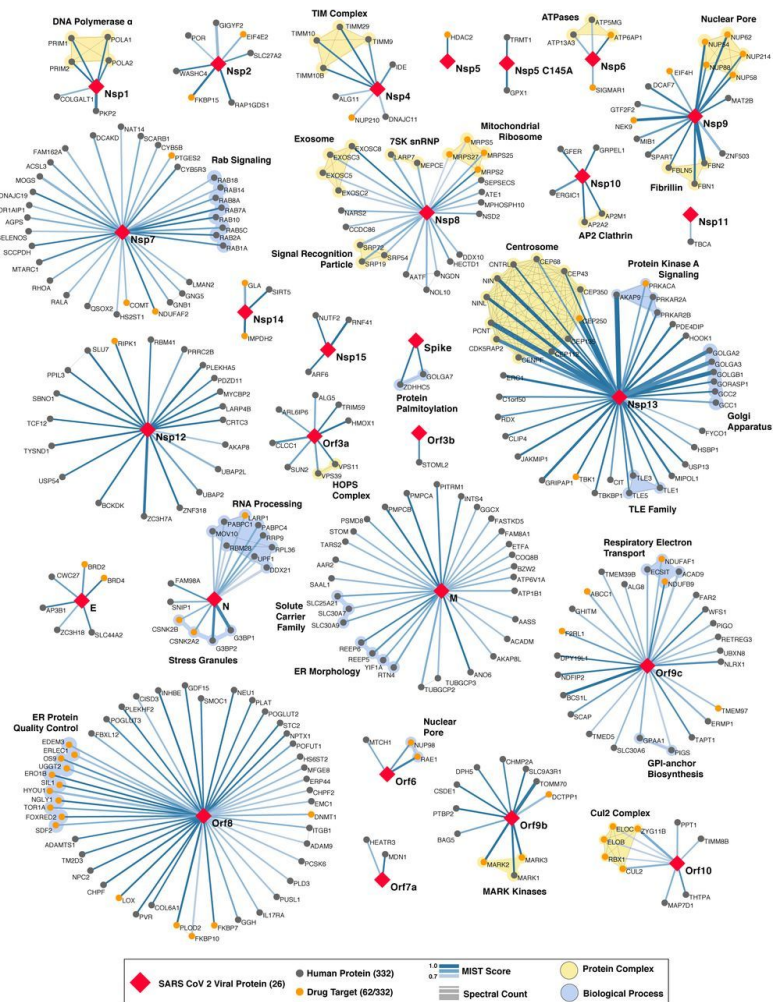
- Better range of mappings between states and rules
 - Mappings with more diverse BDM values
 - One to many, one to one, many to one, ergodic
- Bigger CA ($w > 3$)
- CA of different sizes
- $N > 2$ interacting CA system

Preprint: Alyssa M Adams, The Effects of Complex Interaction Rules Between Two Interacting Cellular Automata, ArXiv Submission 2020

(More specific) Questions I study

- How does biology create new state spaces?
 - (What are the mechanisms of strong emergence?)
- How does biology discover new states?
 - (What are the mechanisms of weak emergence?)
- How do state spaces interact with each other?
- What gives a state more predictive power than other states, according to an observer?
- Does this have a relationship with complexity?
- How can we use real biological data to inform models?





A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing, D. Gordon et al 2020, Preprint

BDM of nCov-19/Host PPIs

Data:

- Interactions from paper's supplementary material: Table 2
- Emailed authors for nCov-19 protein sequences
- Human protein sequences from UniProt

BDM measures:

- BDM of the entire protein sequence
- Sliding window along sequence
 - BDM density
 - Second and third order BDM values

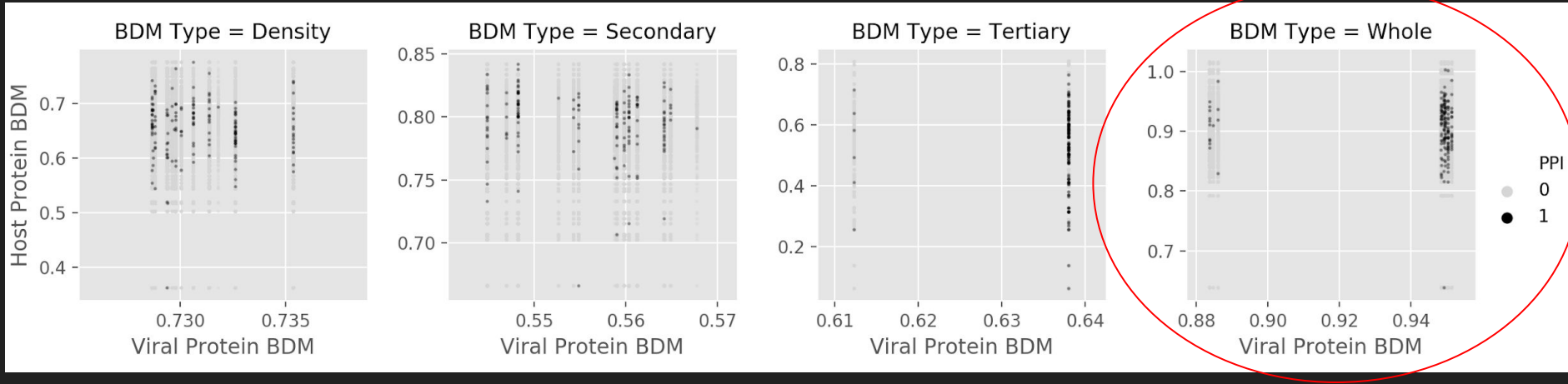
BDM as an approximation to Algorithmic Complexity:
Zenil, H.; Hernández-Orozco, S.; Kiani, N.A.; Soler-Toscano, F.; Rueda-Toicen, A.; Tegnér, J. *A Decomposition Method for Global Evaluation of Shannon Entropy and Local Estimations of Algorithmic Complexity*. Entropy 2018, 20, 605.

