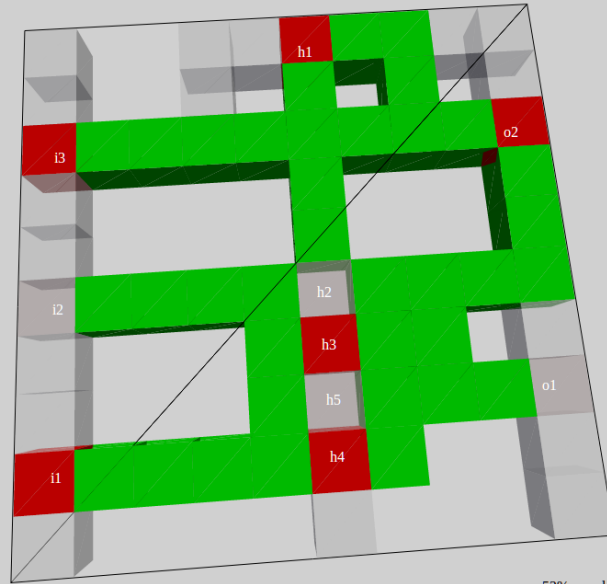


Feedforward Networks generated by Cellular Automata and tuned via optimization algorithms

Walt Woods, 2014

Click and drag to rotate; right click and drag to move; mouse wheel to zoom
i1 - 1



53% populated after 200 step(s); 0 possible updates
Using 67.9% of wires in connections; 100% after 1800 evaluations
2.0 avg connectivity; 6.8 avg length
3:5:2 inputs:middle:outputs, updated via METHOD_TWO
10 cells per side; ☐ Flatten hidden layer
o1=(i1+i2+i3)&1; o2=i1+i2+i3 > 1
☐ 3D

Reset

Next

Finish

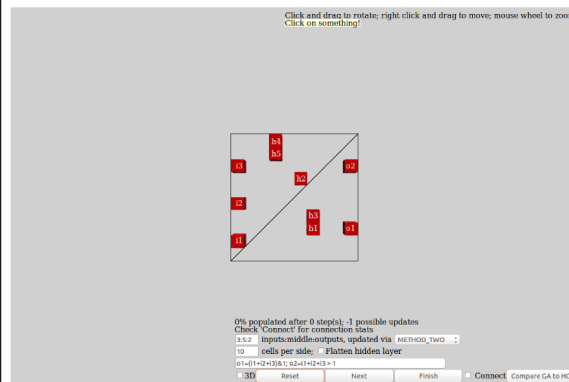


Connect

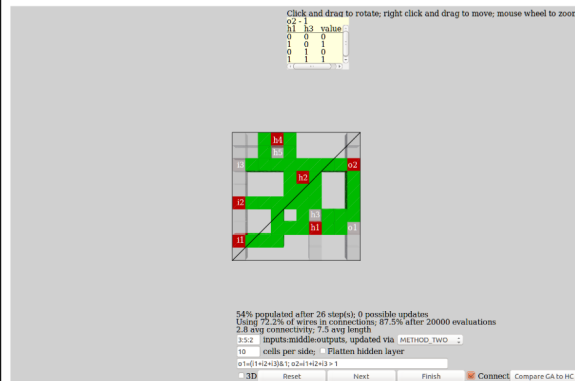
Compare GA to HC

Screenshot

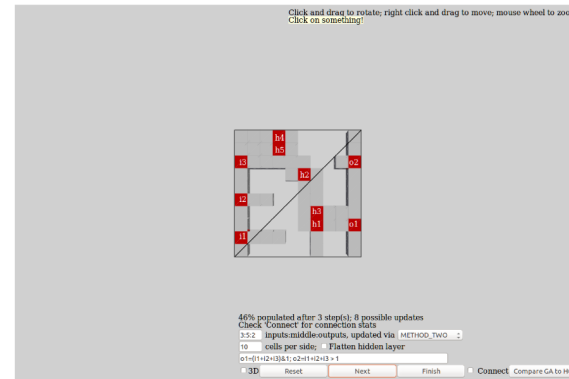
Basic operation - adjust parameters and press "Reset"



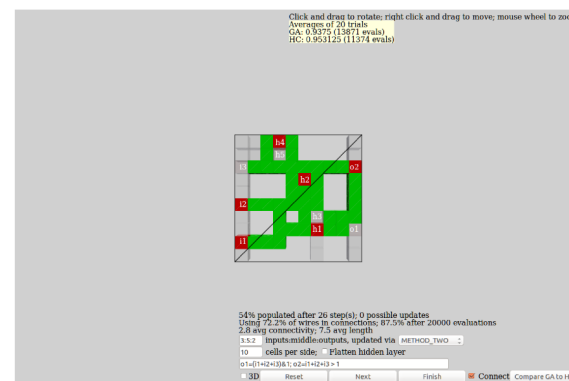
When done, click "Connect" checkbox to determine which nodes are valid inputs for other nodes and run GA; clicking on a node shows its connectivity table.



