Mini Great Ideas in **Comp Bio**

Source: https://thehealthcaretechnologyreport.com/microsoftillumina-and-twist-bioscience-lead-the-way-in-dna-data-storage/

Part 1: DNA Computing

What is DNA Computing?

DNA Computing: Using DNA as hardware of computer due to its molecular-scale storage capabilities.



Barriers to DNA Computing

DNA Computing: Using DNA as hardware of computer due to its molecular-scale storage capabilities.

STOP: What practical barriers do you see for using DNA as a system of storage?

Barriers to DNA Computing

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STOP: What practical barriers do you see for using DNA as a system of storage?

Answer: Reading DNA is expensive, and (until recently) editing DNA has been impossible.

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However, there are some things that aren't hard:Synthesizing a strand (**oligonucleotide**) of DNA.

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- Forcing a DNA strand to base pair given free nucleotides and DNA polymerase.

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However, there are some things that aren't hard:

- Synthesizing a strand (**oligonucleotide**) of DNA.
- Forcing a DNA strand to base pair given free nucleotides and DNA polymerase.
- Filtering all fragments of DNA in a sample of some (approximate) length.

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However, there are some things that aren't hard:

- Synthesizing a strand (**oligonucleotide**) of DNA.
- Forcing a DNA strand to base pair given free nucleotides and DNA polymerase.
- Filtering all fragments of DNA in a sample of some (approximate) length.
- Amplifying a strand of DNA with given start/end into many copies (PCR, Nobel Prize in 1993).

Recall: Easy and Difficult Problems

Hamiltonian Cycle Problem

NP-Complete

Input: a directed network with *n* nodes. **Output:** "Yes" if there is a cycle visiting every *node* in the network; "No" otherwise.

Eulerian Cycle Problem

Polynomial

Input: a directed network with *n* nodes.Output: "Yes" if there is a cycle visiting everyedge in the network; "No" otherwise.

Recall: Easy and Difficult Problems

Hamiltonian Cycle Problem

NP-Complete

Input: a directed network with *n* nodes. **Output:** "Yes" if there is a cycle visiting every *node* in the network; "No" otherwise.

In particular, all *NP*-Complete problems are equivalent; if we solve the Hamiltonian Cycle Problem, then we solve them all.

Programming a DNA computer to solve the Hamiltonian cycle problem

Molecular computation of solutions to combinatorial problems

LM Adleman - Science, 1994 - science.sciencemag.org

The tools of molecular biology were used to solve an instance of the directed Hamiltonian path problem. A small graph was encoded in molecules of DNA, and the" operations" of the computation were performed with standard protocols and enzymes. This experiment demonstrates the feasibility of carrying out computations at the molecular level.

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Key insight: Rather than trying to use DNA as storage, why not use it to *solve* difficult problems?

Note: Adleman is also famous for public key cryptography (he is the "A" in "RSA" cryptosystem).

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Key insight: Rather than trying to use DNA as storage, why not use it to *solve* difficult problems?

The difficulty here is that it's not clear at all what it means to "program" a DNA computer.

Algorithm for Determining if there is Hamiltonian Path in Graph *G* Connecting v₁ to v_n 1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is captured.

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- 2. Keep only those paths that begin with v_1 and end with v_n .

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- 2. Keep only those paths that begin with v_1 and end with v_n .
- 3. Keep only those paths that have *n* nodes.
- 4. Keep only those paths that enter all the nodes of the graph at least once.
- 5. If any paths remain, return "Yes"; otherwise, return "No".

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is present.



Adleman's original G

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is present.

Associate every node *i* of *G* with a DNA *k*-mer denoted O_i . Call its complement O'_i .



 O_i TGACGC O'_i ACTGCG

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is present.

Associate every edge (*i*, *j*) with a DNA *k*-mer $E_{i,j}$ consisting of last k/2 symbols of O_i followed by first k/2 symbols of O_j . (Preserves edge orientation.)



1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is present.

Note: If i = 1, use all k symbols of O_1 . If j = n, use all k symbols of O_n .



1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is present.

Key Point: recall that generating oligonucleotides is cheap and easy.

1. Generate many "random paths" through G to ensure that any Hamiltonian path is present.

Produce many oligonucleotides:

- copies of $E_{i,j}$ for every edge (i, j)copies of O'_i for every node other than v_1 and v_n .