With these measures of BDM...

1. Do COVID-19 proteins interact with human proteins with similar BDM values?
2. Do viral proteins with the same function have the same BDM values?

BDM as an approximation to Algorithmic Complexity:
Zenil, H.; Hernández-Orozco, S.; Kiani, N.A.; Soler-Toscano, F.; Rueda-Toicen, A.; Tegnér, J. *A Decomposition Method for Global Evaluation of Shannon Entropy and Local Estimations of Algorithmic Complexity*. Entropy 2018, 20, 605.

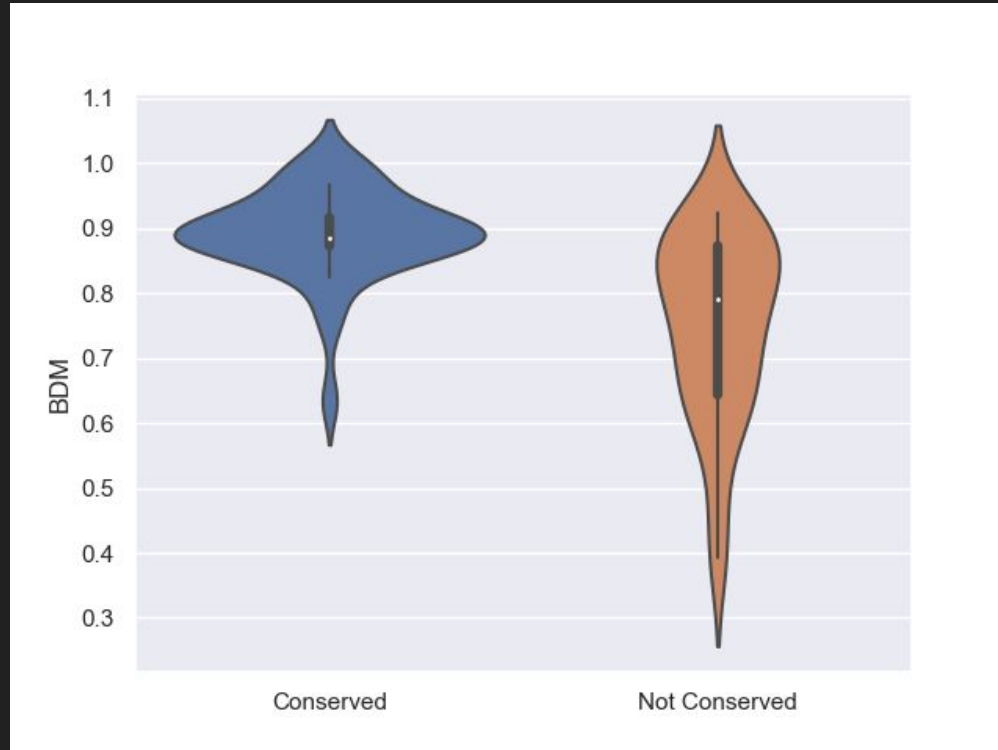
Are the BDM values the same for proteins that interact? ... Results!



Highly complex proteins are *very likely* to interact with humans over proteins of lower complexity!

BDM and regions of mutations?

Preliminary results for bacteriophage T7 tail protein with mutations



What we know so far

- Regions of mutations within the T7 virus have *lower* complexity values
 - True for every virus? Covid-19?
 - Only the most complex proteins in Covid-19 interact with human proteins
 - True for viruses in general?
-
- Currently looking at all experimentally confirmed PPIs between viruses and hosts.
 - The adventure continues...

Thank you & Acknowledgements!

