

# Introduction to GAs

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## Evolutionary Computing (EC)/Evolutionary Algorithms (EAs)

- used for black-box function optimization/design
  - e.g., find a wing design with low drag & weight and good lift
- also used for discovering software agent strategies, robot control structures, neural network designs, art, etc. ...
- and sometimes used for biological modelling
- or even exploring “life-as-it-could-be” (“Artificial Life”)

## Biological Inspiration

Evolutionary algorithms are a nature-inspired/bio-inspired computing paradigm, of which there are many examples:

- Neural Networks
- Ant Colony Optimization
- Swarm Intelligence
- Artificial Chemistry
- DNA Computing
- Artificial Immune Systems

## Biological Inspiration

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Nature is a great source of inspiration, but:

- All of these paradigms are simplified compared to nature
  - is something important missing?
  - has something irrelevant been included?
  - what exactly makes these paradigms work well in nature?
  - in what situations will they work well for us?

## Biological Inspiration

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Nature is a great source of inspiration, but:

- Nature's solutions may not be best for us:
  - brains: highly parallel, but individual elements are very slow
  - desktop computer: mostly serial, very fast components
- Nature has only explored a subset of possible solutions:
  - e.g., what about three or four parents, rather than just two
  - e.g., what if kids inherited parents' knowledge in their genes?
    - Not possible in nature, but it is possible in a computer...

Nature is a great source of inspiration, but:

- Natural systems have limits
  - Evolved creatures are amazing, but they evolved to fit a *niche*
  - They did not evolve to be general purpose or universal
  - An immune system has limits; An ant colony has limits
  - Even a brain has limits – it is not good at all types of thinking
  - Just because biology is cool, doesn't mean a bio-inspired approach is the best... Copying nature is not a magic bullet!
  - Naturalistic Fallacy: “You can’t get an *ought* from an *is*.”

EC is a form of stochastic (randomized) search

- We seek the highest quality solution in the least time
- Evaluating all solutions is guaranteed to find the best one
  - ...but it is slow!
- EC's defining feature: a *population* of solutions search over the (possibly infinite) space of solutions
- EC is often used when traditional search methods are not appropriate or the problem is poorly understood...

- Nature rewards effective behaviour with more offspring:
  - Better at catching food => more offspring 😊
  - More effective immune system => more offspring 😊
  - Better eyesight => more offspring 😊
  - Tendency to fall off cliffs => fewer offspring 😞
- “Fit behaviour”: Behaviour that “fits” its environment.
- “Fitness”: The tendency to generate more offspring.
  - ...*in a context*, environment, task, setting...

Nature is a ‘blind watchmaker’:

- Creates complex things... ...that seem *consciously designed*
- But it is just a noisy copying process that rewards success
  - ‘heredity+variation+selection’ ..or.. ‘copying+error+constraints’

To breed dogs, we hijack the mechanisms that nature uses:

- To get faster dogs / we select the fastest doggy parents
- We do ‘artificial selection’ .. Nature does ‘natural selection’

## Evolution in an Algorithm

We need to have a few elements:

1. A *population* of individuals, each represented by ‘genes’
2. A way to evaluate their fitness: a *fitness function*
3. A way to *select* the fitter individuals as parents
4. A way to introduce some *variety* in their offspring:
  - copying errors ('mutation')
  - mixing genes from two parents ('sex')
5. A *loop* over steps 2, 3, & 4 + a *stopping condition*

## Evolution in an Algorithm

We specify what we want evolution to find by defining a *fitness function*

- Analogous to an *objective function*, or *reward function* in Machine Learning or Reinforcement Learning
- A fitness function assigns a fitness score to one entire individual, based on its overall performance:
  - A Wing:  $fitness_i = f(drag_i, weight_i, lift_i)$ , e.g.,  $lift_i / (drag_i + weight_i)$
  - A Robot Cat:  $fitness_i = 1 / (1 + num\_rats\_in\_my\_house)$

## Law of Unintended Consequences

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- An unwritten assumption: Defining a good fitness function is easier than working out the solution yourself by hand
- But designing the fitness function can be difficult...
- It may be tricky to exploit our knowledge of the problem:
  - E.g., assigning a fitness boost to a chess player when it captures the queen may end up rewarding poor chess-playing strategies
  - Fitness functions can encourage *degenerate* solutions:
    - E.g., car fitness = “don’t crash” => a car that never moves

## Further Reading/Watching

- *The Blind Watchmaker*, Richard Dawkins, Norton & Co., 1986.
- *Biomorphs*: Interactive Web App + Explanation + Simple Code  
<https://www.defy.org/hacks/biomorphs/>
- Karl Sims' *Genetic Images*: Explanation + Gallery + Papers,  
<https://www.karlsims.com/genetic-images.html>
- David Ha's *Neurogram*: <https://blog.otoro.net/2015/07/31/neurogram/>
- Video of Richard Dawkins' *Horizon* Episode (45 min.):  
<http://www.dailymotion.com/video/x223a3n>
  - “Methinks it is like a weasel”, Biomorphs, Rechenberg, Holland..

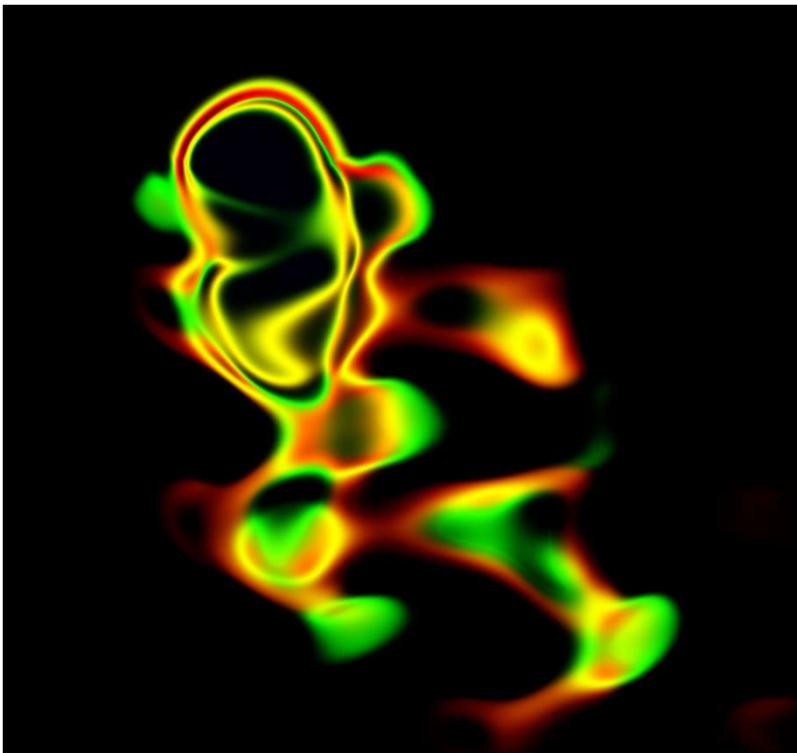
Karl Sims (1991)



<https://www.karlsims.com/papers/siggraph91.html>

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# David Ha, Google Brain (2015)



<https://blog.otoro.net/2015/07/31/neurogram/>

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## Applications: Optimization

- Some papers from last year (top page of Google Scholar):
  - *Automatically designing CNN architectures using the genetic algorithm for image classification*, Y Sun, B Xue, M Zhang, G Yen ..
  - *Solving the open vehicle routing problem with capacity and distance constraints with a biased random key genetic algorithm*, E Ruiz, V Soto-Mendoza, AER Barbosa ..
  - *Extended genetic algorithm for solving open-shop scheduling problem*, AAR Hosseiniabadi, J Vahidi, B Saemi, AK Sangaiah ..
  - *Hybrid genetic algorithm and a fuzzy logic classifier for heart disease diagnosis*, GT Reddy, MPK Reddy, K Lakshmanan ..

## Applications: AI, ALife & Robotics

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- Karl Sims (Blockies): <https://youtu.be/mA8z0GndiYI>
- Hod Lipson (GOLEM): <https://youtu.be/qSIOHSkzG1E>
- Hod Lipson (Walking Robot): [https://youtu.be/iNL5-0\\_T1D0?t=273](https://youtu.be/iNL5-0_T1D0?t=273)
- OpenAI (Hide & Seek): <https://openai.com/blog/emergent-tool-use/>
- Josh Bongard (Soft Robots): <https://youtu.be/gXf2Chu4L9A>
- F. Corucci (Swimming Robots): <https://youtu.be/4ZqdvYrZ3ro>
- Joachimczak et al. (Development) <https://youtu.be/CXTZHHQ7ZiQ>

## Example Questions

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- Which of the following are/are not required for evolution:  
*selection, sex, metabolism, reproduction* [1 mark]
- Name three kinds of bio-inspired algorithm . [1 mark]
- Was Richard Dawkins' Biomorphs system an example of natural selection or artificial selection? Explain. [3 marks]
- Give one reason why Dawkins' “methinks it is like a weasel” example is a *good* way to introduce evolution as an algorithm and one reason why it is *not*. [4 marks]

**Thank you!**

# Metaheuristics

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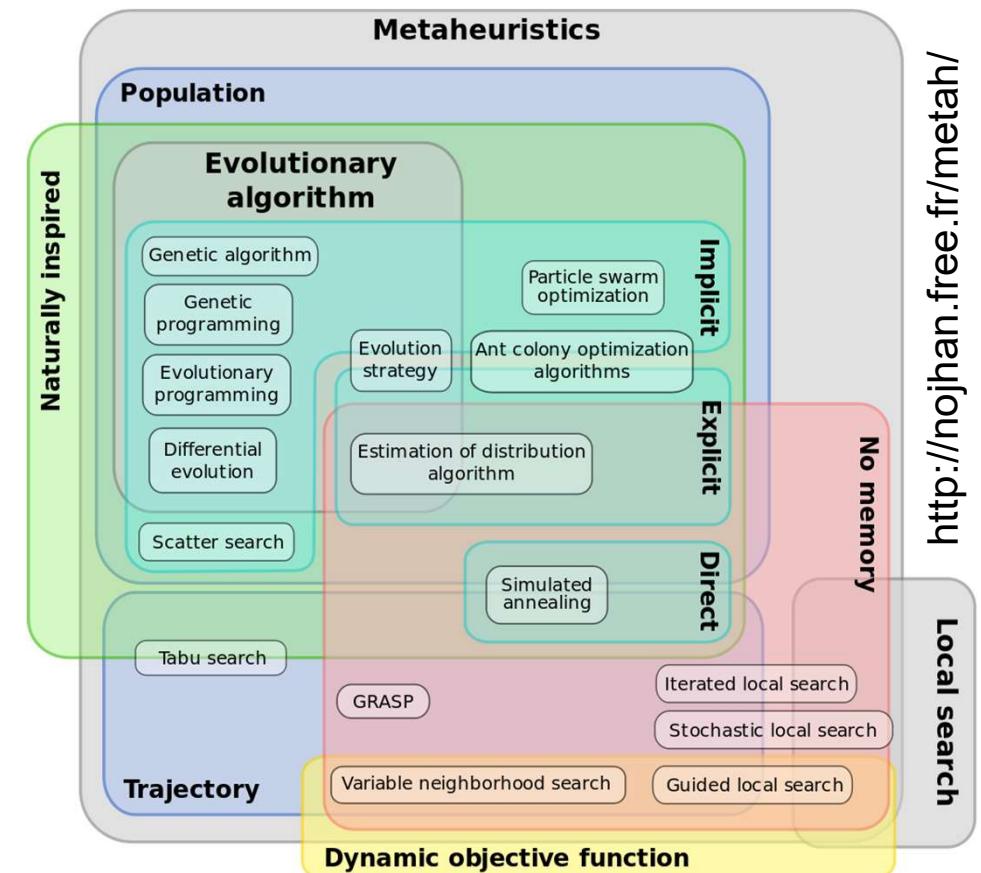
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# What is Evolutionary Computing?

Evolutionary Computing (EC) techniques:

- a diverse collection of ‘nature-inspired’ techniques
- *heuristic*: not guaranteed to find the best solution
  - (the opposite of an ‘exact’ algorithm)
- *stochastic*: they use random number generators
  - (the opposite of ‘deterministic’ algorithms)
- intended for hard optimization problems (e.g., NP-hard)

- EC techniques are examples of *metaheuristic* approaches.
  - A metaheuristic is a way to guide search
  - Some are nature inspired
  - Some are population based
  - Some build an explicit model of the problem as it's being solved



There are several different kinds or flavours of EC algorithm:

- Genetic Algorithms (GA)
- Genetic Programming (GP)
- Evolutionary Strategies
- Differential Evolution
- Etc.

..often invented (quasi-)independently by different people.

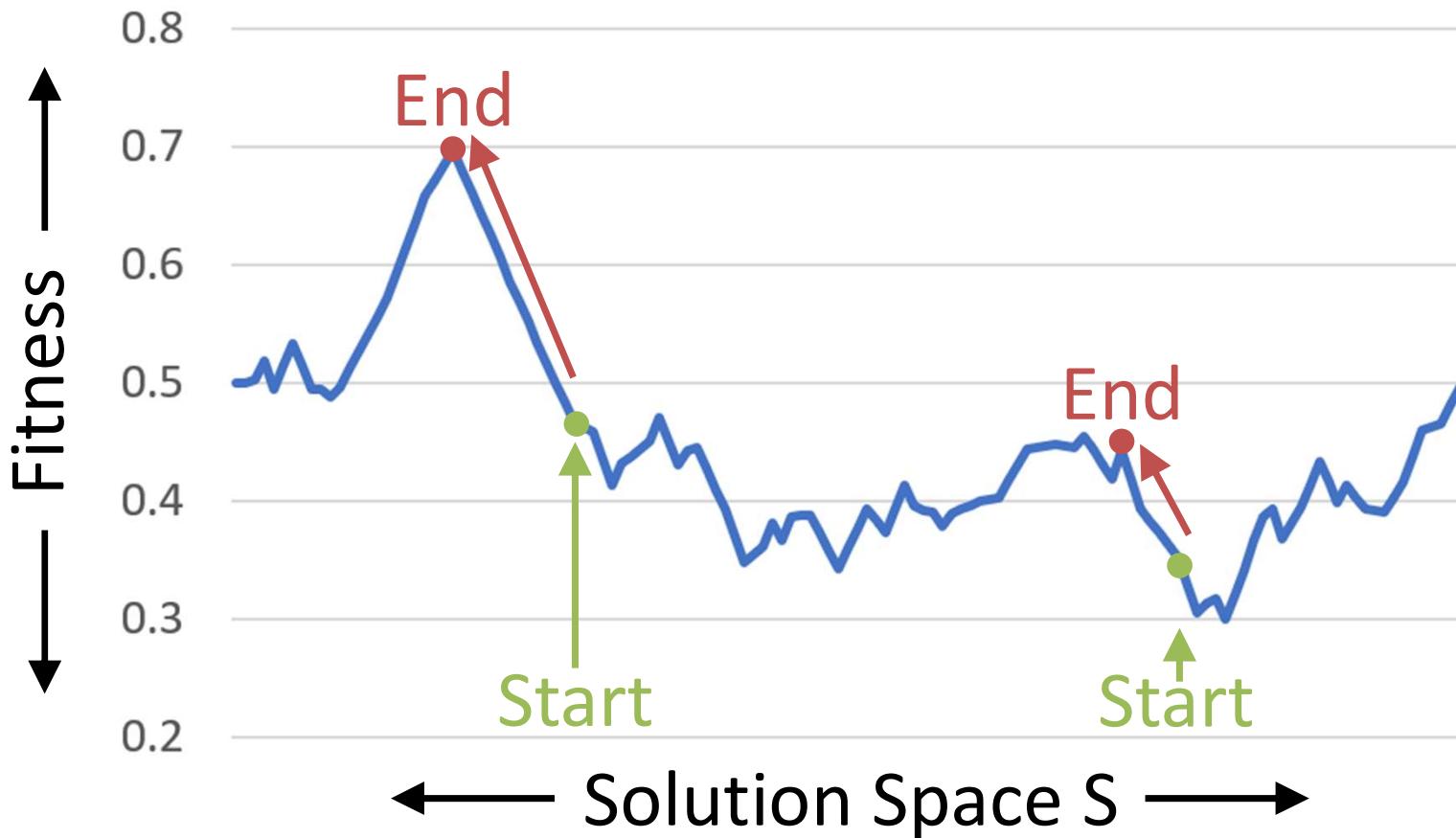
## Individual-based Metaheuristics

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In contrast to EC approaches, some metaheuristic approaches do *not* use a population of solutions; e.g.,

- Hillclimbing
- Simulated annealing
- Tabu search
- ...

## Hill Climber



1. Make a random starting solution
2. Change it a little
3. If the new solution is better: keep it  
Else: discard it
4. If stuck: stop  
Else: go to 2

*Consider: Is this a good diagram?*

# Simple Hill Climbing

*Repeatedly switch to the first better solution found in the local neighbourhood of the current solution*

start with any solution  $p$  chosen from solution space  $S$   
repeat:

```
choose_a_better_neighbour( $p$ ) =>  $q$ 
if  $q$  is None return  $p$ , else  $q$  =>  $p$ 
```

```
def choose_a_better_neighbour( $p$ ):
    for each neighbour  $q$  of  $p$ :
        if  $q$  is better than  $p$ :
            return  $q$ 
    return None
```

*Consider:*

- *How do we pick the first solution  $p$  from  $S$ ?*
- *What counts as the neighbourhood of a solution?*
- *In what order should we consider  $p$ 's neighbours?*

# Steepest Ascent Hill Climbing

*Repeatedly switch to the best solution found in the local neighbourhood of the current solution*

start with any solution  $p$  chosen from solution space  $S$   
repeat:

```
choose_the_best_neighbour( $p$ ) =>  $q$ 
if  $q$  is  $p$  return  $p$ , else  $q$  =>  $p$ 
```

```
def choose_the_best_neighbour( $p$ ):
     $p$  => fittest
    for each neighbour  $q$  of  $p$ :
        if  $q$  is better than fittest:  $q$  => fittest
    return fittest
```

*Consider:*

- Does the order in which we consider  $p$ 's neighbours still matter?*

## Simple Tabu Search

*Hillclimb, but don't consider solutions on a (finite) list of previously visited solutions*

start with any solution  $p$  chosen from solution space  $S$   
 $p \Rightarrow \text{best\_so\_far} ; [p] \Rightarrow \text{tabu\_list}$

repeat:

```
    best(neighbours_of_p_not_in_tabu_list) => p
    if p is better than best_so_far: p => best_so_far
    add p to tabu_list
    if tabu_list too long:
        remove oldest item
    if time_to_stop: return best_so_far
```



*Consider:*

- What's the significance of the tabu\_list max length?*

# Simulated Annealing

*Hillclimb, but tolerate moves to worse solutions with a probability that is initially high, but decreases as more steps are made*

start with any solution  $p$  chosen from solution space  $S$

```
for step from 1 through max_step:  
    pick_a_random_neighbour(p) => q  
    if allow(fit(p), fit(q), temp(step)):  
        q => p  
return p
```

```
def allow(p, q, T):  
    return True if q>p or rand(1)<=exp(-(q-p)/T), else False
```



*Consider:*

- The ‘schedule’  $\text{temp}(step)$  needs to be defined
- It should return a high temperature for step 1
- And reduce it gradually as more steps are taken

## The Explore/Exploit Tradeoff

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- Recall: Breadth-first search *explores*, while depth-first *exploits*.
- Hill Climbers *exploit* current local knowledge of the search space – not even interested in fully exploring the local neighbourhood.
- Steepest Ascent Hill Climbers do explore the local neighbourhood fully before *greedily* exploiting the best local next step.
- Tabu is a little more *exploratory* than regular hill climbing. It keeps a record of solutions that have not yet been fully exploited.
- Simulated Annealing starts off more *exploratory* (at high temps) but gets more *exploitative* over time (as temp falls).