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is present.

Produce many oligonucleotides:

- copies of $E_{i,j}$ for every edge (i, j)
- copies of O'_i for every node other than v_1 and v_n .

STOP: What will happen when we combine all these DNA oligonucleotides in the lab?

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is present.

Produce many oligonucleotides:

- copies of $E_{i,j}$ for every edge (i, j)
- copies of O'_i for every node other than v_1 and v_n .

Answer: edge $E_{i,j}$ will hybridize to O'_i and O'_j. Adjacent edges will therefore join into a path.

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is captured.

Hypothetical path in G $1 \rightarrow 4 \rightarrow 2 \rightarrow 7$ O_1 CATTAT $E_{1,4}$ O_2 CGTCCA CATTATAAG CATTATAAG O_4 AAGACT O_7 CTTTAG

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is captured.

Hypothetical path in G 4 →(2) САТТАТ O_1 O_2 CGTCCA $E_{4.2}$ $E_{1.4}$ CATTATAAGACTCGT O_4 AAGACT TTCTGA O'_{A} CTTTAG O_7

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Hypothetical path in G $\rightarrow (2) \rightarrow (7)$ 4 САТТАТ O_1 O_2 CGTCCA $E_{1,4}$ $E_{4,2}$ E_{2.7} CATTATAAGACTCGTCCACTTTAG O_4 AAGACT TTCTGAGCAGGT $O'_{4} O'_{2}$ CTTTAG \mathbf{O}_{7}

1. Generate many "random paths" through *G* to ensure that any Hamiltonian path is captured.

As a result, every path in the graph will be present as some double-stranded DNA molecule.

2. Keep only those paths that begin with v_1 and end with v_n .

Use PCR to amplify only those remaining fragments of DNA that begin with O_1 and end with O_n .

3. Keep only those paths that have *n* nodes.

Filter remaining DNA fragments by length, and throw out all fragments that don't have length approximately equal to n * k nucleotides.

4. Keep only those paths that enter all the nodes of the graph at least once.

Convert all DNA to single strands, and hybridize DNA against O'_i for some *i*. Filter out strands that don't bind. Repeat for all O'_i .

CATTATAAGAAGCGTCCACTTTAG

 O_1 CATTAT O_2 CGTCCA

GACCGT

 O_3

4. Keep only those paths that enter all the nodes of the graph at least once.

Convert all DNA to single strands, and hybridize DNA against O'_i for some *i*. Filter out strands that don't bind. Repeat for all O'_i .

CATTATAAGAAGCGTCCACTTTAG GTAATA O'₁

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CATTAT

CGTCCA

GACCGT

 O_1

 O_2

 O_3

4. Keep only those paths that enter all the nodes of the graph at least once.

Convert all DNA to single strands, and hybridize DNA against O'_i for some *i*. Filter out strands that don't bind. Repeat for all O'_i .

CATTATAAGAAGCGTCCACTTTAG O_1 CATTAT GCAGGT O_2 CGTCCA O'_2 O_3 GACCGT
Converting Each Step to Experiment

- 4. Keep only those paths that enter all the nodes of the graph at least once.
- Convert all DNA to single strands, and hybridize DNA against O'_i for some *i*. Filter out strands that don't bind. Repeat for all O'_i .
 - CATTATAAGAAGCGTCCACTTTAG
 - O'₃ = CTGGCA doesn't align!

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CATTAT

CGTCCA

GACCGT

 O_1

 O_2

 O_2

Converting Each Step to Experiment

5. If any paths remain, return "Yes"; otherwise, return "No".

If any DNA remains from our experiment, then we know that the answer must be "Yes"! Otherwise, it is "No".



We've Solved an NP-Complete Problem?!

STOP: What issues do you see with this approach?

We've Solved an *NP*-Complete Problem?!

STOP: What issues do you see with this approach?

Answer: Three immediate barriers:

- 1. Possibility of errors is high.
- We still need to generate, at a minimum, n! strands of DNA. So this is impossible for networks with, say, 100 nodes.
- 3. An enormous amount of lab work needs to be done, with hours of waiting times.