Click "Next" (or press and hold) to watch CA grow



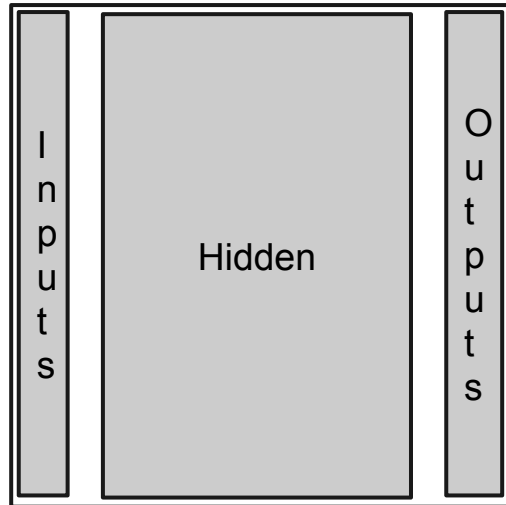
The "Compare GA to HC" button runs the current network through both Genetic Algorithms and Hill Climbing algorithms, and shows stats about which performed better.



Basic GUI usage

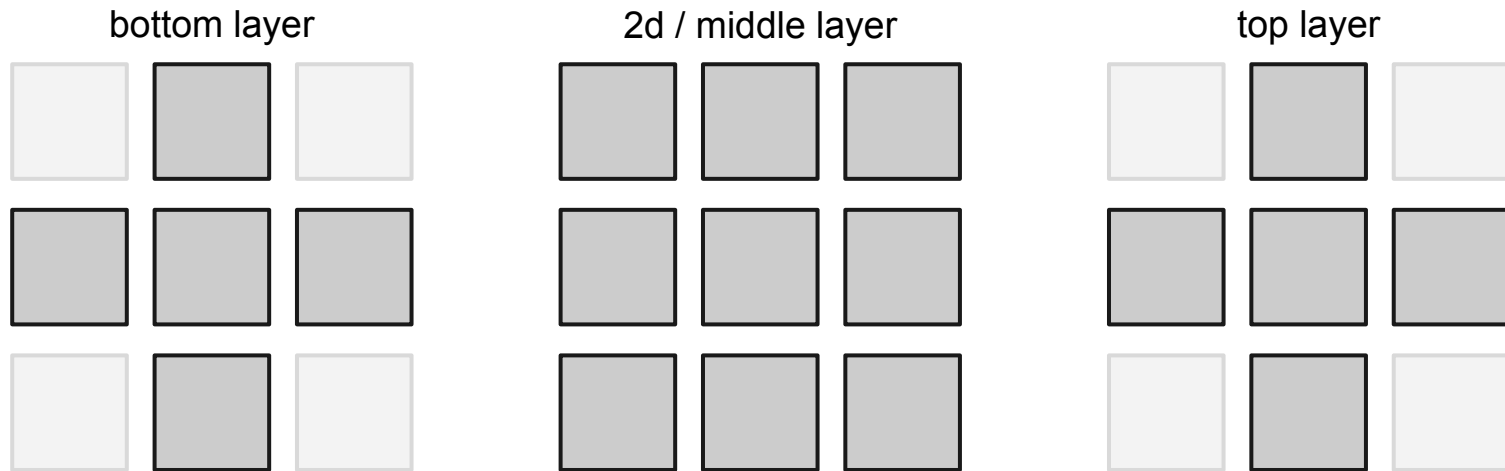
Seed distribution

- Left edge, right edge, hidden layer in the middle (buffered, possibly flattened)

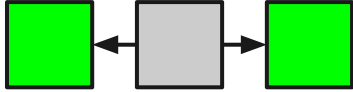


Growing a network

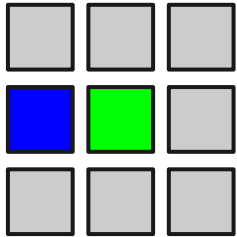
- Stolen from Project 2
- Moore-ish neighborhood



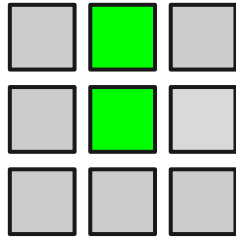
Neighborhood rules

- Axis-aligned neighbors are “spawners”; diagonals (other cells) are “inhibitors”
- Poles 
- If a neighbor is a spawner and a seed, then cell becomes populated
- Otherwise, if there is at least one spawner...