## Going Populational

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- All the algorithms that we've looked at work with only *one* hill climber moving across the solution space.
- By contrast, Genetic Algorithms maintain a *population* of solutions to help balance the explore/exploit trade-off.
- A population of solutions allows exploration to take place in *multiple* parts of the solution space.
- Competition & crossover allow success in one part of the space to be exploited by the rest of the population

## Example Questions

- What's the difference between a stochastic algorithm and deterministic algorithm? *[1 mark]*
- Why does the temperature of a simulated annealing algorithm start off high and get lower over time? *[2 marks]*
- If a hill-climber is stuck, what can you infer about the solution that it has found? *[3 marks]*
- Explain the explore/exploit trade-offs made by best-first search, tabu search & simulated annealing. *[8 marks]*

**Thank you!**

# The Genetic Algorithm

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- Genetic algorithms share the same basic form:
  - Repeatedly: assess, breed, mutate a population of solutions
- But different types of GA vary in many different ways:
  - Selection scheme, genetic operators, population structure, etc.
  - ‘Steady state’ GA vs. ‘generational’ GA
  - + Many special tricks of various kinds...
- Here we present a very simple version
  - (and mention some of the most frequent variants)

- *Population* – the set of individual solutions that the GA is acting on
- *Individual* – a member of the population
- *Genotype* – a string of symbols from some alphabet that encodes a particular solution (sometimes: *Genome* or *Chromosome*)
- *Phenotype* – the actual solution encoded by a genotype
- *Genotype-Phenotype Mapping* – analogous to development
- *Genes* (also *Loci*) – chunks of genome, each taking a value: “*Allele*”
- *Fitness* – the value or quality of an individual solution phenotype
  - *Fitness Function* – returns the fitness of a solution

- *Selection* – choosing which current individuals reproduce
- *Parents* – individuals selected to reproduce
- *Offspring* – the new individuals that result from reproduction
- *Crossover* – the recombination of alleles from multiple parents
- *Mutation* – replacing offspring alleles with random alternatives
- *Fitness Landscape* – an ‘evolutionary search space’ organising all possible solutions according to the neighbourhood relationships that result from the GA’s **Genotype Structure & Genetic Operators**, with landscape ‘altitude’ set by each solution’s **Fitness**.

## Simple Genetic Algorithm

- A Simple GA:

```
initialise() => population
```

```
repeat:
```

```
    evaluate(population)
```

```
    select(population) => parents
```

```
    breed(parents) => offspring
```

```
    offspring => population
```

```
    if timed_out or good_enough:
```

```
        return best(population)
```

- Compare with a Hillclimber

```
initialise() => individual
```

```
repeat:
```

```
    evaluate(neighbours)
```

```
    select(neighbours) => chosen
```

```
    chosen => individual
```

```
    if timed_out or stuck:
```

```
        return(individual)
```

## Generate Initial Population and Evaluate

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- We start with a population of individual random genotypes
  - Each is a random string of symbols from the genetic ‘alphabet’
  - A typical (classic) GA alphabet: {0,1} – binary genotypes
- To evaluate an individual we use the fitness function:
  - How well does the robot specified by the genotype behave?
  - How good is the wing design specified by the genotype?
  - How good is the exam timetable specified by the genotype?
  - How successful is the chess strategy specified by the genotype?

## Genotype-Phenotype Mapping

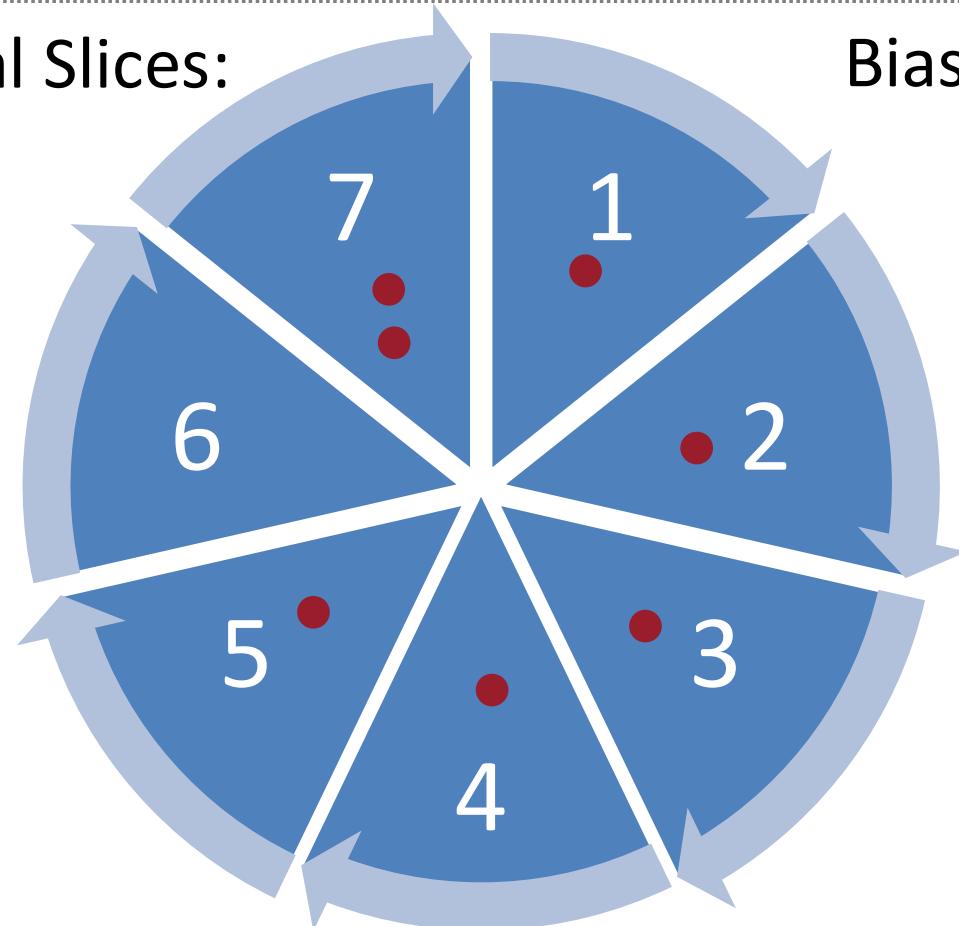
- The genotype is just a way to write down a solution:
  - #1: [Thin, Cheese, NoTomato, NoOlives, NoAnchovy]
  - #2: [Deep, Cheese, Tomato, Olives, Anchovy]
- To allocate fitness to genotypes, we must decode them.
- We must build ('develop') the *phenotypes* they encode:
- The *genotype-phenotype mapping* characterises this 'developmental' encoding relationship...



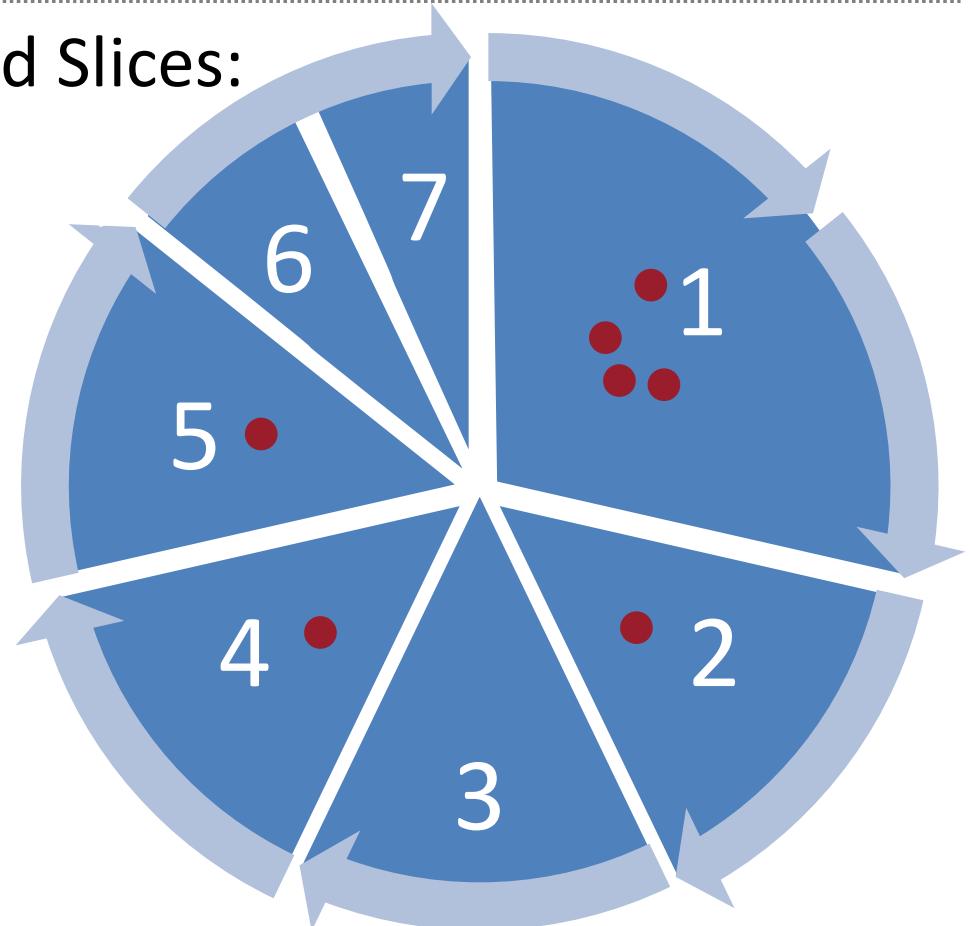
- A key idea is that we should tend to select the *fitter* individuals from the current population to become parents
- We can pick parents with a chance proportional to fitness:
  - $p_i \propto f_i/S$  where  $p_i$  is the chance that we pick individual  $i$
  - $S$  is the sum of fitnesses in the current population:  $S = \sum_{j=1}^N f_j$
  - $N$  is the number of individuals in the current population
- One way of doing this is using ‘roulette wheel’ selection:
  - Spin a wheel where: probability of landing in slice  $i = p_i$

## Roulette Wheel Selection

Equal Slices:



Biased Slices:



## Roulette Wheel Selection

*Run a roulette wheel that selects element i with probability  $p_i$*

start with a population: N individuals, each with a fitness score

```
sum(fitnesses(population)) => S
```

```
rand(0,S) => roll
```

```
0 => running_total
```

```
loop i from 1 to N:
```

```
    running_total + fitness(i) => running_total
```

```
    if running_total >= roll:
```

```
        return(i)
```

*Consider:*

- Is it worth sorting the population by fitness before using the roulette wheel to pick N parents?*

## Rank-Proportionate Selection

- Alternatively we could pick each parent with a chance proportional to the *rank* of their fitness in the population
- One way of doing this is using ‘tournament’ selection:
  - Sample  $k$  (unique) individuals at random from the population
  - Pick a winner (e.g., the one with highest fitness) to be a parent
- To find  $N$  parents, run  $N$  independent tournaments.

*Consider:*

- *How is selecting on fitness rank different from selecting on fitness?*

*Consider:*

- *What is happening if  $k=1$ ?*
- *What is happening if  $k=N$ ?*

- Having selected parents, we reproduce them:
  - we make a copy of their genes and put it into the next generation of the population
- Genetic operators are applied during reproduction:
  - Mutation: each offspring gene is replaced by a random allele with probability  $m$
  - Crossover: the offspring genotype inherits genes from multiple parents
- Mutation is almost always used. One mutation per offspring is a typical rate.
- Crossover is sometimes not used at all ('asexual' reproduction).
- ...or is only applied to some offspring (e.g., it occurs with probability  $c$ )
- Elitism: the fittest current individual is copied into next generation perfectly

Consider:

- *What if all parents were just copied perfectly?*

## Types of Crossover

- One-Point: pick a point along the genotype,  $k \in [0, L]$ 
  - The offspring inherits the first  $k$  genes from their mother's genotype and the remainder from their father's genotype
- Two-Point: pick two points along the genotype,  $j, k \in [0, L]$ 
  - The offspring inherits genes  $j$  thru  $k$  from their mother's genotype and the remainder from their father's genotype
- Uniform: merge the genes from both parents at random
  - Each of the offspring's genes, is inherited from their mother with probability 0.5, else from their father.

# Crossover Schemes

*Consider:*

- *How do different crossover schemes disrupt genotypes in different ways?*

Mum: 

Dad: 

**One-Point Crossover Kid:**  A horizontal bar divided into 10 segments. The first 6 segments are blue (labeled 1, 0, 0, 0, 0, 0) and the last 4 segments are green (labeled 0, 0, 0, 0). A vertical black line labeled 'k' is positioned at the boundary between the 6th and 7th segments.

**Two-Point Crossover Kid:**  A horizontal bar divided into 10 segments. The first segment is green (labeled 0), the second is blue (labeled 1). From the third segment onwards, there are 5 blue segments (labeled 0, 0, 0, 1, 0) followed by 4 green segments (labeled 0, 0, 0, 0). Two vertical black lines are shown: one at the boundary between the 1st and 2nd segments labeled 'j', and another at the boundary between the 2nd and 3rd segments labeled 'k'.

**Uniform Crossover Kid:**  A horizontal bar divided into 10 segments. The first 6 segments are blue (labeled 1, 1, 1, 0, 0, 0) and the last 4 segments are green (labeled 0, 0, 0, 0).

## Generational GAs vs Steady State GAs

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- Typically the GA population size,  $N$ , is held constant...
- Two common ways to ensure this:
  - Generational Reproduction: ...we continue selecting and reproducing parents until we have a  $N$  new offspring. Then we discard the old population and replace it with the  $N$  new individuals.
  - Steady-State Reproduction: ...as soon as we have generated *one* new offspring, we pick a member of the current population (either at random or biased toward the unfit) and kill it, replacing it with the new offspring.
- There are many different wrinkles on these basic schemes:
  - E.g., only ever let a new offspring displace a less fit individual

- Two simple stopping conditions:
  1. We've found the perfect solution, i.e., a genotype that achieves maximum fitness
  2. We've run out of time, i.e., our generation counter has reached `max_generation`
- A more subtle stopping condition:
  3. We think the GA has run out of steam and things are as good as they are going to get
- Checking for conditions 1 and 2 is easy. How do we check for condition 3?
- Fitness scores have *stagnated* – no improvement for many generations:
  - Current “best” genotype is (very) old...
  - The population is strongly converged...

