I will describe a computational experiment in which a selection-mutation process evolves neuron-like cells, combining evolutionary and biochemical dynamics. The simulated organisms, called agents, are designed to resemble single cells, each of which has an internal state consisting of counts of abstract molecules, plus a genome that specifies how they interact. These artificial reaction networks can perform any bit-wise computation. For this project, the goal is to start with random genomes and subject them to selective breeding, mutation, and recombination so that they evolve the ability to detect coincidences in a spike train, one of the essential timing-based computations performed by living neurons. When two input spikes arrive separated by a short delay, the agent should fire an output spike of its own, but when spikes arrive widely separated, the agent should produce no output spike. During the selective breeding process, agents are rated based on how well they process a variety of spike trains, and are more likely to survive and reproduce if they earn a high rating. Once the population has discovered good solutions to that basic coincidence detection task, agents are given an additional Hebbian learning task. After receiving many closely spaced spikes, they should fire more eagerly even when spikes arrive somewhat separated. After a period of low activity, they should fire more skeptically, only after spikes arrive very close together. The simulation generally succeeds, discovering genomes encoding reaction networks that transfer activity from input to output, but with feedback loops that inhibit the transfer and only allow it to succeed when input spikes are close. Some of these inhibitory reactions are themselves inhibited by sustained input activity, accomplishing the Hebbian learning task using a mechanism similar to that of NMDA receptors. The population maintains considerable genetic variation, and takes advantage of gene duplication as it evolves successful mechanisms.

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