DNA is nevertheless promising as hard drive storage

DNA Fountain enables a robust and efficient storage architecture Y Erlich, D Zielinski - Science, 2017 - science.sciencemag.org

DNA is an attractive medium to store digital information. Here we report a storage strategy, called DNA Fountain, that is highly robust and approaches the information capacity per nucleotide. Using our approach, we stored a full computer operating system, movie, and …
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November 12, 2020 03:15 PM Eastern Standard Time

SOUTH SAN FRANCISCO, Calif.--(BUSINESS WIRE)--Twist Bioscience Corporation (NASDAQ: TWST), Illumina, Inc. (NASDAQ: ILMN) and Western Digital (NASDAQ: WDC) today announced the formation of an alliance with Microsoft to advance the field of DNA data storage. These founding companies, alongside member organizations, will work together to create a comprehensive industry roadmap that will help the industry achieve interoperability between solutions and help establish the foundations for a cost-effective commercial archival storage ecosystem for the explosive growth of digital data.

Part 2: Self-Replicating Cellular Automata

Can a Machine Replicate Itself?



Cornell University. Taken from https://www.youtube.com/watch?v=gZwTcLeelAY

Why Haven't We Seen Alien Spacecraft?

Fermi paradox: No evidence of alien life has been found in the galaxy despite its likelihood.



Why Haven't We Seen Alien Spacecraft?

von Neumann Probes: a theorized space probe that can use resources it finds to self-replicate.



Von Neumann's Question

What is the simplest possible self-replicating system?



John von Neumann

Von Neumann's Question

What is the simplest possible self-replicating system?

Learn some biology, John!

Stanislaw Ulam

John von Neumann

Cells are Self-Replicators •



Elon Musk 🤣 @elonmusk

We are the Von Neumann machines

4:22 PM · Jun 20, 2019 · Twitter for iPhone

1.6K Retweets 36.8K Likes

Source: https://singularityhub.com/2017/11/10/the-dream-of-regenerative-medicine-is-alive-and-well/

Psst ... There's a Simpler Self-Replicator



Cellular Automata

Cellular Automaton: A grid of (typically square) cells, along with a collection of simple rules that allow the cells to change from one "state" to another.

Cellular Automata

Cellular Automaton: A grid of (typically square) cells, along with a collection of simple rules that allow the cells to change from one "state" to another.

A lot of the cellular automata you could come up with are pretty boring, but then there is ...

The Game of Life: Rules



Neighborhood

A: If a cell is alive and has either two or three live neighbors, then it remains alive.

B: If a cell is alive and has zero or one live neighbors, then it dies out.
C: If a cell is alive and has four or more live neighbors, then it dies out.
D: If a cell is dead and has more than or fewer than three live neighbors, then it remains dead.

E: If a cell is dead and has exactly three live neighbors, then it becomes alive.

What's the Next Generation?



Dark = alive

A: If a cell is alive and has either two or three live neighbors, then it remains alive.

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What's the Next Generation?

D	D	D	D	D	D
D	В	E	E	D	D
D	D	С	С	А	D
D	А	С	С	D	D
D	D	E	E	В	D
D	D	D	D	D	D



Quick Quiz

Exercise: What is the next generation?

A: If a cell is alive and has either two or three live neighbors, then it remains alive.

B: If a cell is alive and has zero or one live neighbors, then it dies out.
C: If a cell is alive and has four or more live neighbors, then it dies out.
D: If a cell is dead and has more than or fewer than three live neighbors, then it remains dead.

E: If a cell is dead and has exactly three live neighbors, then it becomes alive.



Stable Forms



Quick Quiz

Exercise: Carry out the next few generations of this board. What happens?







































Getting More Complicated ...



In case you were curious ...

[Submitted on 5 Dec 2023]

Conway's Game of Life is Omniperiodic

Nico Brown, Carson Cheng, Tanner Jacobi, Maia Karpovich, Matthias Merzenich, David Raucci, Mitchell Riley

In the theory of cellular automata, an oscillator is a pattern that repeats itself after a fixed number of generations; that number is called its period. A cellular automaton is called omniperiodic if there exist oscillators of all periods. At the turn of the millennium, only twelve oscillator periods remained to be found in Conway's Game of Life. The search has finally ended, with the discovery of oscillators having the final two periods, 19 and 41, proving that Life is omniperiodic. Besides filling in the missing periods, we give a detailed history of the omniperiodicity problem and the strategies used to solve it, summarising the work of a large number of people in the decades since the creation of Life.