- Anantharaman Lab

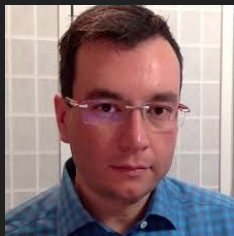
- Karthik Anantharaman
- Kristopher Kieft



- CIBM Program and NIH NLM

- Algorithmic Nature Lab

- Hector Zenil



- UCSF & QBI COVID-19 Research Group

- David Gordon
- Nevan Krogan

Special Thanks



Sara Walker



Hector Zenil

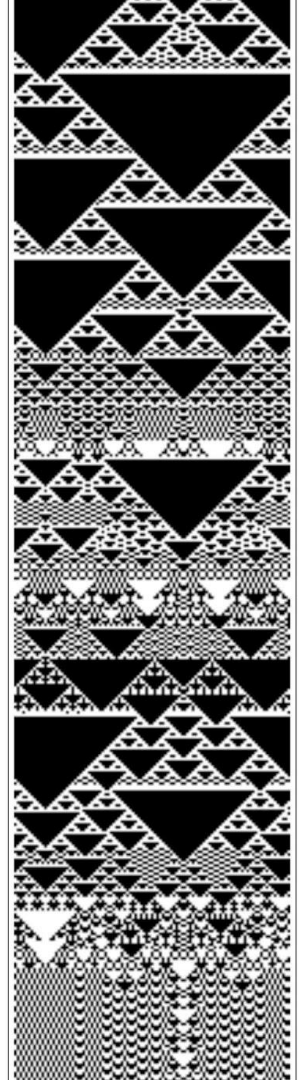
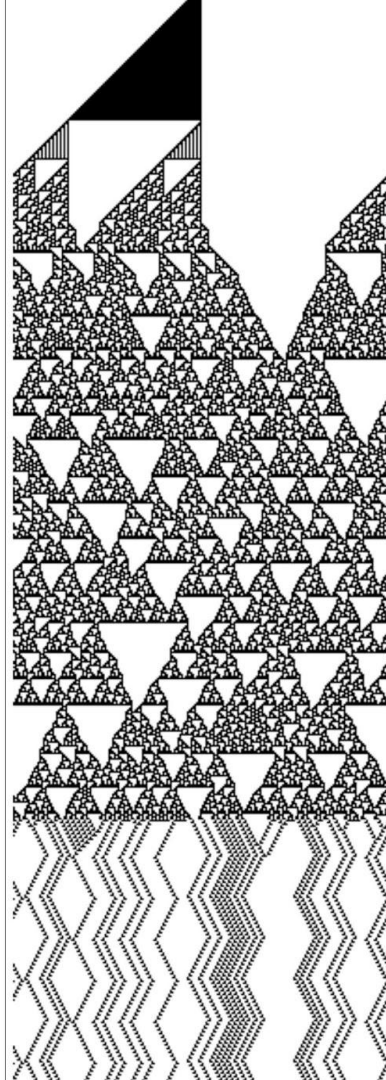
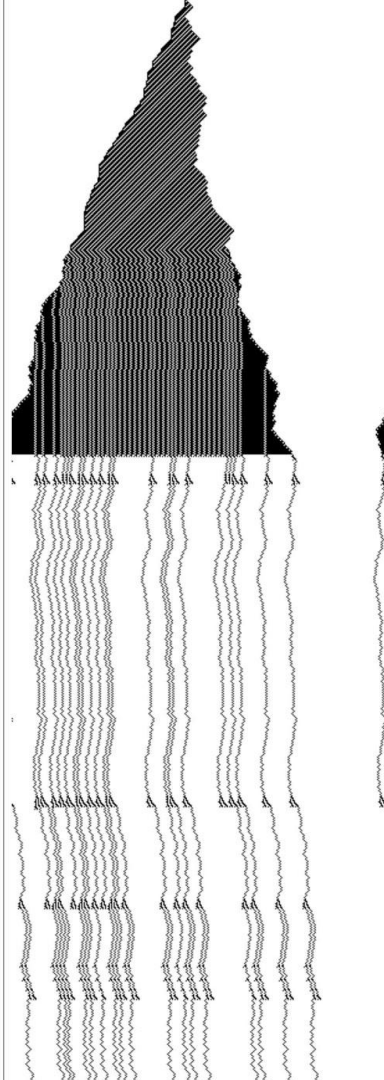
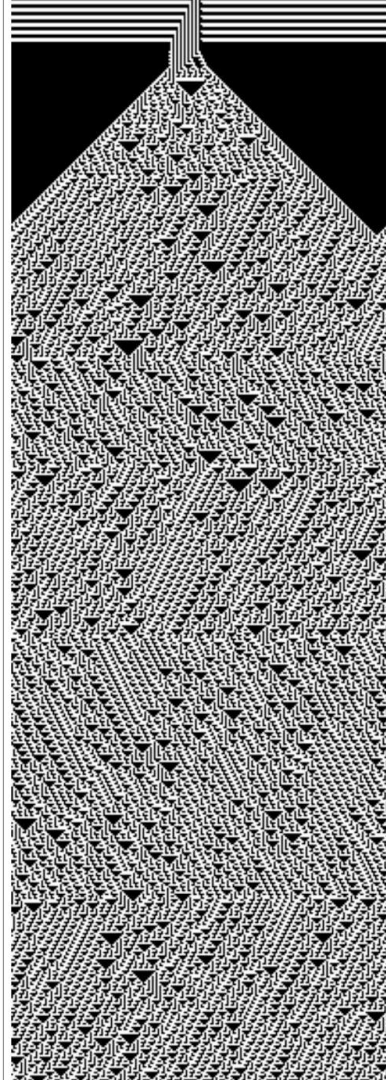
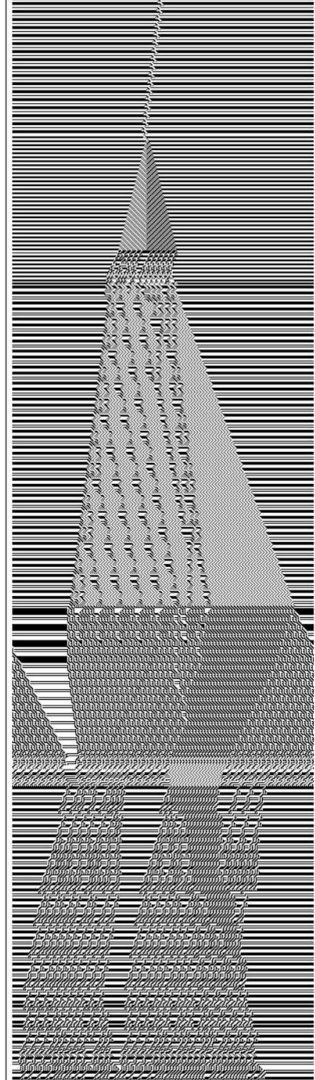