Consider:

- *Might the population still be exploring new solutions?*
- *How could we know for sure?*

- Remember: Each genotype is made of symbols from the genetic ‘alphabet’
  - $\{0,1\}$  – bit strings;  $\{A, C, G, T\}$  – nucleic acids;  $\{A, B, C, \dots Z\}$  sentences
  - Or maybe parameters of some kind:  $\{\langle \text{integers} \rangle\}$ ,  $\{\langle \text{floats} \rangle\}$
  - Note that choice of alphabet has implications for mutation and crossover
  - Mutation = a bit flip; or a random letter; or a random perturbation
- And there could be constraints on some genes:
  - `pizza_radius` must be *positive* and *less than oven\_width*
  - `num_robot_legs` must be *even*;
    - a 3-bit encoding of `exam_day` leaves `101`, `110`, and `111` unused?
    - illegal genotypes must be discarded... causing search *biases*

## Simple Genetic Algorithm (Recap)

- The Simple GA:

```
initialise() => population
repeat:
    evaluate(population)
    select(population) => parents
    breed(parents) => offspring
    offspring => population
    if timed_out or good_enough:
        return best(population)
```

- Simple Example

```
# generate N random bit strings
# employ a generational GA
# fit. func. assigns  $f_i \in [0,1]$ 
# tournament selection, use k=3
# bitflip mutation & 1-pt xover
# elitism on: always copy best
# gen > max_gen or fitness = 1
```

## Example Questions

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- Name two different kinds of cross-over operator. [1 mark]
- Uniform crossover of two L-bit binary genotypes can result in how many different offspring genotypes? [2 marks]
- What is the difference between roulette-wheel selection and tournament selection? [4 marks]
- Define a good fitness function for evolving a university time-table schedule. Explain your answer. [8 marks]

**Thank you!**

# Fitness Landscapes

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# Fitness Landscapes

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This time:

- Visualizing search problems as fitness landscapes
- Kinds of landscape (unimodal, multimodal, deceptive...)
- How search operators interact with fitness functions
- How search moves across landscapes
- The need to both explore new areas and exploit existing knowledge while searching

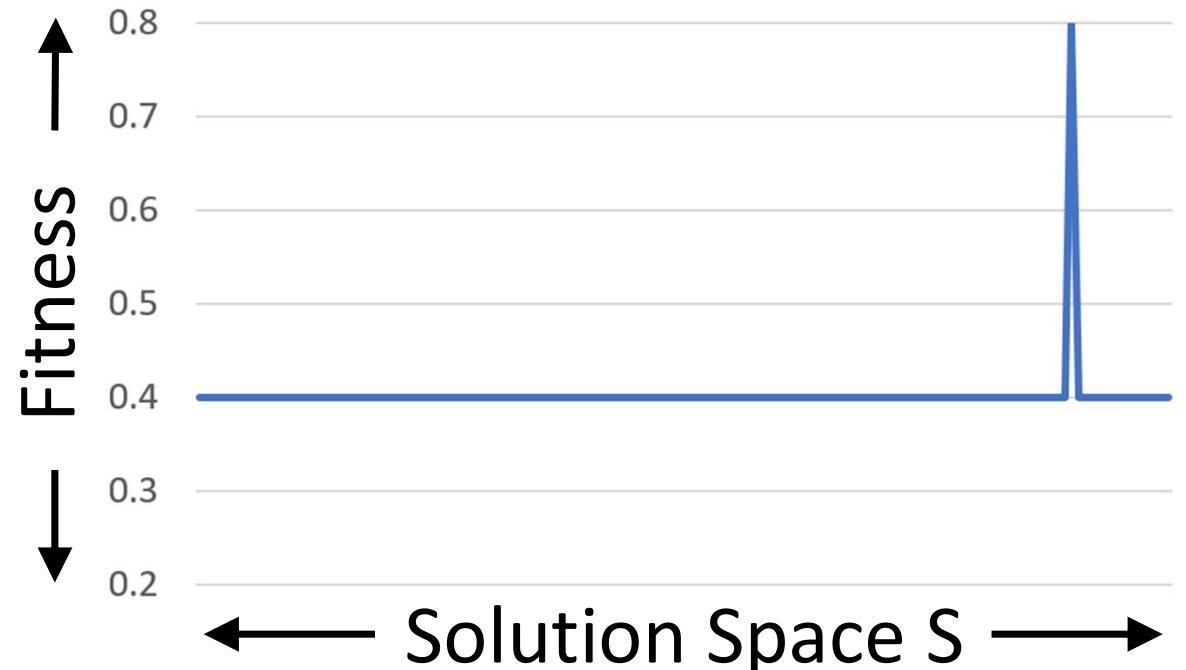
- The set of possible genotypes is the GA's search space,  $S$
- Given genotypes of length  $L$  from an alphabet of size  $A$ :
  - The space has  $L$  dimensions which each have  $A$  possible values
  - There are therefore  $A^L$  possible genotypes in  $S$
- Each genotype is a *point* in the search space
- Genotypes are 'neighbours' if they differ by one mutation
- The *structure* of a search space influences how challenging it is for an algorithm to search it

## Fitness Landscapes

- A search space can be visualized as a *fitness landscape*
  - A plot of the fitness of all possible genotypes: fitness => height
  - Called a landscape because it can have peaks, valleys, ridges...
  - Introduced by biologist Sewall Wright in 1932
- We can think of search as movement across the landscape
  - A population of points move in discrete steps and jumps
  - The shape of the landscape influences this movement

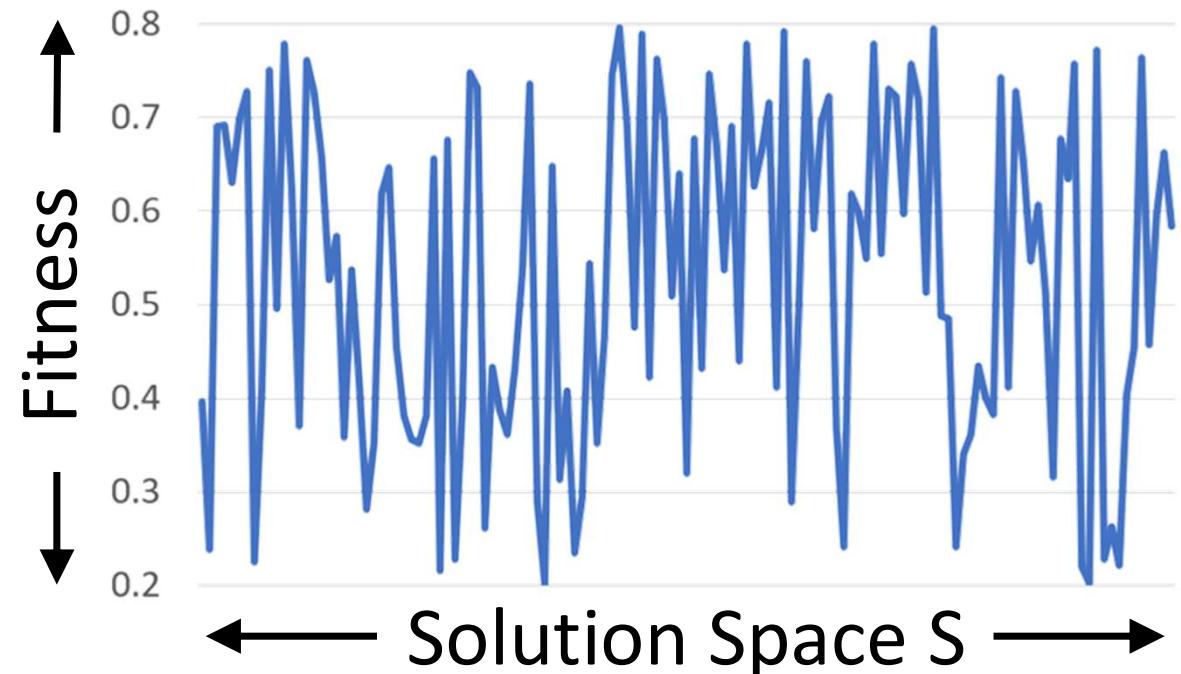
## Needle-In-A-Haystack Landscape

- Suppose all genotypes except one have the *same* low fitness
- This kind of problem is *hard* for any search algorithm:
  - The fitness function is very unhelpful; it has no structure to exploit
  - The fitness of suboptimal genotypes tells the algorithm no information about where the optimal genotype is



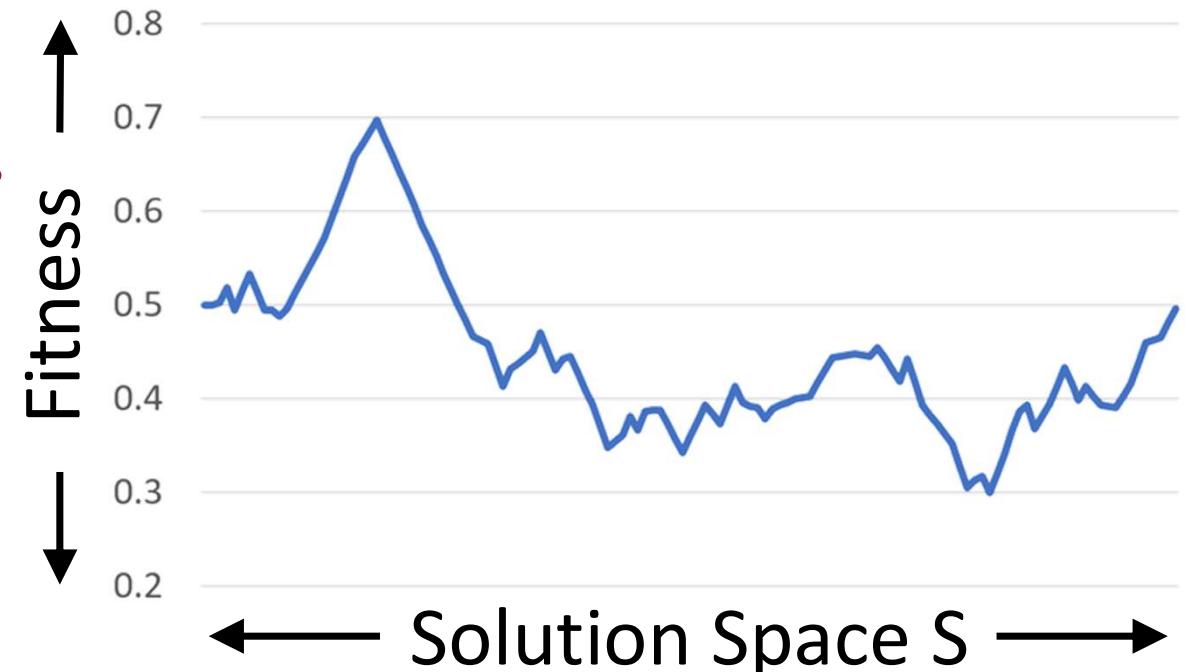
## Random Landscape

- Suppose all genotypes had a *randomly* assigned fitness
- Again, this problem is *hard* for any search algorithm:
  - The fitness function is still very unhelpful; it still has no structure to exploit
  - The fitness of suboptimal genotypes still tell the algorithm no information about the optimal genotype



## A Nicer Landscape

- Luckily, real-world problems do tend to have useful structure
- The algorithm's job is to be able to exploit this structure:
  - Local smoothness, i.e., nearby points have similar fitness = *correlation structure*
  - Ideally, higher peaks are also broader = *non-deceptive*
  - The problem can be divided into parts = *decomposable*



## Search Neighbourhoods

- What does ‘local’ mean in the term ‘local smoothness’?
  - It depends on how we represent and search the space,  $S$
- We could say two points,  $a$  and  $b$ , in  $S$  are ‘local’ to each other if the ‘distance’ between their genotypes is beneath a threshold
  - What distance measure to use? Hamming distance? Euclidian distance?
- Alternatively we could define the ‘distance’ between  $a$  and  $b$  in terms of how easy it is for the algorithm to move between them.
  - $a$  and  $b$  are *neighbours* if  $a$  can reach  $b$  in one genetic operation
    - (e.g., a single mutation)

**Thank you!**

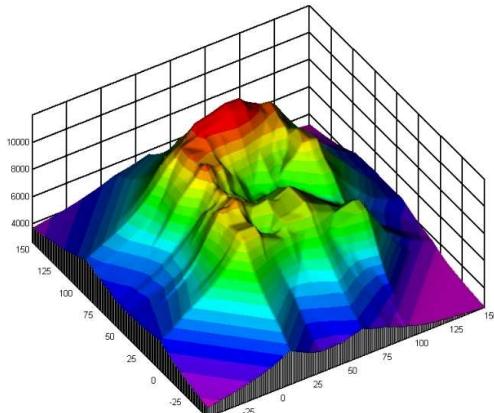
# Fitness Landscapes II

Seth Bullock

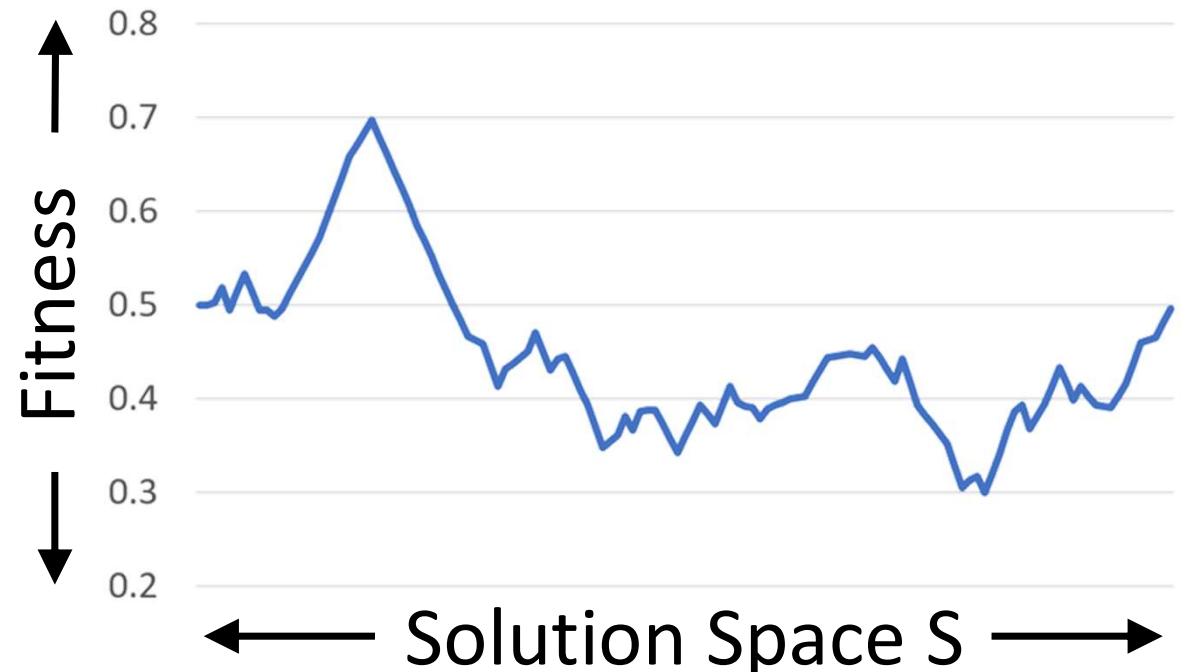
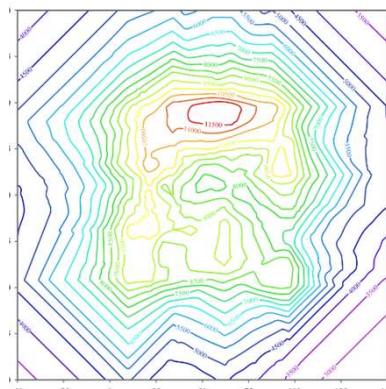
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# Visualizing Neighbourhoods

- So far we have used a very poor diagram of a search space
- It represents  $S$  as a *line*; but  $S$  is typically *high-dimensional*
- Even a 2-D  $S$  is challenging:



[https://en.wikipedia.org/wiki/Contour\\_line](https://en.wikipedia.org/wiki/Contour_line)

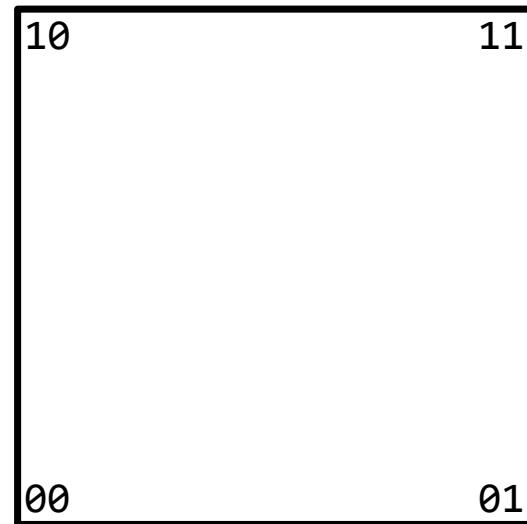


## Visualizing Neighbourhoods

- In fact, it's even worse as many GAs search *discrete* spaces:
- Consider a binary genotype of length 1 or 2...

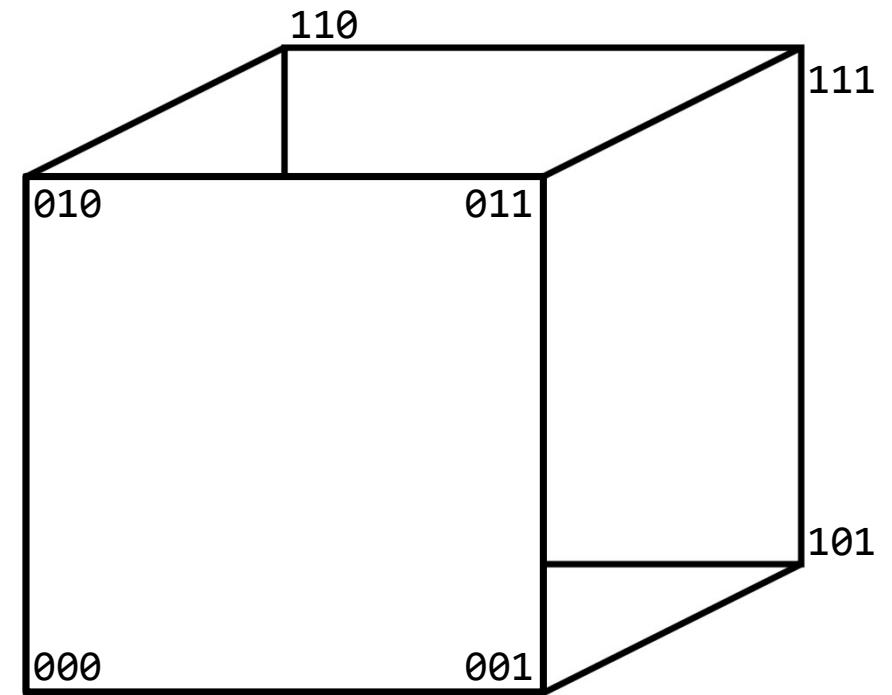
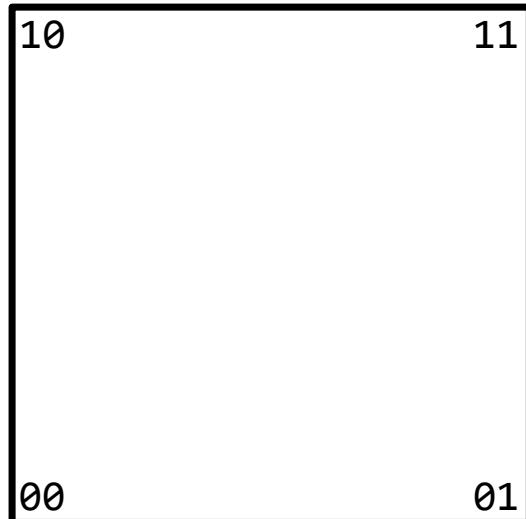
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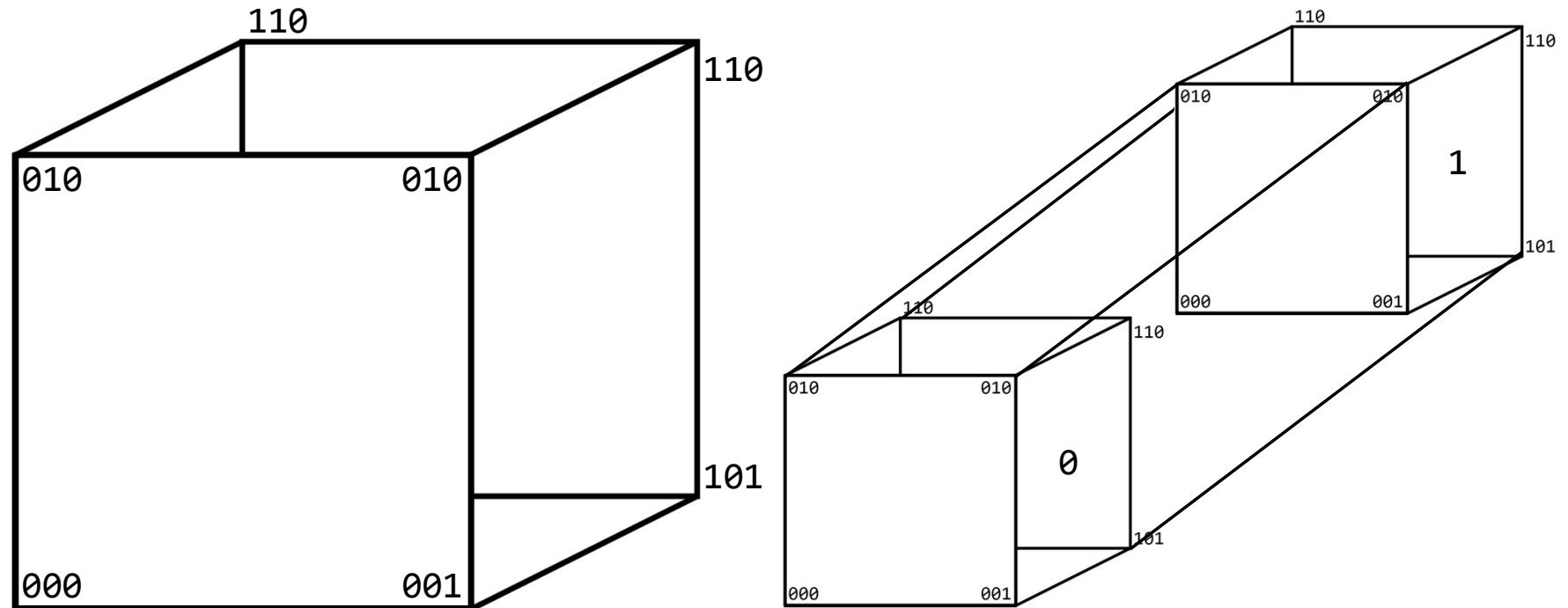
# Visualizing Neighbourhoods

- In one, two and three dimensions we are reasonably ok...