The Curious Case of the R-Pentomino



The Curious Case of the R-Pentomino



John Conway's Question

Is it possible for the number of live cells to grow without bound as time goes on?

Courtesy: Thane Plambeck

Bill Gosper's "Glider Gun"



Bill Gosper's "Glider Gun" Resembles a Factory with *Linear* Growth



Self-Replicating Automata: A History

John von Neumann



Year: 1952 Number of States: 29 Size of Self Replicator: 130,622 cells Year: 1968 Number of States: 8 Size of Self Replicator: 283,126,588 cells

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Edgar Codd



Chris Langton



Year: 1984 Number of States: 8 Size of Self Replicator: 86 cells
Langton Loops: A (Beautiful) Self-Replicating Cellular Automaton



Part 3: Spatial Games

Cooperation is Everywhere. But Why?

P.

Courtesy: milkwood.net

"Prisoner's Dilemma"

Prisoner's Dilemma: A simple two-player game with choices between "cooperation" and "defection" against an opponent.

Partner's decision

Cooperate Defect

Cooperate10Your
decisionDefectb > 10

"Prisoner's Dilemma"

Prisoner's Dilemma: A simple two-player game with choices between "cooperation" and "defection" against an opponent.

STOP: Why would you cooperate?

Partner's decision

Cooperate **Defect**

Cooperate10Your
decisionDefectb > 10

Axelrod's Tournament (1978): What if the game is played *multiple times*?

Group Exercise: Design a strategy.

- We are playing an (unknown) *m* number of games.
- Opponent's strategy is hidden.
- We play a variety of opponents but use same strategy.

Partner's decision

Cooperate Defect

1

3

Your decision Defect 7

Idea 0: "Poor-Trusting Fool"

for every integer *i* between 1 and *m* cooperate!

STOP: What are its strengths and weaknesses?

Idea 1: "All-Defect"

for every integer *i* between 1 and *m* defect!

STOP: What are its strengths and weaknesses?

Idea 2: "Grudger"



STOP: What are its strengths and weaknesses?

The Clear Winner: "Tit-for-Tat"

cooperate in game 1 **for** every integer *i* between 2 and *m* do whatever opponent did in game *i* – 1

This was the winning strategy (and the simplest!) among 15 submissions.

STOP: What properties of this strategy make it so good?



Anatol Rapoport

Words to Live By ...

More tournaments have shown that the highestscoring strategies tend to have four qualities:

- Niceness: Never be the first to defect.
- **Provocability:** Get mad quickly at defectors and retaliate.
- Forgiveness: Do not hold a grudge once you have vented your anger.
- **Clarity:** Act in ways that are straightforward for others to understand.

http://www2.econ.iastate.edu/classes/econ308/tesfatsion/axeltmts.pdf

Spatial Games: Every cell in a 2-D field plays a simplified Prisoner's Dilemma with each of its neighbors.



Your

Spatial Games: Every cell in a 2-D field plays a simplified Prisoner's Dilemma with each of its neighbors.

All use same strategy: in "generation" i, each cell adopts the strategy of its "bestscoring" Moore neighbor (including itself) in generation i - 1.



b > 1

0

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Your

Defect

STOP: What is the score of the central square on the right?





Your decision

STOP: What is the score of the central square on the right?

Answer: It is a cooperator, and its neighborhood has three cooperators, so its total score is 3.



Partner's
decisionCooperateDefect10Defectb > 10

Your decision

After computing the score of all neighbors, we ask "Do any neighbors have higher score?"

- If "no", the cell remains a cooperator in the next generation.
- If "yes", the cell adopts the • strategy of its highestscoring neighbor (it may be cooperation or defection) in the next generation.



b > 1

0

Your

Defect

Idea: Let's animate the spatial game board over the generations.

- Cells choosing to cooperate with their neighbors
 = blue
- Cells choosing to defect = red

Idea: Let's animate the spatial game board over the generations.

- Cells choosing to cooperate with their neighbors
 = blue
- Cells choosing to defect = red

Let's put one defector in the middle of our board. I wonder what we will see?

Idea: Let's animate the spatial game board over the generations.