Paul Davies



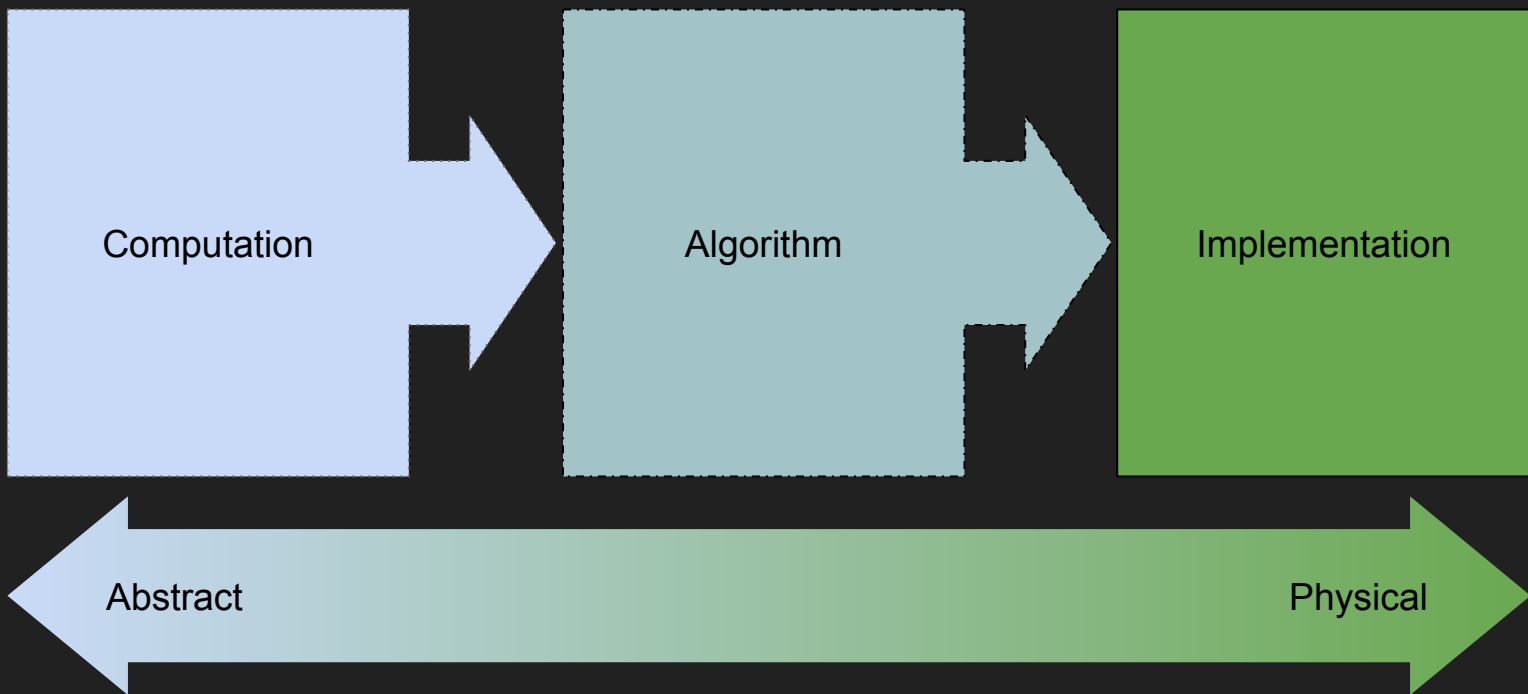
Angelica Berner

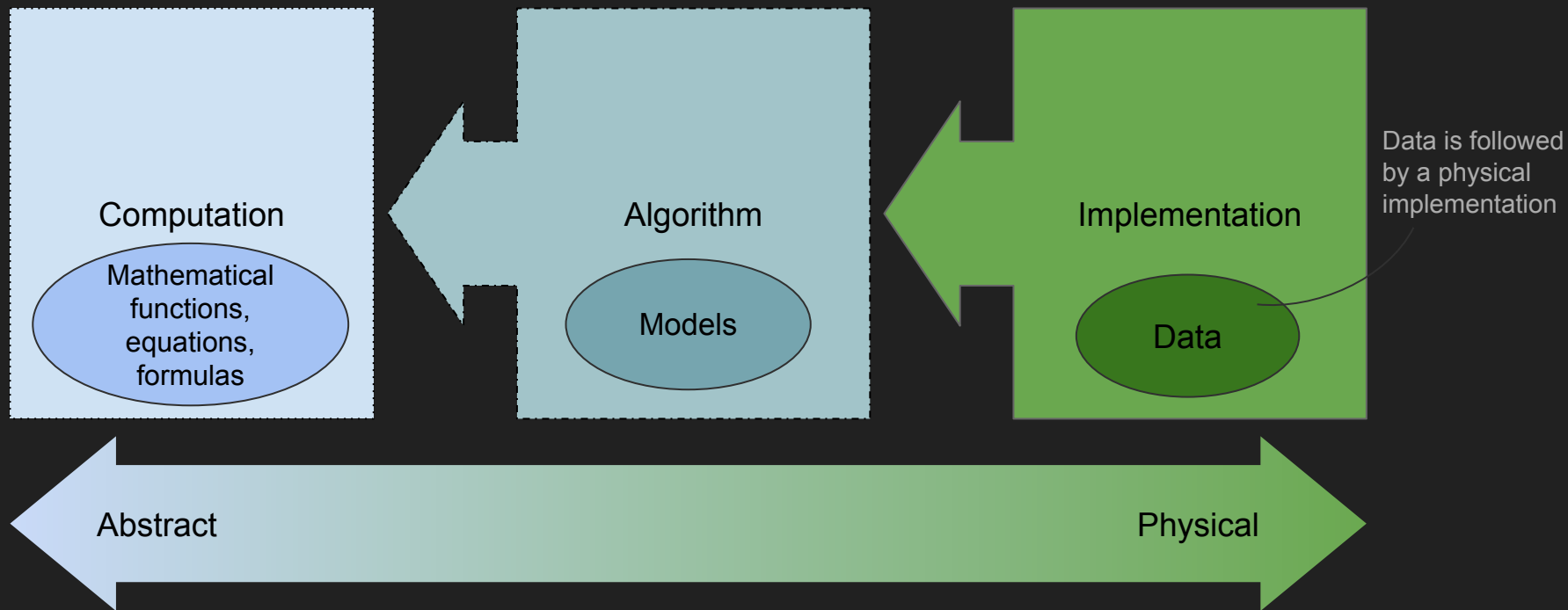




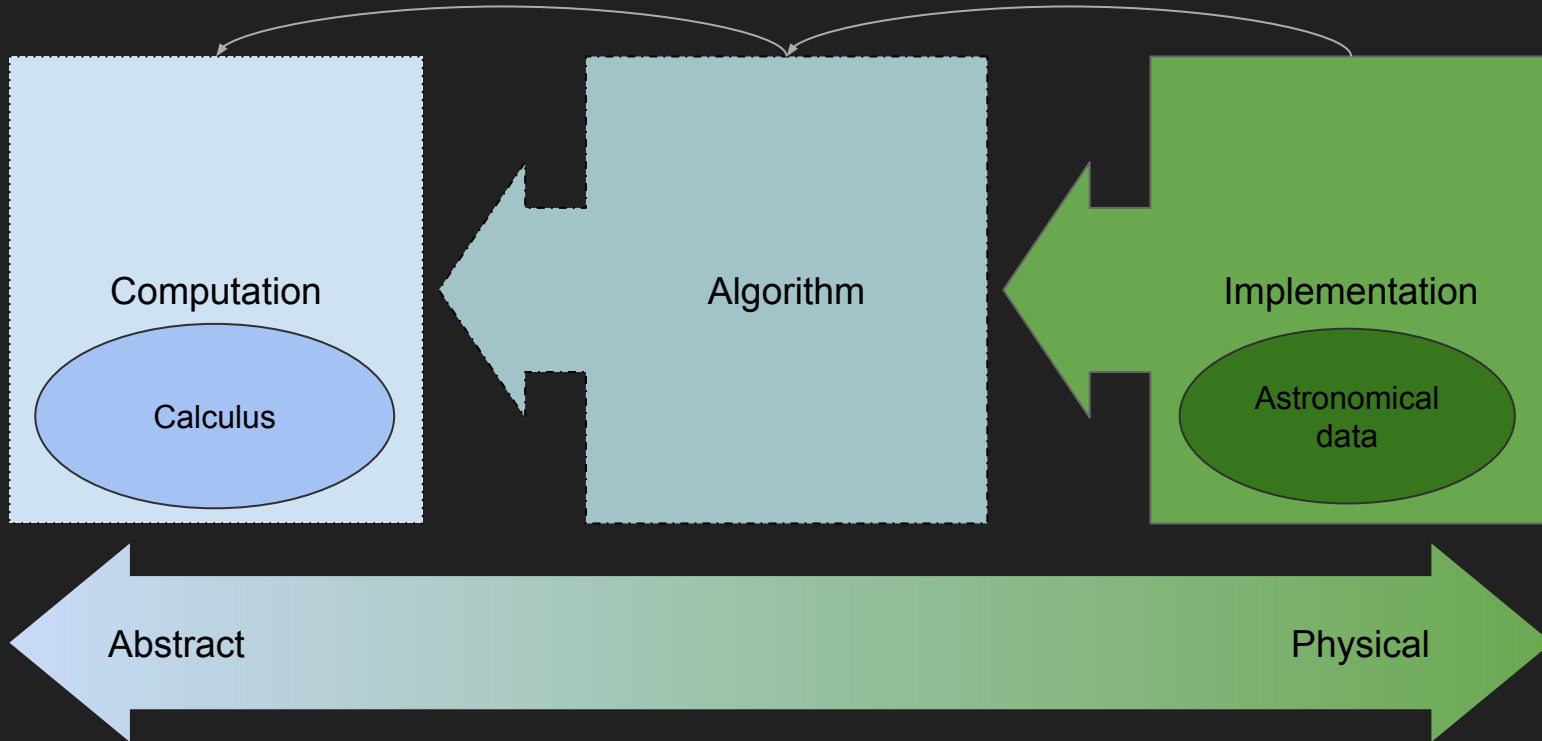
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Both calculus and quantum mechanics
are successful paths along this direction