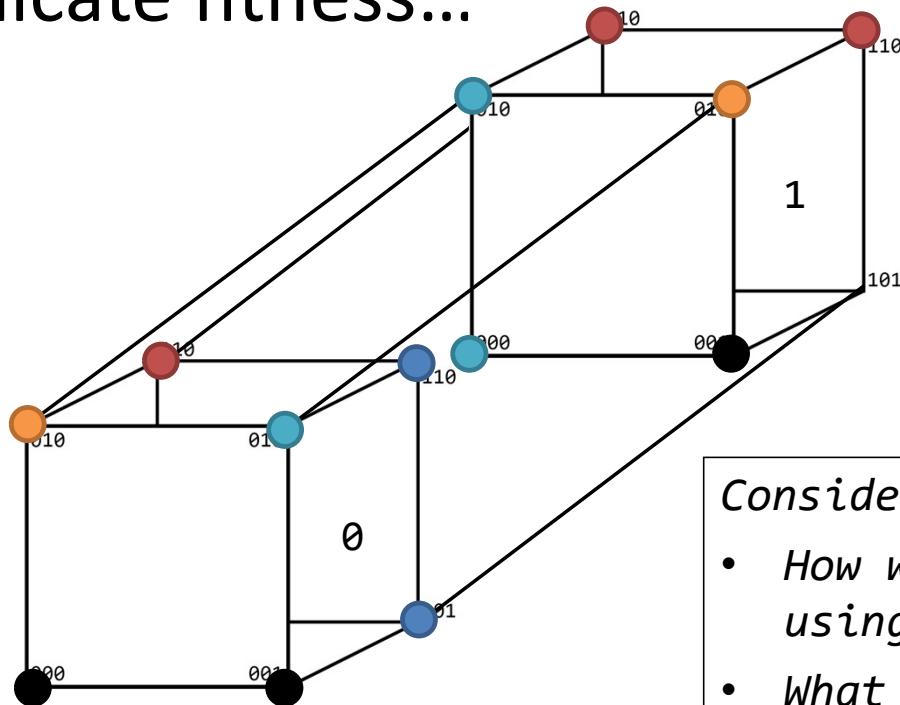
# Visualizing Neighbourhoods

- ...but a solution space of all length- $L$  bit-strings implies that genotypes are located on an  $L$ -dimensional binary hypercube...



# Visualizing Neighbourhoods

- ...and each visualized point also needs an extra dimension to indicate fitness...



- Comprehending the structure of real search spaces is challenging!

Consider:

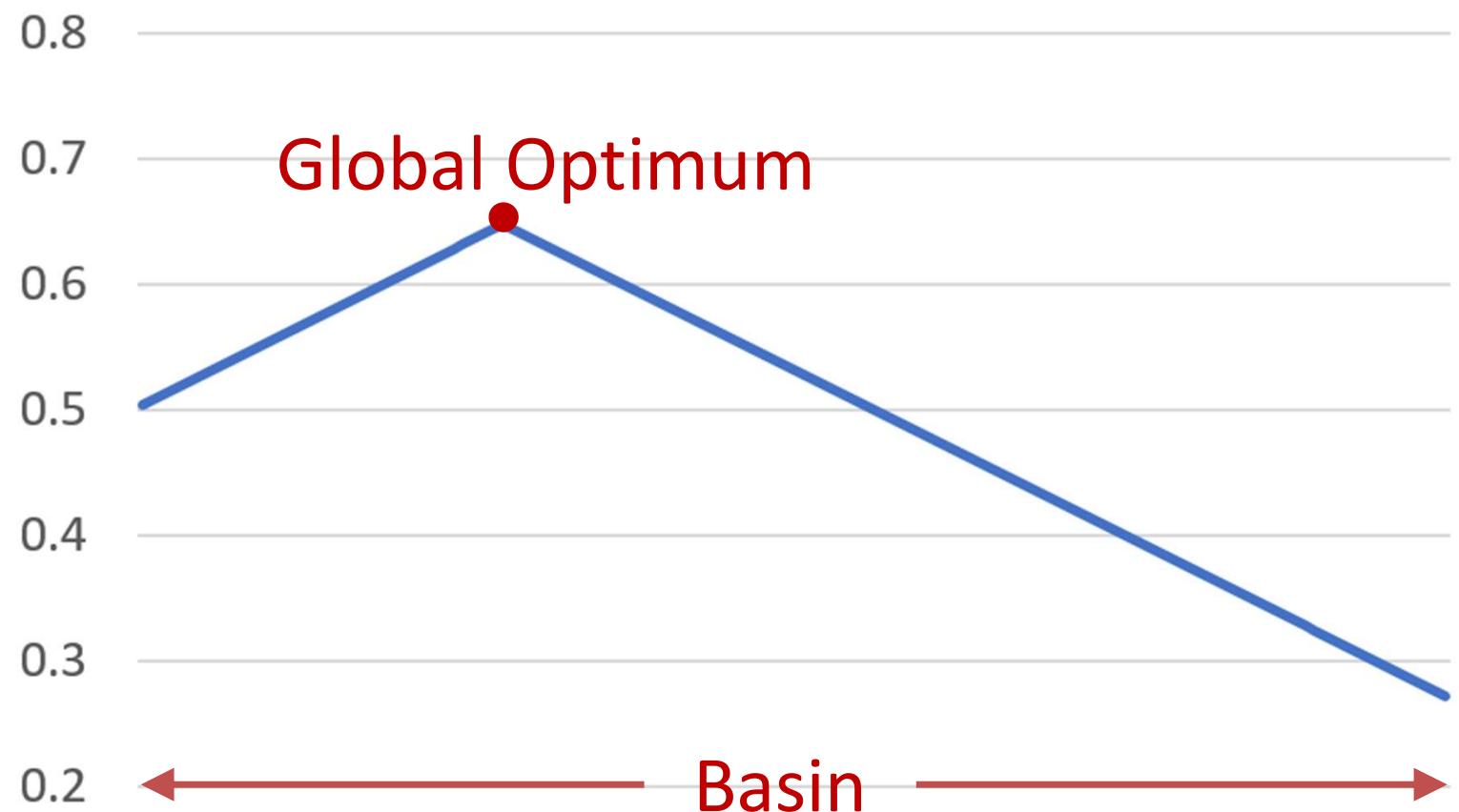
- How would this diagram change if we were using a ternary alphabet:  $\{-1, 0, 1\}$
- What about genes with integer alleles?

## Landscape Metaphors

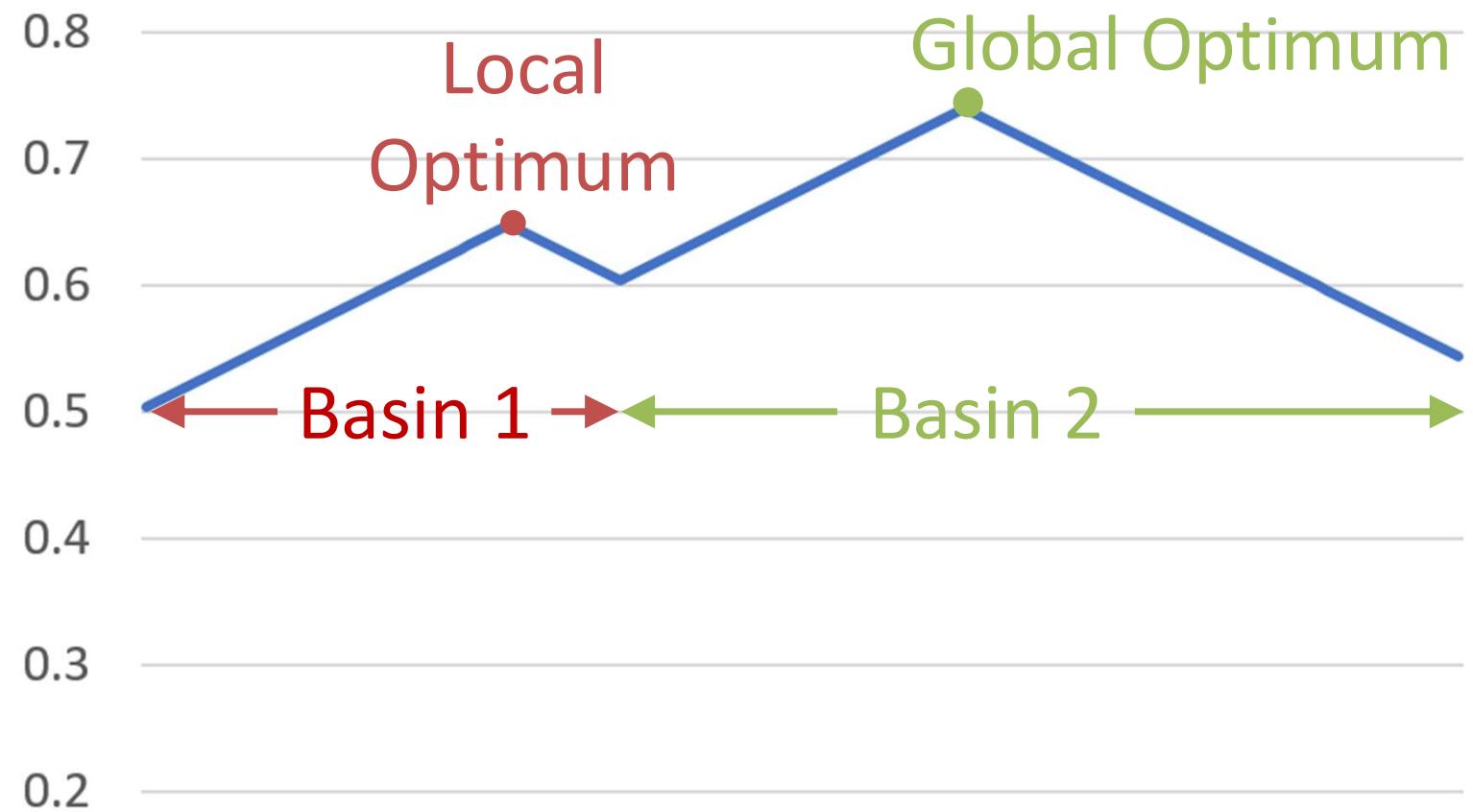
- A real landscape is three-dimensional, continuous, defined, relatively smooth, and static or changing very slowly.
- But fitness landscapes don't share these properties.
- This means we have to be careful when we use “landscape” language to describe search spaces:
  - Peaks
  - Valleys
  - Ridges
  - Basins
  - Plateaus
  - Smoothness
  - Ruggedness
  - Climbing
  - Drifting

- A landscape with one global optimum solution (i.e., it has no local optima) is called *unimodal*
- A landscape with two optima is called *bimodal*
- A landscape with many optima is called *multi-modal*
- A set of points that lie on hill-climbing routes that terminate at one local optimum are said to lie within the *basin of attraction* of that local optimum.
  - A unimodal landscape has *one* basin of attraction

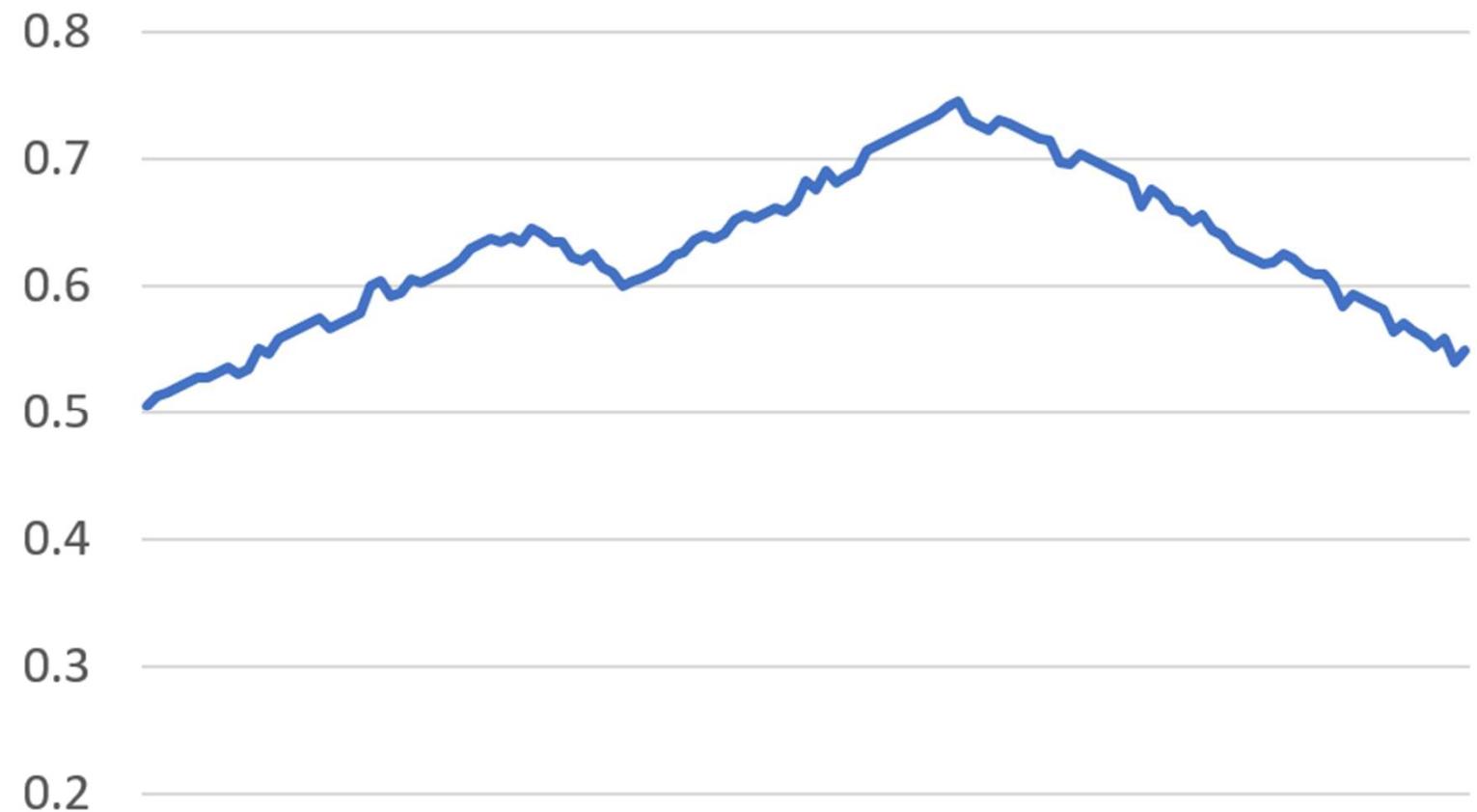
- Trivial problem
- EC is overkill
- Each gene has a *best* allele, independent of the alleles at all other genes



- The best allele for some genes *depends* on the alleles at some other genes.
- GA can't know which basin its population is in.



- Many basins of attraction for many optima.
- But isn't this landscape still bimodal really?
  - Depends on the algorithm...