- Cells choosing to cooperate with their neighbors
 = blue
- Cells choosing to defect = red

Let's put one defector in the middle of our board. I wonder what we will see?

Note: Our early reasoning would imply that the defectors would take over completely...

Spatial Games with b = 1.65



Citation presented without comment

www.nature.com > letters

Evolutionary games and spatial chaos | Nature

by MA Nowak - 1992 - Cited by 3747 - Related articles

Oct 29, 1992 - Evolutionary games and spatial chaos. Martin A. Nowak &; Robert M. May. Nature ...

Nowak, a Harvard mathematical biologist, seems to have been Epstein's favorite scientist, regularly mentioned in <u>press releases</u> issued by his foundations. The financier <u>donated</u> \$6.5 million to launch Nowak's Program for Evolutionary Dynamics at Harvard in 2003 — although Epstein <u>claimed</u>, apparently <u>falsely</u>, to have given \$30 million.

https://www.buzzfeednews.com/article/peteraldhous/jeffrey-epstein-science-donations-apologies-statements

Part 4: Tripping with Turing

Why Do Animals Have Stripes (or Spots)?









https://en.wikipedia.org/wiki/Leopard#/media/File:Nagarhole_Kabini_Karnataka_India,_Leopard_September_2013.jpg

Alan Turing has the answer!

Turing patterns: stripe/spot patterns that occur due to specific reactions and diffusion.

Well, the stripes are easy. But what about the horse part?

The chemical basis of morphogenesis

AM Turing - Bulletin of mathematical biology, 1990 - Springer

It is suggested that a system of chemical substances, called morphogens, reacting together and diffusing through a tissue, is adequate to account for the main phenomena of morphogenesis. Such a system, although it may originally be quite homogeneous, may later develop a pattern or structure due to an instability of the homogeneous equilibrium, which is triggered off by random disturbances. Such reaction-diffusion systems are considered in some detail in the case of an isolated ring of cells, a mathematically convenient, though ...

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We've already seen reaction-diffusion...





"Prey" molecules enter the system at a constant **feed rate** *f*.

"Predator" molecules are removed at a constant kill rate k.



"Prey" molecules enter the system at a constant **feed rate** *f*.

"Predator" molecules are removed at a constant kill rate k.

The predators can "eat" the prey and reproduce via 2 *Predator* + *Prey* \rightarrow 3 *Predator*



The predators can "eat" the prey and reproduce via 2 Predator + Prey \rightarrow 3 Predator



But the prey are "faster swimmers", having a diffusion rate that is twice as fast.



If the kill rate is too high, then the predators die out more quickly than they can eat the prey, and so only prey will survive.

f = 1,000 and *k* = 500,000



On the other hand, if *f* is too high, then the prey will increase, feeding the predators, and we will see an explosion in the number of predators.

f = 1,000,000 and k = 100,000



Finding a sweet spot set of parameters produces waves of predator "stripes" expanding outward against a background of prey.

f = 100,000 and k = 200,000



Holding *k* fixed and increasing *f* by a little increases the likelihood of predatorprey interactions, producing even more predator stripes.

f = 140,000 and k = 200,000



Increasing *f* further produces a chaotic stripe pattern because there are so many pockets of predators that they constantly collide and mix.

f = 175,000 and k = 200,000



Increasing *f* further produces a chaotic stripe pattern because there are so many pockets of predators that they constantly collide and mix.

f = 175,000 and k = 200,000



Once *f* equals *k*, the stripes disappear. We might expect to see a uniform mix, but instead, we see a "mottling" of red and green clusters, or spots.

f = 200,000 and *k* = 200,000
Turing pattern systems have been identified in fish (but not zebras)!



These pufferfish are very similar genetically, and yet they display different patterns.



Unlike other *robust* biological systems, Turing patterns are *finetuned*.

An Automaton-Like Model of Reaction-Diffusion

Gray-Scott Model: a "discretized" simulation with improved runtime by partitioning space into blocks and assuming concentration of a given molecule in a block is uniform throughout the block.