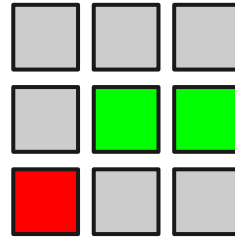
Everybody loves pictures



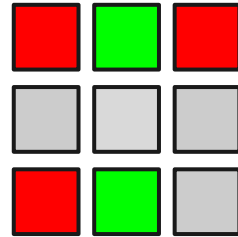
Any spawner is a seed



Exactly 1 spawner,
no inhibitors



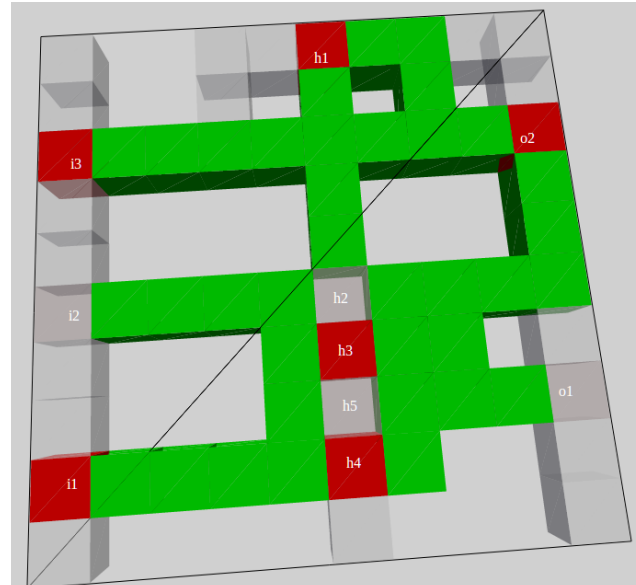
Exactly 1 spawner
and 1 inhibitor, not on
edge of world



Completed pole, less
than 4 inhibitors

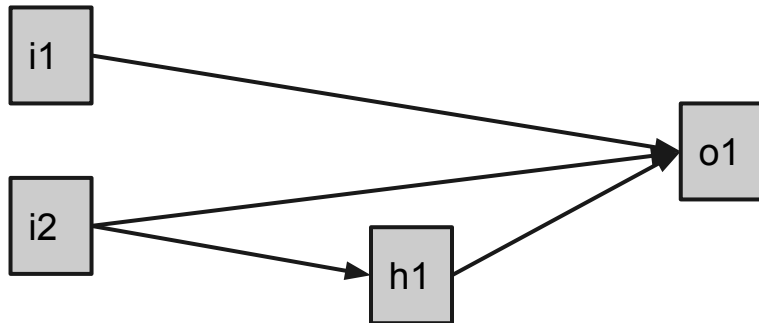
Connectivity rules

- No diagonals
- Feed-forward enforced
- Several signals share a wire
- Output connectivity is forward only, not lateral

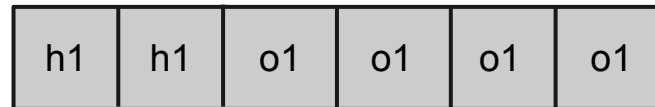


Assembling a genome

- Generate a connectivity table, order it according to calculation order



i2 is input to h1 which is input to o1, so o1 does not register i2 as an input.



h1 has 1 input, o1 has 2 inputs;
genome becomes $h1 = 2^1$ bits,
concat o1 = 2^2 bits \Rightarrow 6 bits long

Mix & match (genetics)

- Choose two parents based on monte carlo selection based on square of score
- A genome scoring 50% correct output has 4x chance of being parent as genome with 25%
- Pick a splice point, generate a single child with genes from $B < \text{splice}$ then Parent 1, $B \geq \text{splice}$ then Parent2
- Mutate at least one bit, but up to 30% of the genome (with decreasing intensity in subsequent generations)

Hill climbing

- Single parent, asexual reproduction. Each child mutates bits in a single segment of the genome (corresponding to a single neuron's output table). If the child performs better than the parent, it modifies the same section, but less bits. If the child performs worse, it resets to the parent and modifies a different segment.

Demo time

<https://wwoods.github.io/nanowire>

Quiz time!

...for me. Questions?

Thank you!

What did the seed say to the nanowire? ...
You're growing on me!