For a deceptive landscape:

- The best optima have small basins.
- Consequently, global optima are hard to find



## Example Questions

- What size is the search space if genotypes each have  $G$  genes and each gene can be one of  $A$  alleles? [1 mark]
- Consider the search landscape drawn below. Which of the following properties does it have [1 mark each]
  - Neutral, Global, Deceptive, Unimodal, Rugged, Coevolutionary
- Tom's GA keeps getting stuck on local optima. He thinks that doubling the mutation rate might be a good idea. Is it? Explain your answer. [5 marks]

**Thank you!**

# More Advanced GA Concepts

Seth Bullock

[bristol.ac.uk](http://bristol.ac.uk)

This lecture covers a number of Evolutionary Computation concepts:

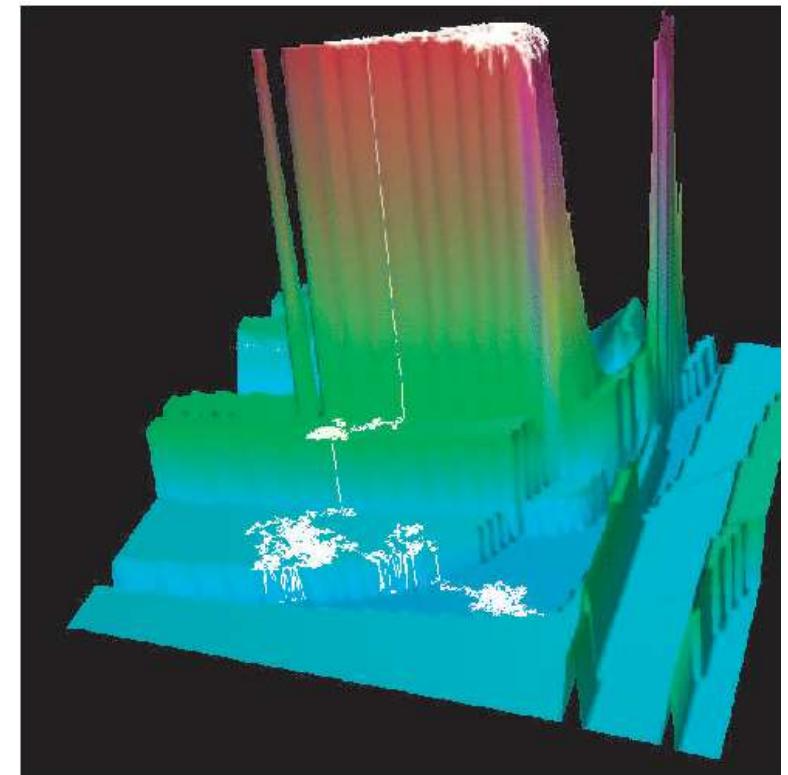
- Premature Convergence
- Neutrality
- Quasi-Species
- Epistasis
- Problem Modularity
- No Free Lunch
- Evolvability

## The Problem of Local Optima

---

- Hill-climbers get stuck on local optima; Exhaustive search does not
- GAs are less likely to get stuck on local optima than hill-climbers:
  - ...because they maintain and evolve a *population of solutions*
  - ...because genetic operators may generate a *wider range of neighbours*
  - These reasons exploit and rely on *diversity* in the evolving population
- Local optima are still a problem as *pop diversity is not guaranteed*
- Should a population of solutions end up *converged* within one basin of attraction they can find it difficult to escape
  - Getting stuck like this is called: *premature convergence*

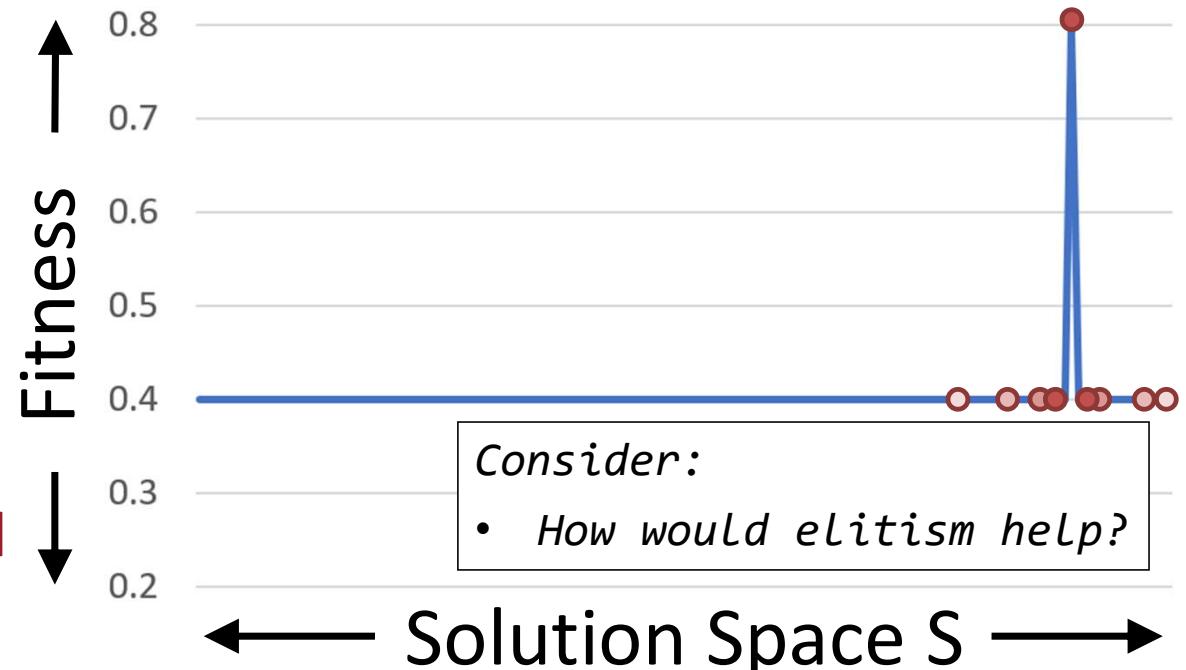
- Neighbouring genotypes with equal fitness are ‘selectively neutral’
  - ...even if their phenotypes are different.
  - Evolution cannot choose between them...
  - ...which results in ‘evolutionary drift’
- Neutrality is often easy to overlook and hard to visualize, but it can be key...
  - E.g., ‘neutral networks’ that percolate the search space may allow converged populations to escape “local optima”



Barnett (2002).  
[Explorations in Evolutionary Visualisation](#)

## The Invisible Needle

- Recall the “needle” fitness landscape we saw in a previous lecture
- The needle is hard to find because there’s no gradient to climb
- But even if we start the pop *on the needle*, we still might not find it...
  - Notice: it’s very rare for an offspring to be an exact copy of their parent
  - So a perfect solution will tend to have unfit offspring...



# The Quasi-Species Concept

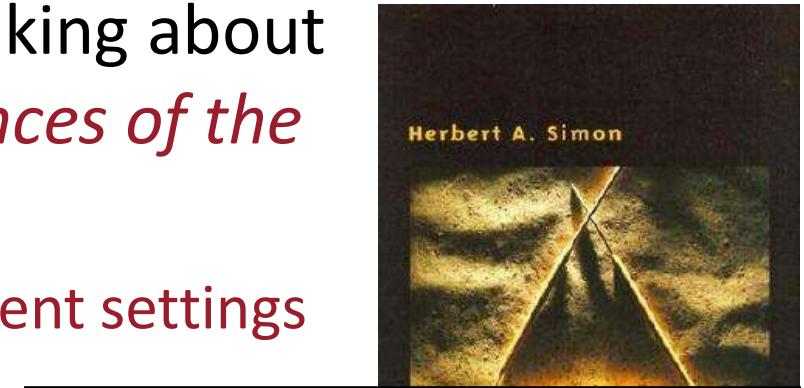
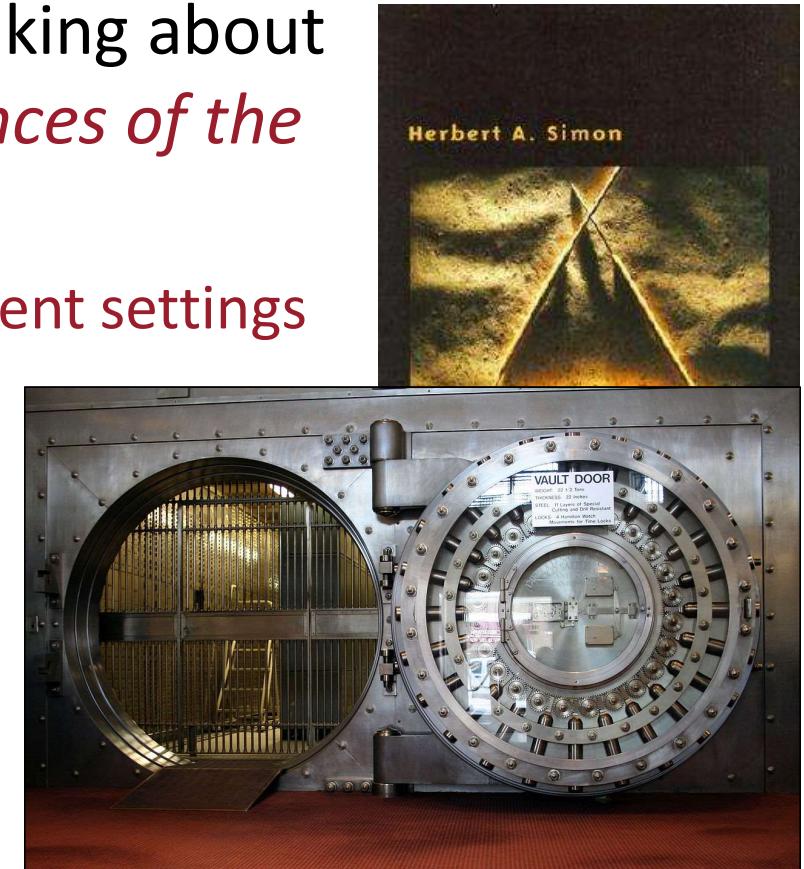
- Manfred Eigen & Peter Schuster developed the *quasi-species* concept to explain what's happening here:
  - High GA mutation rates (much higher than for DNA) mean that the evolving population is a *cloud* of points on the landscape: a *quasi-species*
  - If the selection pressure on the population to reward good solutions...
  - ...is overcome by the mutation pressure that constantly corrupts them...
  - ...then the population effectively cannot even “see” the needle.
- Conversely: if an evolving population *is* able to find a good solution, *and stay there*, we can infer that the solution must be surrounded by other pretty good solutions – it is *robust*

- If we're very lucky, fitness is a *linear function* of the gene alleles:
  - The contribution of each gene to fitness is *independent* of other genes
  - 1-max is a linear fitness function: fitness = the number of 1s in a bitstring
  - Trivial to optimize: optimize each gene independently
- But almost always, fitness is a *non-linear function* of gene alleles:
  - The contribution of genes to fitness is *interdependent* to some extent
  - The best allele choice at one gene *depends* on the alleles at other genes
  - E.g., baby skull size  $\leftrightarrow$  size of birth canal; weapon range  $\leftrightarrow$  visual range
    - This is *epistasis*: more epistasis makes a search problem harder

- The presence of epistasis  $\Leftrightarrow$  the existence of local optima.
  - Epistasis / local optima are different ways of describing the same thing:
  - Non-linearities in the mapping of fitness onto the search space
- Epistasis means we can't optimize each gene *independently*
  - Instead our algorithm must *co-optimize* the alleles of multiple genes
- How big is the set of interacting genes? (the 'order' of interaction)
- How many sets of interacting genes? How do they overlap?
- More generally, what is the *structural modularity* of the problem?

# Modular Decomposability

- Herb Simon introduces a nice way of thinking about problem modularity in his book *The Sciences of the Artificial* (1969): trying to crack a safe
  - A bank safe has  $N$  dials, each with 100 different settings
  - Only *one* setting is correct on each dial
  - *All* dials need to be correct to open the safe
  - (Recall that Dawkins uses the same example in his *Horizon* episode...)
    - How hard is it to open the safe?



## Modular Decomposability

The answer depends on the *modularity* of the safe

- For a safe with perfectly silent dials: we must search all  $100^N$  possibilities
  - We can expect to have to check  $\frac{1}{2}$  of them =>  $100^N/2$  to crack the safe
  - No modularity; no useful problem structure; solution has strong epistasis
- But if each dial gives a little *click* only when it is at the correct setting:
  - We can expect to have to check  $\frac{1}{2}$  of the 100 possibilities *for each dial*
  - =>  $100N/2$  tries to crack the whole safe (much less time)
  - Full modularity; useful problem structure; solution has zero epistasis
    - The same as the “Methinks it is like a weasel” & 1-max problems

# Partial Decomposability

- But real problems tend to lie somewhere in between:
  - Partial modularity; useful problem structure; solution has some epistasis
  - Compare: “Methinks...” vs. evolving any correct English sentence
  - English sentences have modules (words) that depend on each other
- Watson (2006): consider a safe with dials that are sensitive to each other. For each dial,  $n$  settings (including the correct one) give a little click:
  - $n=1$  (full modularity);  $n=100$  (no modularity);  $n=20$  (some modularity)
  - We must try  $n^N/2$  combinations (much less than  $100^N/2$ ) to crack the safe
  - (After we find which are the  $n$  clicky settings on each dial:  $100N$  tries)
    - What if  $n$  is halved for every dial that is in the correct setting?

## No Free Lunches

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- Wolpert and Macready (1997): No Free Lunch for Optimization:
    - When algorithm performance is averaged across *all possible problems*:
    - *Any two optimization algorithms will exhibit equivalent performance*
    - *i.e., no optimization algorithm can do better than blind random search*
  - The insight here is that every search algorithm other than random search has a *search bias*: it works on a hunch, gamble, or heuristic
  - For every time the hunch pays off, there's a time where it doesn't
  - Perhaps need to shift focus to *satisficing* rather than optimising...
  - Algorithm quality depends on the *problem structure* that it faces
-

## Learning How to Search

---

- Recall that the structure of  $S$  (including its modularity) is influenced by our choice of *representation* and *genetic operators*
- So, we can restructure the space by making different choices
- Good choices could be the difference between success and failure
  - Might it be possible to learn which operators to use when?
  - Or to learn a good genetic representation?
  - ..either for a whole class of different, related problems (e.g., timetables)?
  - ..or *online* for one problem *as we are trying to solve it*
    - Could a GA implement evolution that gets more + more powerful?

# The Evolution of Evolvability

- Natural evolution has got more powerful over time:
  - cf. the ‘major transitions’ in evolution (Maynard Smith and Szathmáry)
  - E.g., Single=>Multi-cellularity; A-sex=>Sex; Non-Social=>Social/Cultural
- In fact, Dawkins’ paper at the first Artificial Life conference is on what his *Biomorphs* tell us about “the Evolution of Evolvability”.
  - ‘The ability of a population to generate *adaptive* genetic diversity’
  - (Here *adaptive* means ‘well adapted’ to the problem at hand)
  - i.e., evolvability is: how good is a population at evolving
    - A poor GA has low evolvability; Nature exhibits high evolvability

# The Evolution of Evolvability

- More subtle mechanisms in nature:
  - DNA repair – maintains some parts of the genome more carefully
  - Chromosome Organisation – nearby genes less likely to be disrupted
- Genetic Algorithms can look to exploit similar tricks:
  - Analyse how fitness varies in the current population – build a model
  - Use this model to predict what type of genotypic variation will be best
  - Effectively learning the structure of the problem during evolution
- E.g., “How can evolution learn?” (Watson & Szathmáry, 2015)
  - <http://www.bbc.com/earth/story/20170301-life-may-actually-be-getting-better-at-evolving>

## Example Questions

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- Complete the missing fitness entries in the two tables of genotypes and their associated fitness values, below, such that there is (i) no epistasis, (ii) some epistasis. [2 marks]
- Give an example of two aspects of a real-world problem that are linked epistatically. Explain your answer. [4 marks]
- A problem comprises two complex but almost independent sub-problems. How should a GA's genotype be structured, and what type of crossover should be used? [6 marks]

**Thank you!**

# Coevolution

Seth Bullock

[bristol.ac.uk](http://bristol.ac.uk)

## Fitness Function Design Is Hard

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- As we have seen, a GAs success or failure is often down to our design decisions:
  - Our choice of genetic representation of the phenotype space
  - Our choice of genetic operators and selection scheme
  - Our design of a fitness function
- The third of these is particularly trying:
  - Many fitness functions are hard for GAs to make progress on due to local optima, ruggedness, neutrality, deception, etc.

- But what if we could skip that tricky bit?
- Real evolving populations *do not consult a fitness function* to find out how many offspring each individual is allowed.
  - They just get on with it
  - Organisms co-operate & compete with the other organisms in their environment, and have offspring as part of this activity
- Coevolution: *when multiple populations of evolving organisms influence each other's evolution*

- Coevolution = An automatic fitness function:
  - There is no fitness function designer in nature
- Coevolution = An implicit fitness function:
  - Instead of being set an *explicit* objective target by the fitness function, real organisms are assessed *relative* to their current environment
- Coevolution = A dynamic fitness function:
  - Instead of being assessed against a *fixed* target, real organisms cope with environments that change/evolve over time

## Example

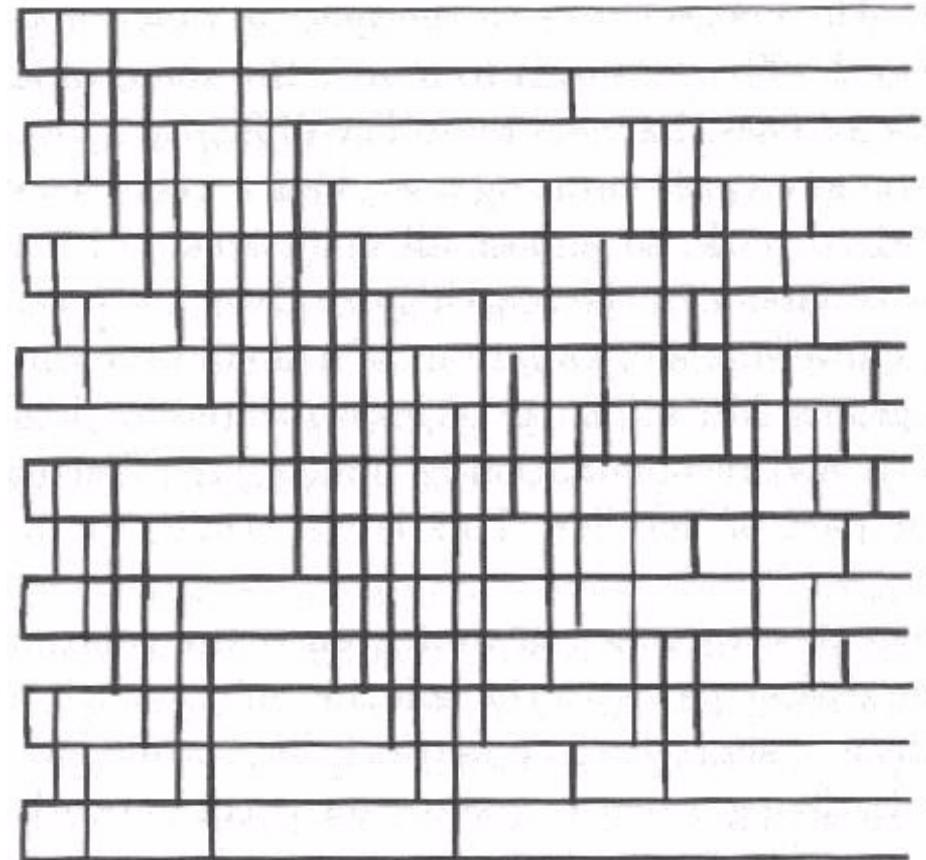
- We would like to evolve a robot goalkeeper for RoboSoccer
  - Designing a fitness function has proven to be quite hard
- Instead, we decide to *coevolve* a population of goalkeeper robots against a population of robot penalty takers
  - We start off with random penalty takers and random goalkeepers
  - As soon as penalty takers start to be able to beat random goalkeepers..
    - ..there is pressure on the goalkeepers to get better..
    - ..putting pressure on the penalty takers to get better.. ..and so on.
      - If things work out, coevolution generates a good solution without us having to define a ‘good’ strategy via an explicit fitness function

- Co-operative Coevolution:
  - Each population deals with a separate part of the overall problem
  - A solution combines individuals from each population
  - Appropriate when the overall problem is highly structured
- Competitive Coevolution:
  - One population of “solutions” to the problem that we are interested in coevolves against a population of “challengers” that must be defeated
  - Solutions are fit if they defeat many challengers.
  - Challengers are fit if they defeat many solutions.
    - Reminiscent of natural host-parasite or predator-prey coevolution.