Going backwards...

What are the mechanisms that result in *this*?

...ttggctttgtgtgctgactctatcattattggtggagctaaacttaaagccttgaatttaggtgaaacatttgtcacgc
actcaaagggattgtacagaaagtgtgttaaataccagagaagaaactggcctactcatgcctctaaaagcccaaaa
gaaattatcttcttagagggagaaacacttcccacagaagtggttaacagaggaagttgtcttgaaaactggtgattta
caaccattagaacaacactactagtgaagctgttgaagctccattgggttggtacaccagtttgtattaacgggcttatgt
tgctcgaaatcaaagacacagaaaagtactgtgcccttgcacctaataatgatggtaacaaacaataccttcacactca
aaggcgggtgcaccaacaaagggttacttttgggtgatgacactgtgatagaagtgcaagggtacaagagtgatgaatc
acttttgaacttgatgaaaggattgataaagtacttaatagagaagtgctctgcctatacagttgaactcggtacagaa
gtaaatgagttcgcctgtgttggtggcagatgctgtcataaaaactttgcaaccagtatctgaattacttacaccactgg
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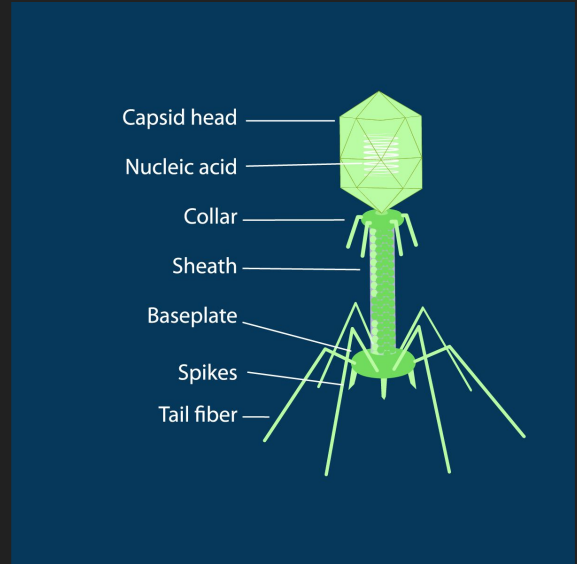
Can everything be approximated to a Turing Machine?

Is evolution computable?

Is life computable?

Are gene sequences computable?

Are the interactions between viruses and hosts computable?




Trivial solution

```
print('insert_all_of_biology_here')
```

```
Insert_all_of_biology_here
```


Trivial solution

```
print('insert_all_of_biology_here')
```



The program is longer than the actual sequence!


```
Insert_all_of_biology_here
```



This is already a very long sequence!

Trivial solution

```
print('insert_all_of_biology_here')
```




The program is longer than the actual sequence!

Being TRULY random means that the ONLY program that generates X is LONGER (or as long) than x itself.

There's no way to “compress” the sequence.

How do we check which TM made the sequence?