Autocatalytic reactions in the isothermal, continuous stirred tank reactor: Oscillations and instabilities in the system A+ 2B \rightarrow 3B; B \rightarrow C P Gray, SK Scott - Chemical Engineering Science, 1984 - Elsevier The prototype, cubic autocatalytic reaction (A+ 2B \rightarrow 3B) forms the basis for the simplest homogeneous system to display "exotic" behaviour. Even under well-stirred, isothermal, open conditions (CSTR) we may find multistability, hysteresis, extinction, ignition and ... 29 Cited by 639 Related articles All 4 versions

An Automaton-Like Model of Reaction-Diffusion

Gray-Scott Model: a "discretized" simulation with improved runtime by partitioning space into blocks and assuming concentration of a given molecule in a block is uniform throughout the block.







Implementing Reactions as Cellular Operations

Parameters d_A and d_B indicate what fraction of a cell's two particle types to diffuse into neighbors.

0, 0	0, 0	0, 0	0, 0	0, 0	$d_A = 0.2$ $d_B = 0.1$	0, 0	0, 0	0, 0	0, 0	0, 0
0, 0	0, 0	0, 0	0, 0	0, 0		0, 0	.01, .005	.04,.02	.01, .005	0, 0
0, 0	0, 0	1,1	0, 0	0, 0		0, 0	.04,.02	.8, .9	.04,.02	0, 0
0, 0	0, 0	0, 0	0, 0	0, 0		0, 0	.01, .005	.04,.02	.01, .005	0, 0
0, 0	0, 0	0, 0	0, 0	0, 0		0, 0	0, 0	0, 0	0, 0	0, 0

Implementing Reactions as Cellular Operations

Parameters d_A and d_B indicate what fraction of a cell's two particle types to diffuse into neighbors.

Then, we apply reactions cell by cell. $[A]_{new} = [A] + f(1 - [A]) - [A][B]^{2}$ $[B]_{new} = [B] - k[B] + [A][B]^{2}$ Here, *f* is the feed rate parameter, and *k* is the kill rate parameter; both are between 0 and 1.



A cell's color is based on its value of [B]/([A])+ [*B*]). If this value is close to zero (many prey), then it will be colored red, and if it is close to 1 (many predators), then it will be colored dark blue.

f = 0.034 and k = 0.095



Creating multiple initial predator locations leads to more complex patterns.

f = 0.034 and k = 0.095



If we hold the feed rate constant and increase *k* by just 0.002, then the patterns change significantly into spots.

f = 0.034 and k = 0.097



If we make the prey just a little bit happier, raising *f* by 0.004 and *k* by 0.002, then we get a striped pattern again, but a different one.

f = 0.038 and k = 0.099



And if we raise *f* by another 0.004 and *k* by another 0.002, we again see a spot pattern.

f = 0.042 and k = 0.101

Convergent patterns are very parameter dependent



This plot shows final convergent patterns for varying values of *k* (*x*-axis) and *f* (*y*-axis).

Key point: Gray-Scott is a faster model that confirms the highly fine-tuned parameters of this system.

Image source: Robert Munafo

PRETTY TRIPPY HUH

We all trip in similar ways. But why?





Form constant (Klüver, 1928): a commonly recurring shape in visual hallucinations.

We all trip in similar ways. But why?



Key point: Hallucinations happen in the blind and don't move in visual field, so they originate in brain.

The brain encodes signals from retina

Cowan 1978: determined details for transformation of retinal coordinates (polar) to cortex (rectangular).



Ermentrout and Cowan, 1979

The brain encodes signals from retina

Cowan 1978: determined details for transformation of retinal coordinates (polar) to cortex (rectangular).

All the form constants reduce to "stripes" in the visual cortex!



Ermentrout and Cowan, 1979

How Does This Relate to Hallucinations?

The visual cortex contains "activator" neurons that tend to be connected more tightly and "inhibitor" neurons with fewer, sparser connections.

Hypothesis: activators/inhibitors are analogous to "predator"/"prey" molecules; some events (migraines, hallucinogens) change the underlying parameters of the system and produce Turing patterns within the visual cortex.

WHAT – IF ANYTHING – DID YOU LEARN?



Some Parting Words

"The Lord gives us so little time for a career: forty years if we start early ... and remain in good health, fifty if fortune smiles. The Devil takes so much away - primarily in administrative burdens that fall upon all but the most resistant and singularly purposeful SOBs." - Stephen Jay Gould

The End?

Time for FCEs!