- The first coevolutionary GA was due to Hillis (1990) and was applied to solving a list-sorting problem.
  - What's the most efficient way to sort a list of length  $n$ ?
  - Hillis pitched a population of 'hosts' (sorting networks) against a population of 'parasites' (each a set of lists to be sorted)
  - He initialised his host population with a reasonable solution and initialised his parasite population with random lists
  - Hosts rewarded for sorting parasite lists; parasites for being unsorted
  - In a few hours, he was able to coevolve a sorter that used 61 'gates'
    - Engineers had taken years to achieve a sorter with 60 gates

- History of  $n=16$  sorting networks
  - Batcher & Knuth (1964) **63** gates
  - Shapiro (1969) **62** gates
  - Green (1969) **60** gates (best known)
  - Hillis (1990): Evolved **65** gates...  
Hillis (1990): Coevolved **61** gates...
- Used in telecoms switches
- Now also relevant to GPUs
  - Saving even one gate can make a huge performance difference

## List Sorting Example



## Why Did Regular Evolution Fail?

Evolution (~65K hosts for 5K generations) had problems:

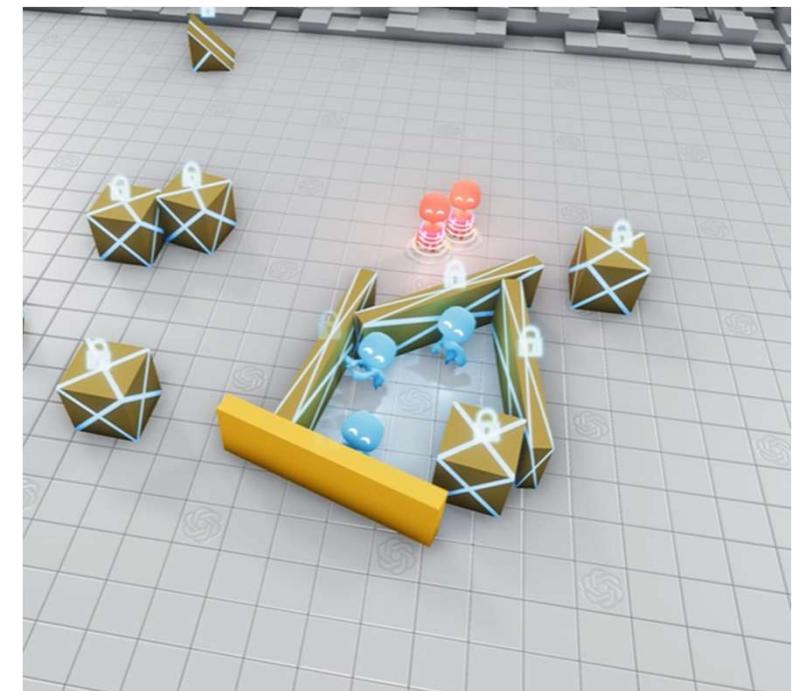
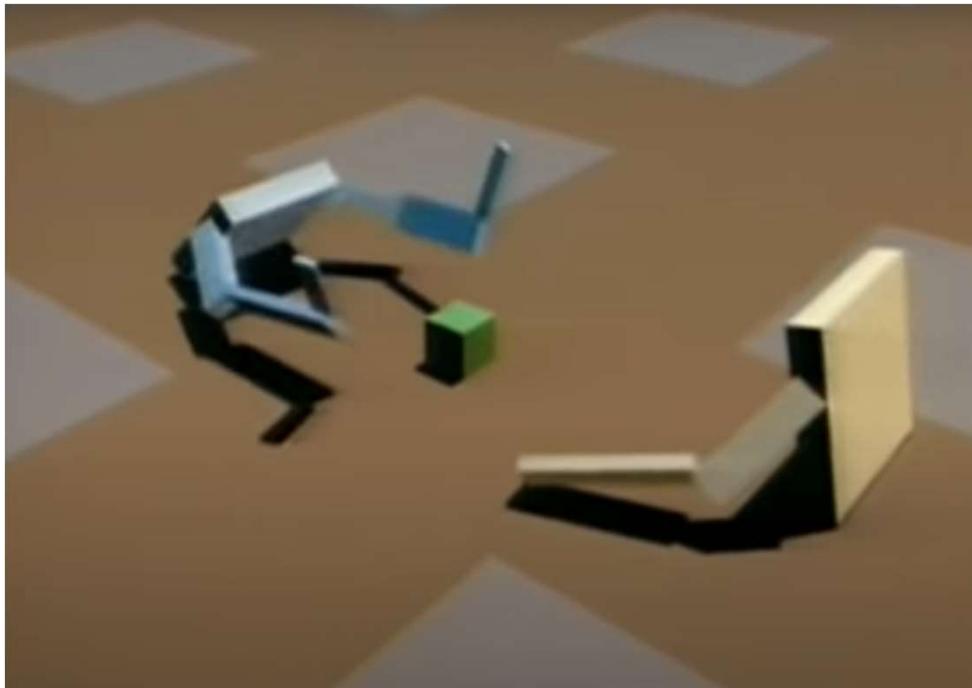
1. Many local optima: reasonable sorters are surrounded by rubbish
2. Exhaustive assessment is prohibitively slow
  - There are  $16!$  different lists to consider...
  - (Even reducing to  $2^{16}$  binary lists is still a lot to check for each sorter)
3. But assessing against a random sample of lists is also inefficient:
  - Most randomly generated lists are sorted by reasonable sorters
  - Really challenging lists are rare, so there's a lack of pressure to improve

## Why Was Coevolution So Much Better?

---

- Coevolution solved these problems automatically:
  - Instead of random lists, sorters needed to sort sets of lists that were selected to become harder and harder.
  - If sorters got stuck on a local optimum, parasites were under pressure to punish that strategy by finding the lists that it couldn't sort.
  - When improvements in the sorter population meant selection pressure got weaker, parasites were selected to get still harder.

From Karl Sims' (1994) *Blockies* to OpenAI's (2019) *Hide & Seek*:



**Thank you!**

# Coevolution II

Seth Bullock

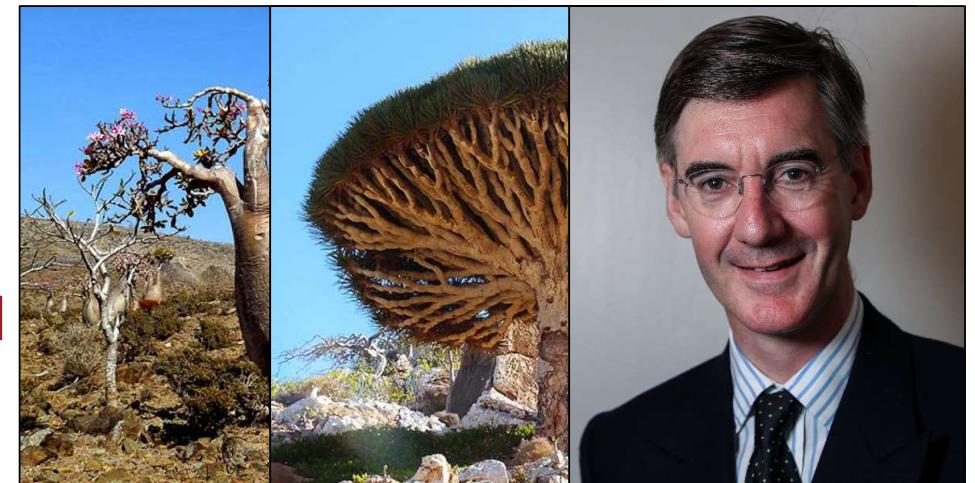
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- Coevolutionary arms races are supposed to *escalate* to increasing levels of sophistication... but sometimes that doesn't happen:
  - Stagnation: populations reach a poised state in which there is a turnover of individuals in the population but no phenotypic progress
  - Cycling: populations repeatedly cycle through the same weak strategies as if they were playing a game of scissors-paper-stone (the Red Queen)
  - Disengagement: every host is beaten by every parasite, all selection pressure is extinguished and coevolution effectively ceases (see Lab 2)
  - Measuring Progress: without a fitness function it can be difficult to assess whether genuine progress is being made by coevolving populations.

- To a large extent the problems with coevolution are familiar:
  - Our old foe: the loss of genetic and phenotypic diversity
- How can we stop the populations from converging and becoming vulnerable to stagnation, cycling, disengagement?
- Three different ideas:
  - Population structure
  - Fitness sharing
  - Reduced virulence

# Population Structure

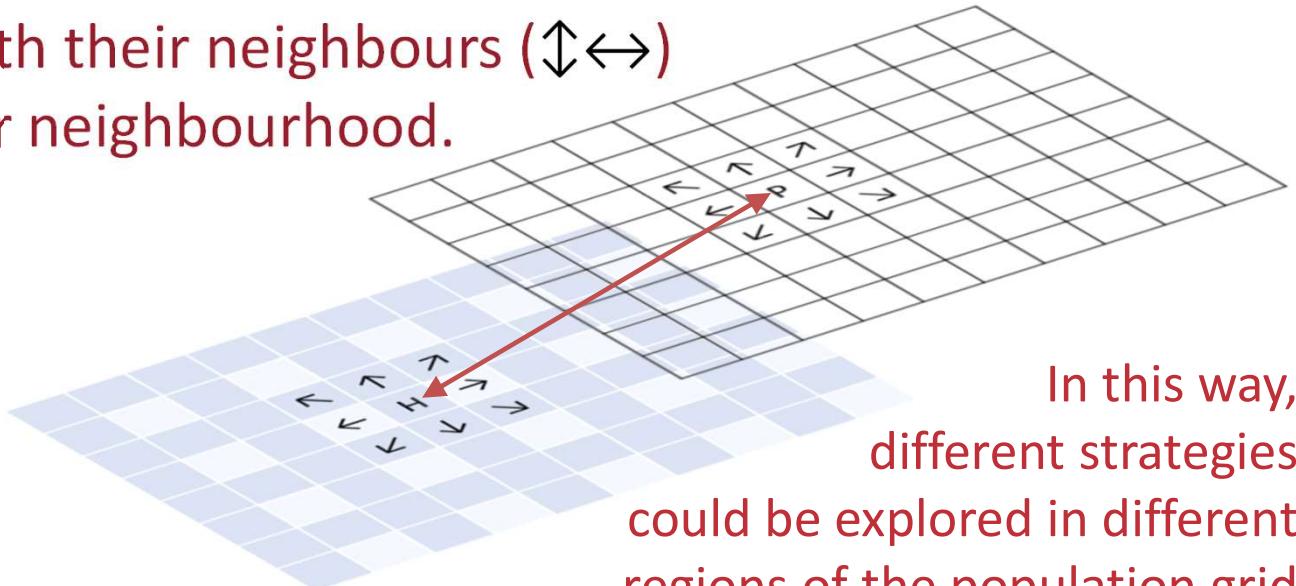
- The natural world is not randomly mixed up like an evolving soup.
- Populations are structured such that not every organism can interact with or compete directly with every other organism
- This is why island ecologies can be so distinctive and interesting
- GAs can do something similar
  - split populations into quasi-isolated sub-populations called ‘demes’
  - spread a population over a space and only allow local interactions



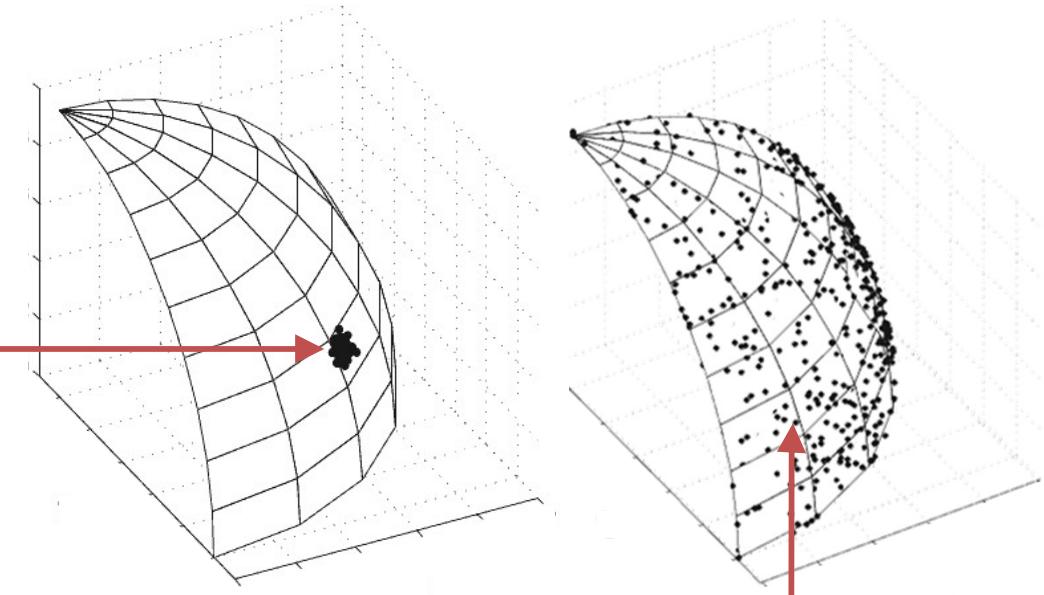
# Population Structure

- Hillis employed this idea in his list sorting work:
  - Each host was placed on a grid. Parasites were placed in a different grid.
  - Each host played the parasite at the same location in the other grid ( $\leftrightarrow$ )
  - Individuals competed with their neighbours ( $\uparrow\downarrow\leftrightarrow$ ) to leave offspring in their neighbourhood.

H	H	H	H	H	H	H	H
H	H	R	↑	↗	H	H	H
H	H	←	H	⇒	H	H	H
H	H	↖	↓	↘	H	H	H
H	H	H	H	H	H	H	H
H	H	H	H	H	H	H	H



- A more deliberate way of maintaining diversity is to punish solutions that are similar to other solutions in the population:
  - Define a similarity measure (e.g., genetic hamming distance < threshold)
  - If solution  $i$  is similar to  $n$  others:
    - $f'_i = f_i / \sum_{j=1}^{j=n} \text{sim}(i, j)$
    - Now, instead of converging on one region of this manifold of equally fit solutions...
      - ...fitness sharing pushes solutions to spread out

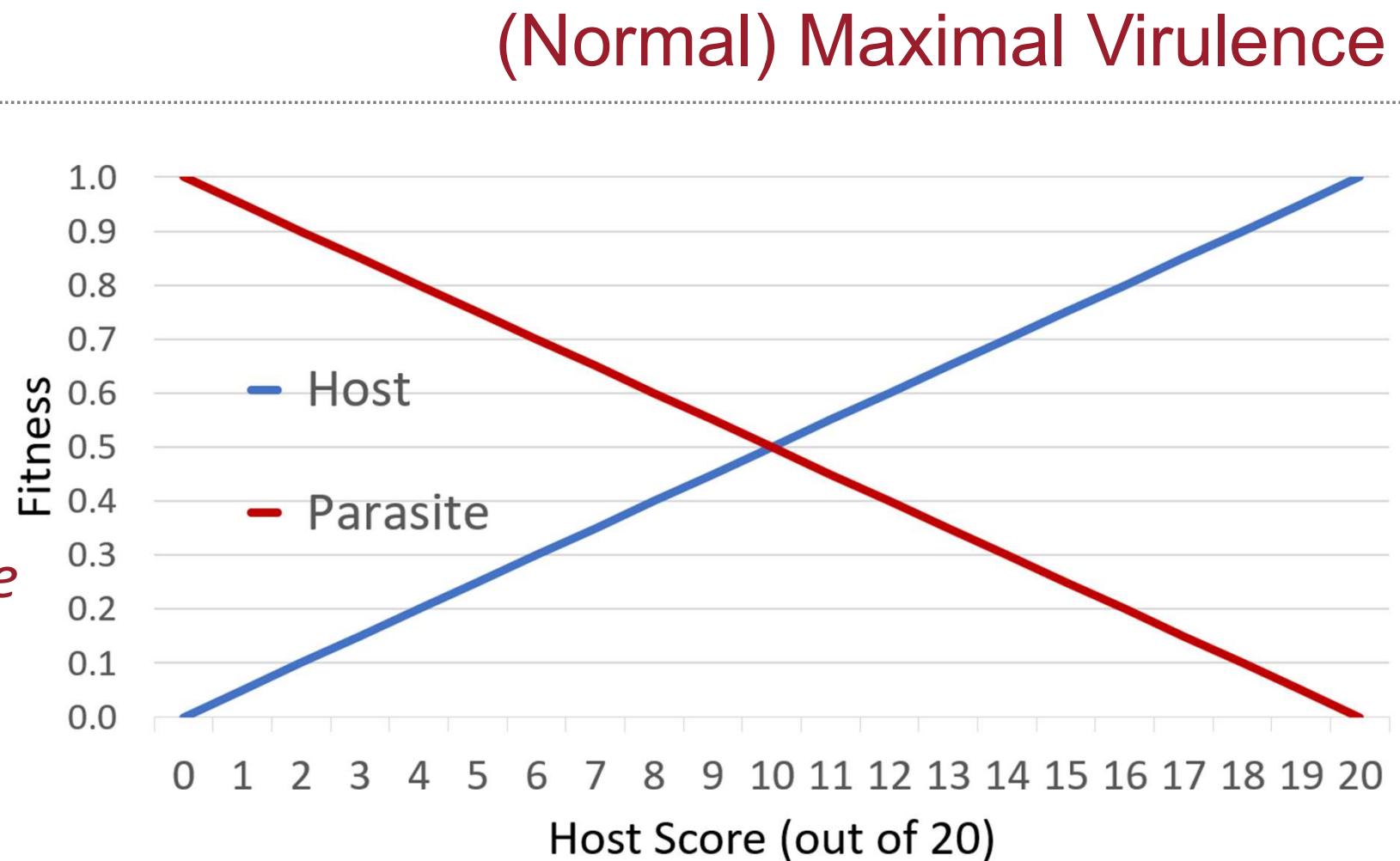


## Reduced Virulence

- Natural parasites / viruses often reduce their *virulence* over time
  - ...it's not in their interest to kill their host quickly.
  - Consider the common cold or a tapeworm vs. extremely virulent Ebola
- But parasites in a coevolutionary GA are often rewarded for being *maximally damaging* to the hosts that they are assessed against...
- Our initial random robot goalkeepers won't benefit from facing penalty takers that smack the ball into the top corner every time.
- It would be better to start off with shots that are easy to save, and then get gradually harder...