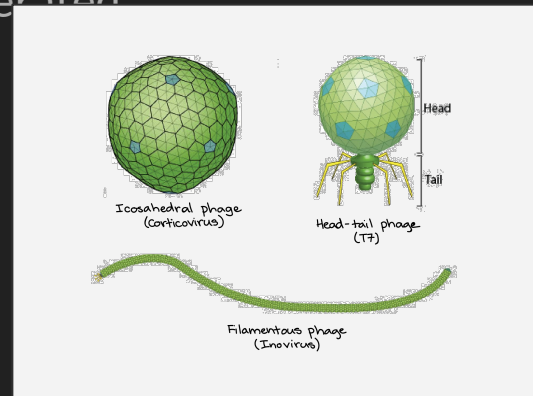
```
Insert_all_of_biology_here
```

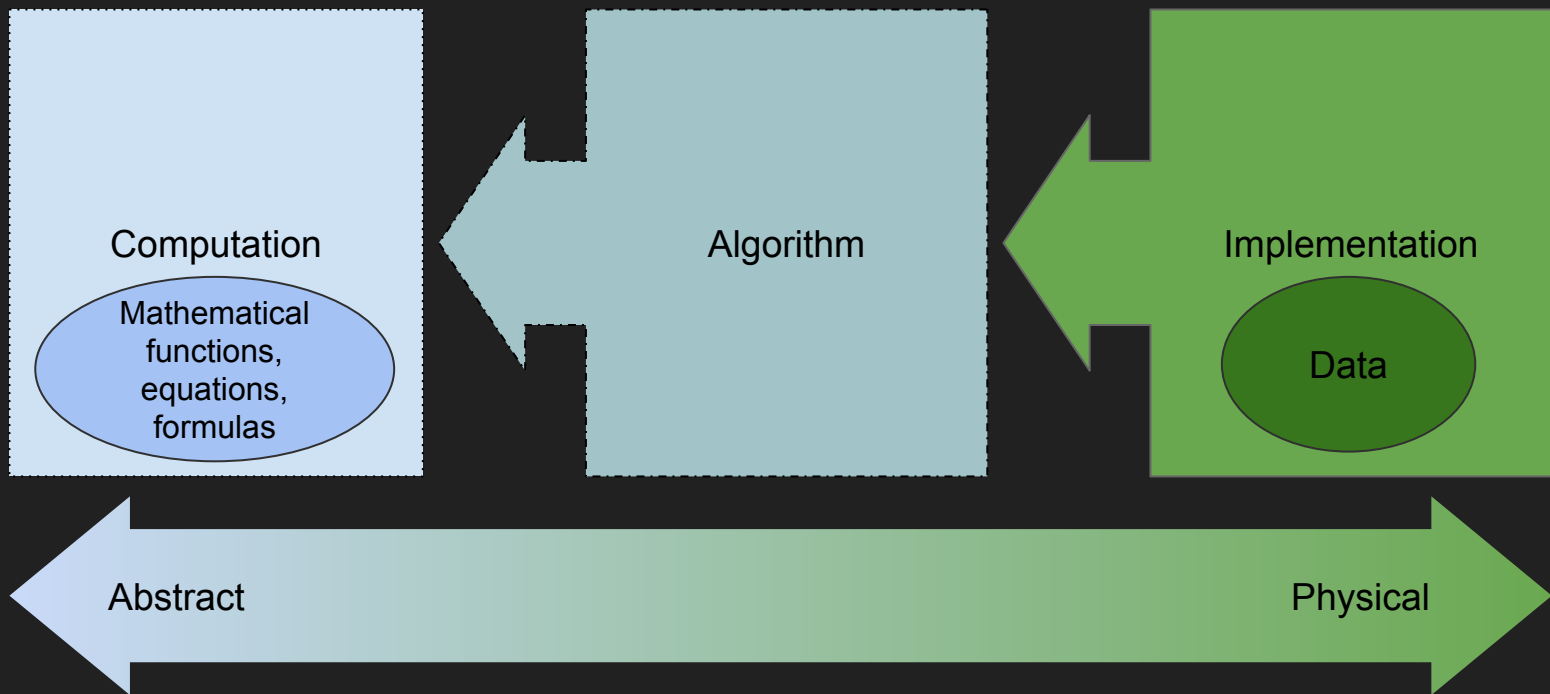


This is already a very long sequence!

Back to biology

- The same object can be represented by *several different strings*.
 - Networks, for example
- Algorithmic complexity provides a measure for complexity *regardless* of how that object is represented as a string.
- Strings generated by short TMs are more likely to be generated by chance and are NOT very complex.
- Strings with high AND similar values of BDM are likely generated by similar mechanisms.
- Genetic sequences!





League of Legends is a system of
{Game Developers + Players} that
produces open-ended **strategy** selection