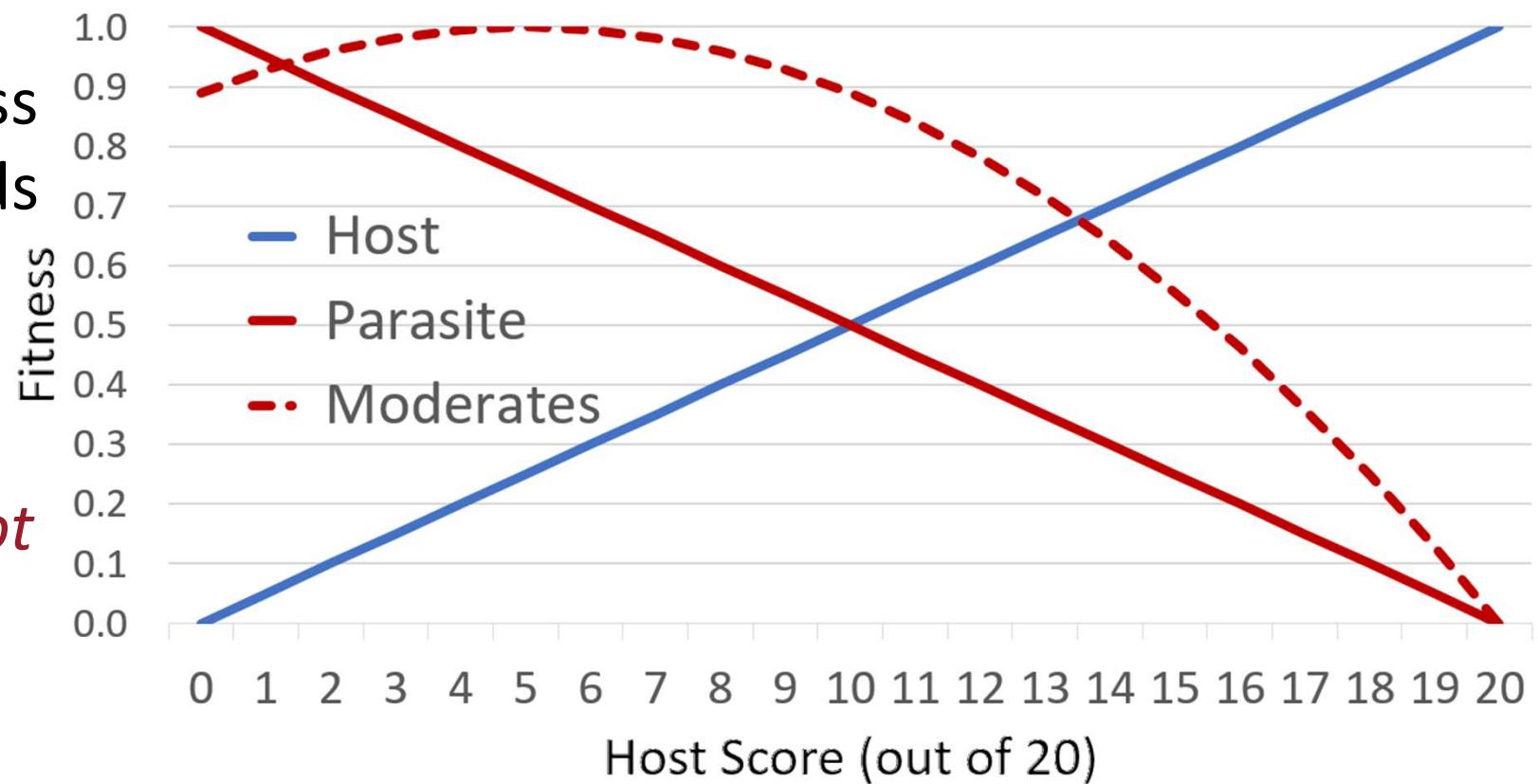
Normally, when a parasite plays against a host:

- If the *Host* scores  $x$  ...
- ... the *Parasite* scores  $1-x$



## Reduced Virulence

A ‘moderate virulence’ fitness function rewards parasites most for defeating hosts *most of the time, but not all of the time...*



- More on these ideas in this weeks' GA Lab
- Ahead of the lab, please take a look at
  - Cartlidge, J. & Bullock, S. (2004). Combating coevolutionary disengagement by reducing parasite virulence. *Evolutionary Computation*, **12**(2), 193-222.
  - This lays out the details of the virulence idea, and introduces a simple game that we will be using to explore it.
  - It's a long paper, so don't feel you need to deep read all of it. ☺
    - Just focus on sections 1-4 (15 pages)

## Free Lunches?

- Recall Wolpert & Macready's (1995) No Free Lunch theorem
  - No search alg. can do better than random across *all* problems.
- More recently, in 2005, the same authors claim that *coevolutionary* free lunches are possible...
  - By using a separate (non-random) population to steer its search, a search algorithm may be able to always rule out some bad solutions, and thus out-perform random search...
- Check this stack exchange [post](#) for some intuitions...

## Example Questions

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- Give an example of coevolution from nature. [1 mark]
  - Name 3 problems that beset coevolutionary GAs. [2 marks]
  - Why did Hillis embed his populations on a grid? [4 marks]
  - What is premature convergence in a GA population. How do coevolutionary GAs hope to avoid it? [4 marks]
  - Explain why a coevolutionary GA might cycle through the same poor solutions over and over again, rather than finding a better general purpose solution. [6 marks]
-

**Thank you!**

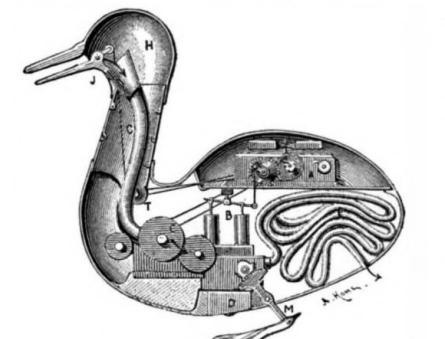
# Artificial Life

Seth Bullock

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- Artificial Life is a sister discipline for Artificial Intelligence
- Both take a functionalist approach to a mysterious subject:
  - AI: an artificial system can be *intelligent* if it is organised right
  - Alife: an artificial system can be *alive* if it is organised right
- Like AI, Alife combines a Strong project and a Weak project
  - Strong Alife: creating life inside a computer or in a robot
  - Weak Alife: understanding life by building life-like systems
    - Alife's pithy strapline: "The study of life-as-it-could-be"

- Chris Langton named + founded Artificial Life in 1987
- But Alife has been going on for much longer than AI
  - Frankenstein, Golem, various ‘Automata’ and ‘Living Machines’:
  - Vaucanson’s Duck (1739): quacking, drinking eating, “excreting”
- The biggest names in CS were in fact Alifers...
  - Babbage: Evolutionary Models of Miracles
  - Turing: Models of Biological Morphogenesis
    - Von Neumann: Self-Reproducing Machines

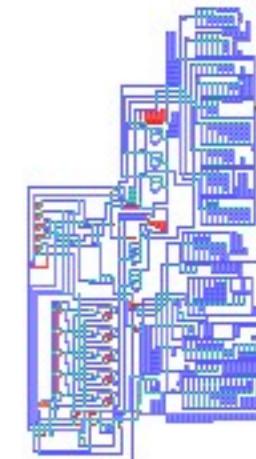


INTERIOR OF VAUCANSON'S AUTOMATIC DUCK.  
A, clockwork; B, pump; C, mill for grinding grain; F, intestinal tube;  
J, bill; H, head; M, feet.

## Self-Reproducing Machines

- How could a machine make a more complex copy of itself?
- This conundrum sounds impossible – paradoxical
- Von Neumann arrived at a two-part solution in 1948:
  1. Information encoding the structure of a machine ...DNA
  2. Machinery that uses the information to make a new machine + a new copy of the information ...cellular machinery
- In doing so, JVM predicted the contents of our cells...  
...before the 1952 discovery of the DNA double helix.

- But John Von Neumann went further than theorising and actually designed the first self-replicating machine!
- The first “Cellular Automaton” (CA):
  - A grid of cells, each containing a value
  - All values are updated according to a set of rules applied to each cell grid
    - Careful design of the rules plus the initial state of the grid, and...

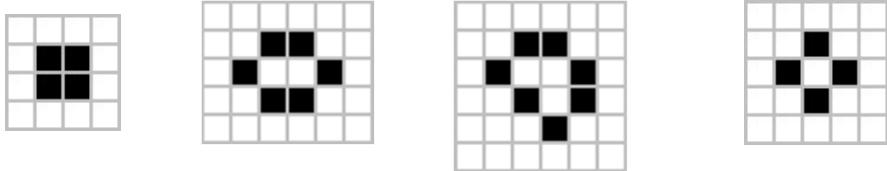


## Conway's Game of Life

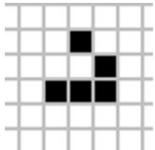
- You may be familiar with the most famous CA: Game of Life
- John Horton Conway (1937-2020) created the *Game of Life* in an effort to make a CA that had interesting behaviour:
  - Proliferating, repeating patterns; universal construction; etc.
- He settled on the following simple rules:
  - Each cell has a binary state – it can be alive or it can be dead
  - A live cell with >3 living neighbours or <2 living neighbours dies
    - A dead cell with three living neighbours becomes alive

# Conway's Game of Life

- Some configurations are static:



- Some oscillate on the move:

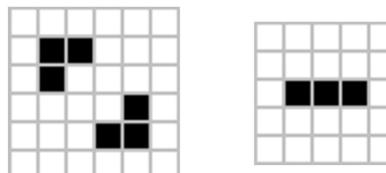


- A “glider”

- Some destroy each other when they collide in the right way...

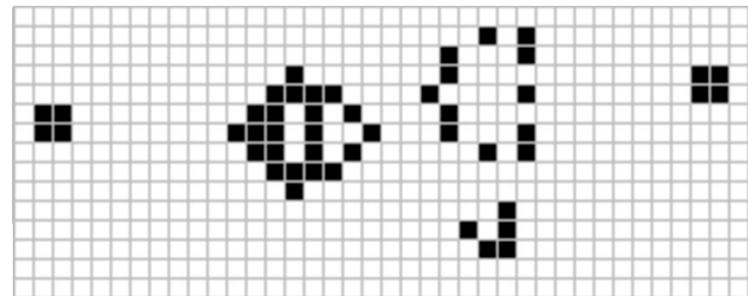
- Amazingly, the Game of Life is provably Turing Complete...

- Some oscillate in place:



- A “beacon” and a “blinker”

- Some *generate* other structures: e.g., a *glider gun*

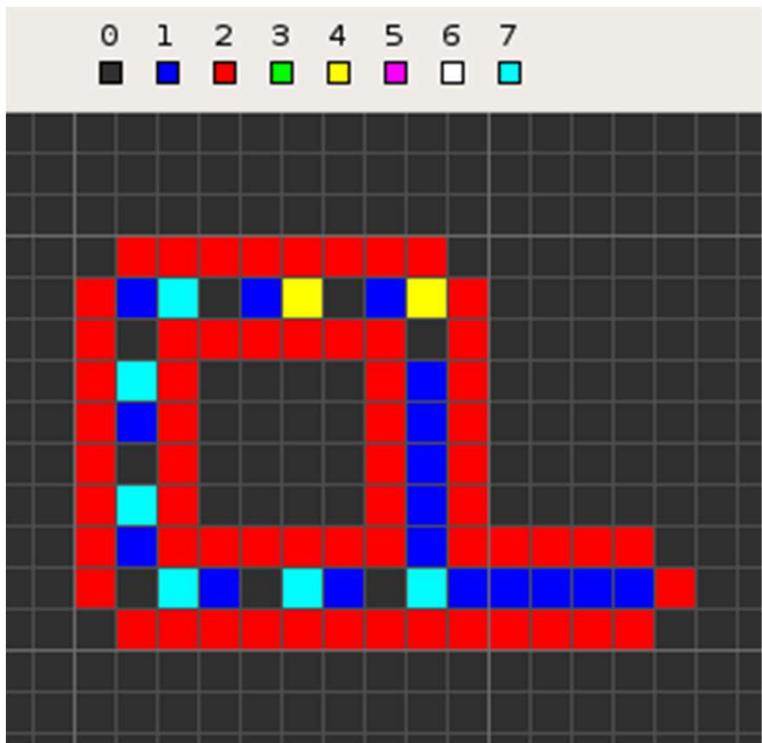


Life in Life  
Phillip Bradbury  
Roger Pincombe

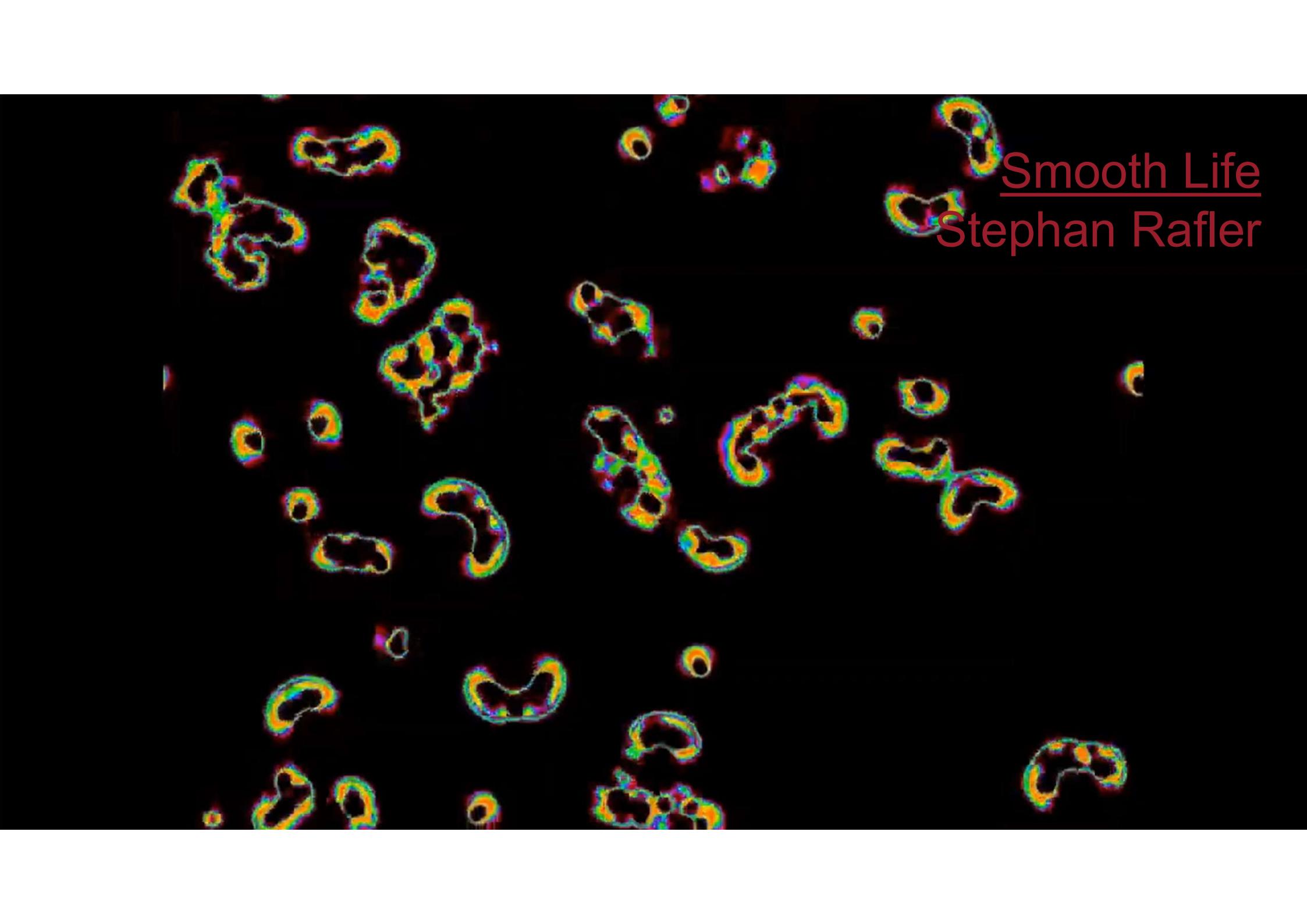


## Langton's Loop

- Langton studied CAs + made a more simple self-replicator:



- Some CAs are boring, dead, inert, fixed;  
...some just repeat; some are messy chaos;  
...and some are ‘interesting’ for a long time
- What is the physics of this complexity?
- Self-replicators + some kind of mutation =  
the possibility of *evolving replicators*...
- But how can truly ‘open-ended evolution’  
be achieved in artificial systems?



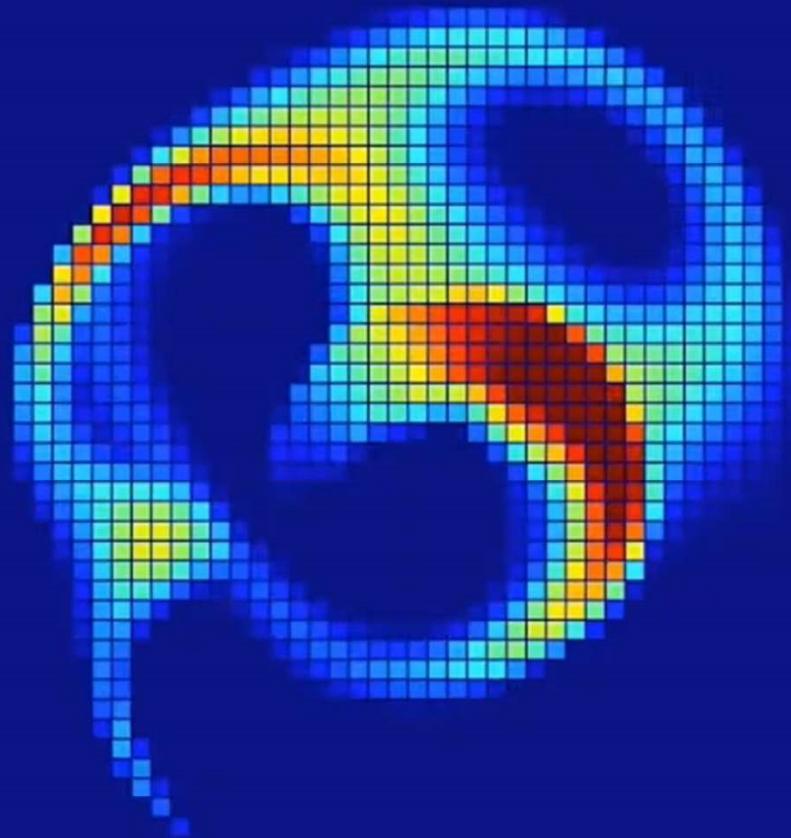
Smooth Life

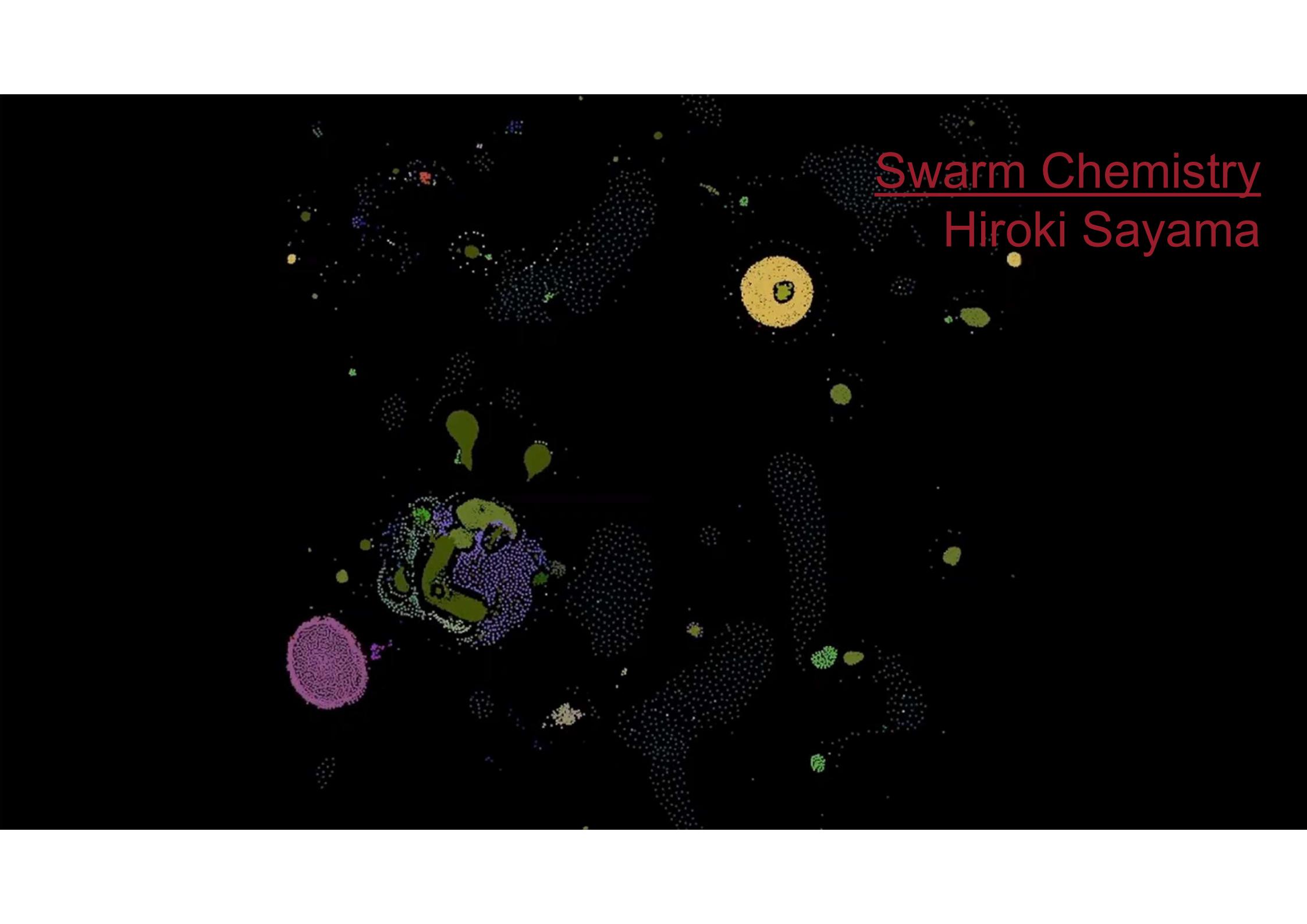
Stephan Rafler



Smooth LifeL  
(Tim Hutton)

Lenia  
Bert Chan

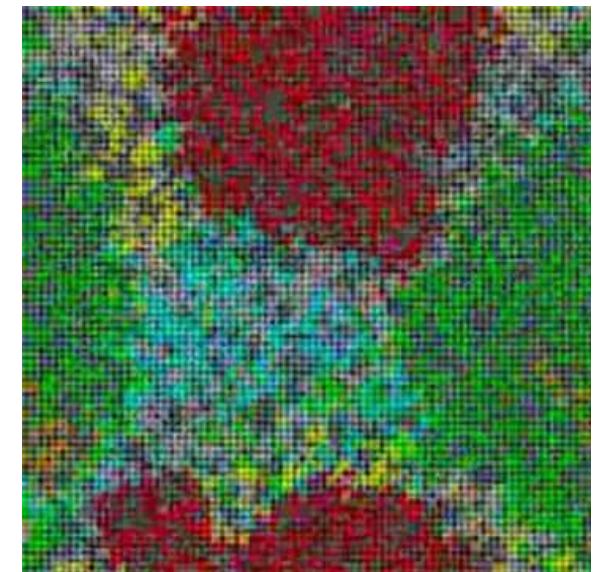
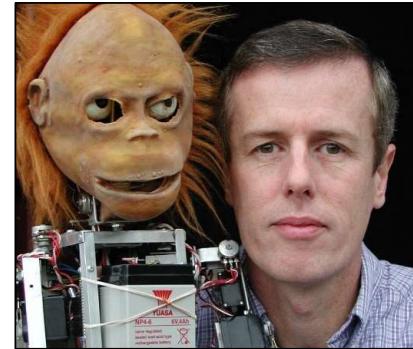




# Swarm Chemistry

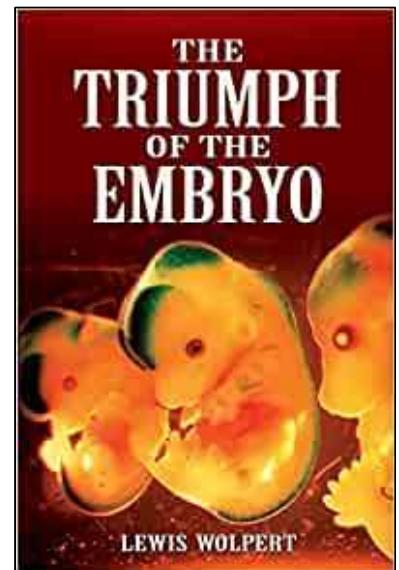
## Hiroki Sayama

- Other Alifers explored the evolution of “digital organisms”:
  - Tom Ray’s *Tierra*: from replicators to parasites to hyperparasites
  - Chris Adami’s *Avida*: a kind of digital evolutionary laboratory
  - Alastair Channon’s *Geb*; Yaeger’s *Polyworld*.
  - Steve Grand’s video game: *Creatures*

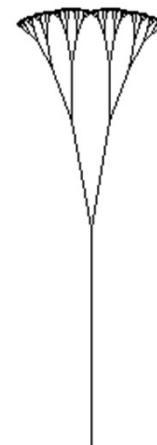


## From Evolution to Development...

- Real biological lifeforms *develop* over time: morphogenesis
- Understanding how exactly an egg grows into a person is still one of the most profound scientific challenges
- Since before Turing: *growing* an AI has looked far more feasible than hand-crafting one
  - How can artificial systems grow and develop?
  - How can this development be steered or guided?



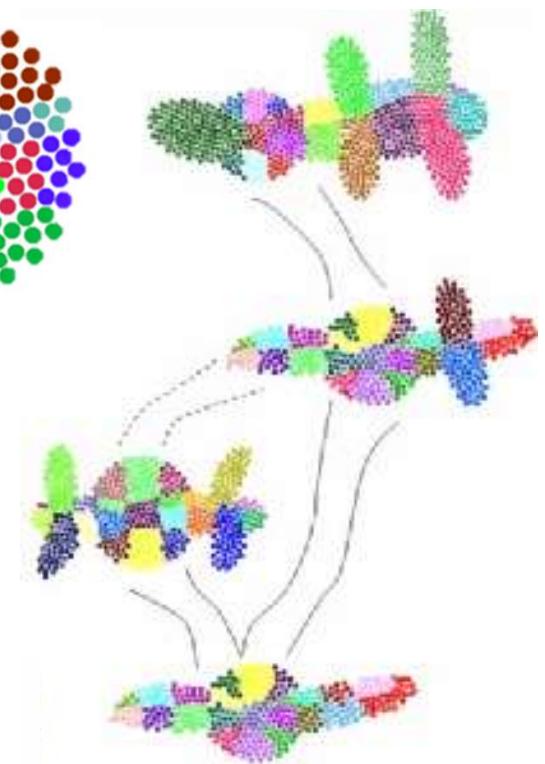
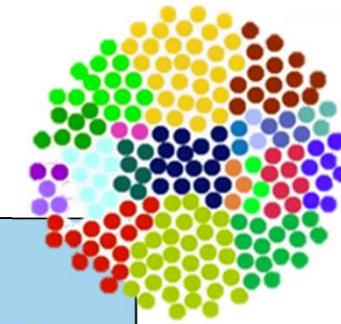
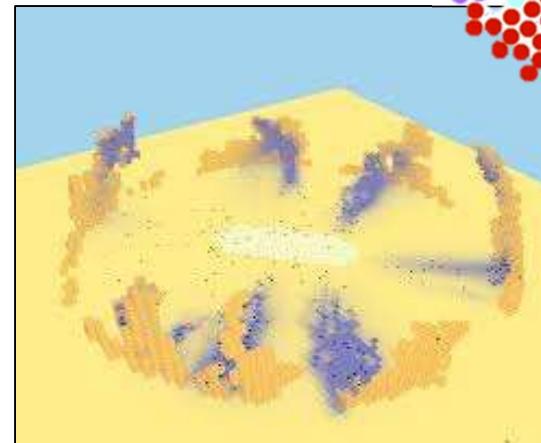
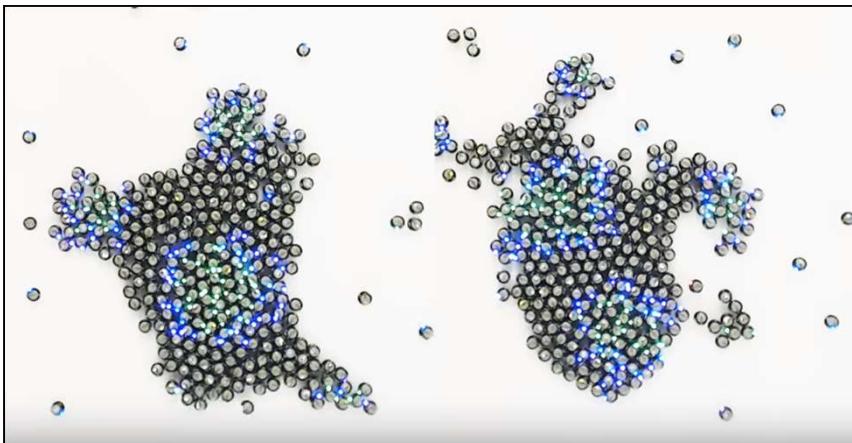
- Lindenmayer Systems, Aristid Lindenmayer (1925-'89)
  - A model of plant development based on grammar rewriting
  - In language:  $S \rightarrow NP+VP$ ;  $VP \rightarrow V+NP$ ; etc., etc.
  - In L-Systems:  $I \rightarrow Y$
  - More complex rules:



Przemysław Prusinkiewicz, A. Lindenmayer (1990). *The Algorithmic Beauty of Plants* [bristol.ac.uk](http://bristol.ac.uk)

# Artificial Morphogenesis

- Morphogenesis is still a growing area of research in Alife: 😅
  - “Morphogenetic Engineering”
  - Swarm Construction

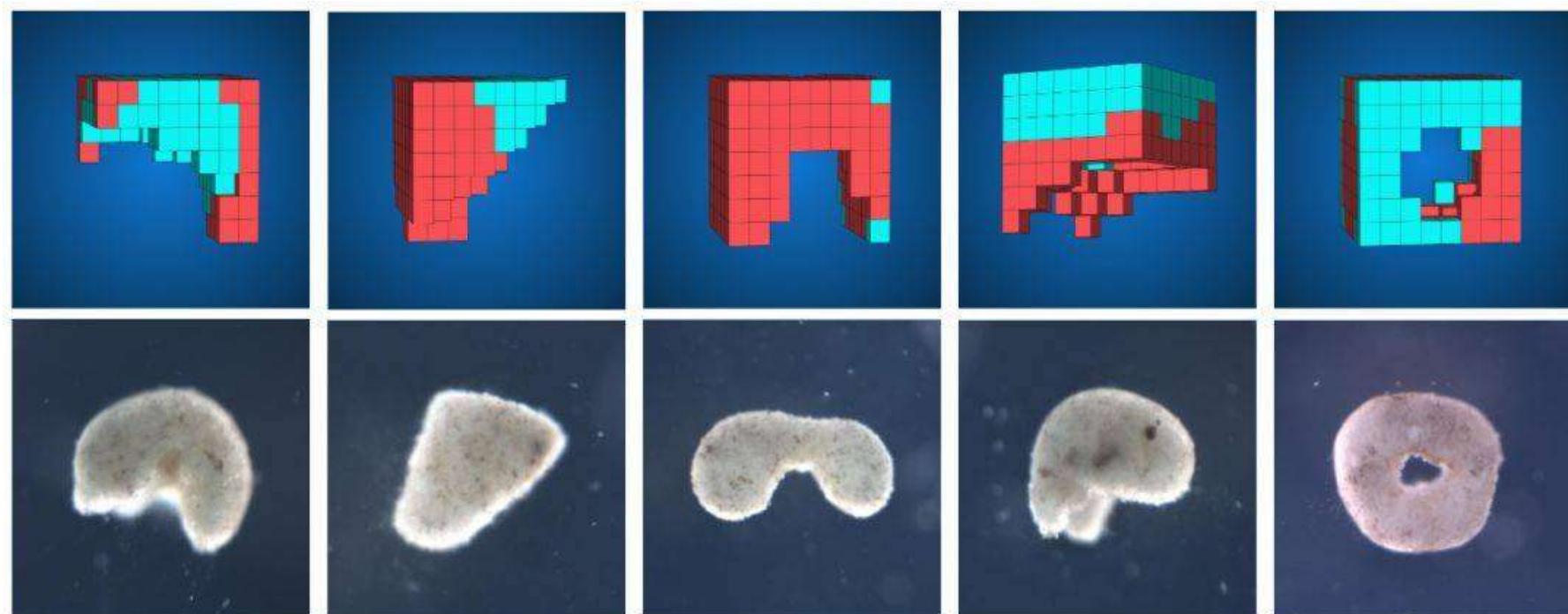


- Evo-Devo Soft Robotics

1



Robotics + soft-body simulation + evo-devo + bio-chemistry...



Josh Bongard (Vermont), Michael Levin (Tufts) and collaborators

[bristol.ac.uk](http://bristol.ac.uk)

## Types of Alife

Alife combines many disciplines ... and considers different life forms:

- Computer Science
  - Robotics
  - Biology
  - Physics
  - Chemistry
  - Philosophy
  - Linguistics
- + more

- Soft Alife: digital life
- Hard Alife: robotic life
- Wet Alife: biochemical life
- Whereas AI has focussed on:
  - Reasoning, Planning, Logic, etc.
- Alife has focussed on:
  - (Co-)Evolution, Development, Learning, Self-Organisation, Emergence, Origins of Life, etc.

# Open Problems

In 2000, a group of nine prominent Alife researchers authored a journal paper: “Open problems in Artificial Life”: 14 challenges that are still live + relevant...

- How does life arise from the non-living? (5 problems)
  - Achieve the transition to life in an artificial chemistry.
  - Simulate a unicellular organism over its entire life cycle.
- What are the potentials and limits of living systems? (5 problems)
  - Determine what is inevitable in the open-ended evolution of life.
  - Develop a theory of information processing, flow and generation for evolving systems.
- How is life related to mind, machines, and culture? (4 problems)
  - Demonstrate emergence of intelligence in an artificial living system.
    - Establish ethical principles for artificial life.

# Women in Alife!

Pauline  
Hogeweg

Janet Wiles

Alex Penn

Jitka Čejková

Katie Bentley

Mizuki Oka

Sabine  
Hauert



Charlotte  
Hemelrijk



Barbara  
Webb



Lana  
Sinapayen



Emily  
Dolson



Melanie  
Mitchell



Hemma  
Philamore



Susan  
Stepney

## Further Reading

- Langton, C. (1989). [Artificial life](#), in *Artificial Life*, Addison-Wesley.
- Lehman, Clune, Misevic, Adami, et al., [52 authors!] (2020). [The surprising creativity of digital evolution: A collection of anecdotes from the evolutionary computation and artificial life research communities](#). *Artificial Life*, 26:2, 274-306.
- International / European Alife Conference proceedings at [alife.org](#)
- The *Artificial Life* journal at [MIT Press](#) | Lana [Sinapayen's Prezi](#) 🔥
- Hiroki Sayama's [PyCX](#) Python package and associated [text book](#)
  - [NetLogo Life](#), [Alife Virtual Seminars](#),  [Alife Papers](#)

## Example Questions

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- Which cells in the Game of Life grid shown below will survive to the next time step, and which will not? *[2 marks]*
- How did Von Neumann's insight into self-replicating machines anticipate the DNA molecule? *[4 marks]*
- Why might it be more feasible to grow a general purpose AI rather than code one by hand? *[4 marks]*
- Apply two iterations of the following L-system rules to the starting shape shown below. *[3 marks]*

**Thank you!**