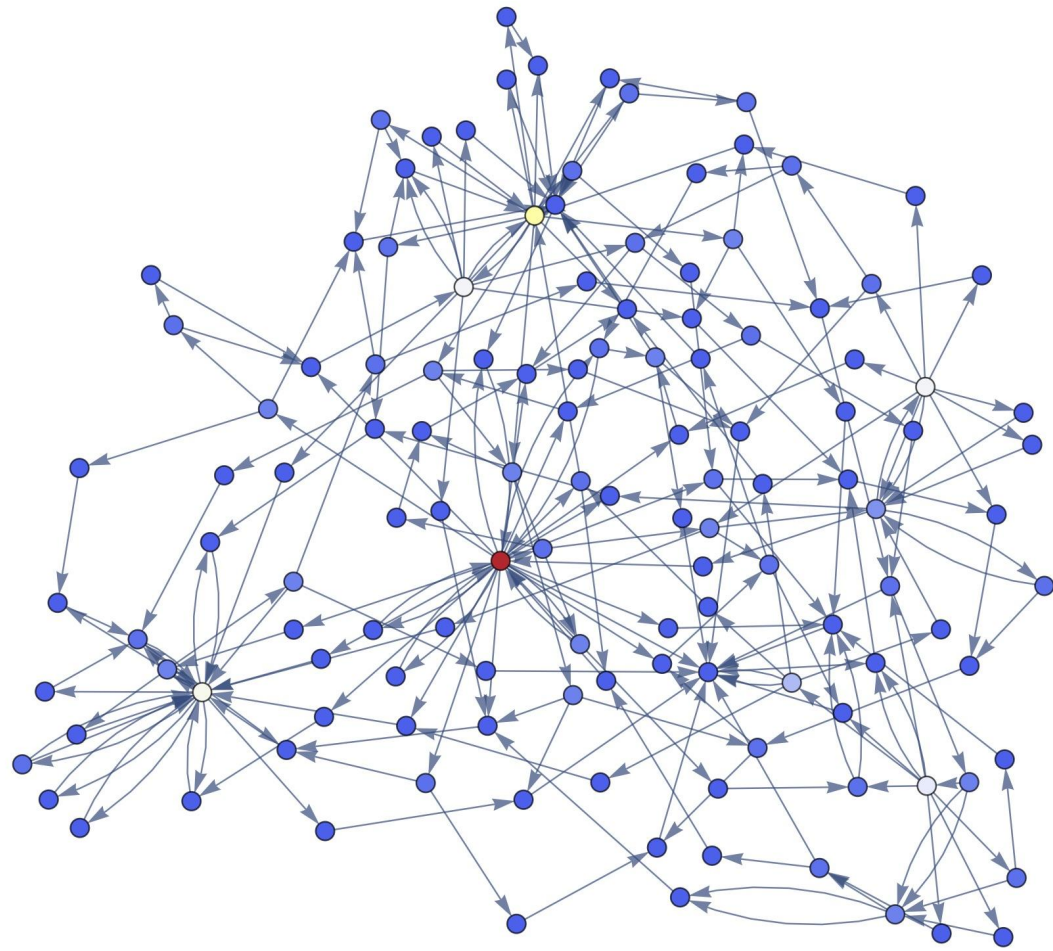
A character named Teemo, a small green frog-like creature with a yellow flame on its head and a red visor, is positioned in the upper right. It is holding a wooden staff and has just cast a spell, indicated by a small cloud of white smoke and a trail of golden sparks leading towards the bottom left. The background is a graveyard with tombstones and flowers.

Teemo

Beat

A character named Tristana, a small girl with black hair and a red headscarf, is positioned in the lower left. She is holding a large black cannon. Three purple spheres are floating above her head. The background is the same graveyard as the top image.

Tristana





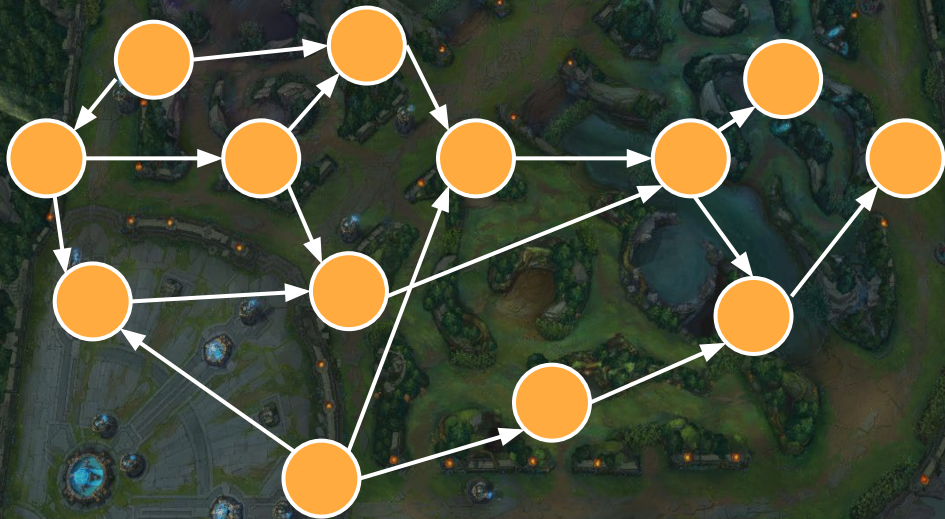
Players explore the available strategy space, with the goal of winning matches.

Player Strategy Space Evolves Open-Endedly

"To keep the game fun", Riot will weaken overwhelmingly successful strategies and strengthen very weak strategies.

Riot changes the game rules. This changes the strategy space that players can explore

Game Developers



League of Legends Players
~80 Million



Players discuss strategies and share information online.

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Player Strategy Space Evolves Open-Endedly

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