**Why epochal evolution "fails"---or why it takes a very large number of steps.**

Figure 6 “log mean evolutionary steps vs log redundancy” shows that the reason why epochal evolution requires many steps: it is because the target phenotype has low redundancy. Recall that K complexity is strongly inversely related to redundancy, so this can be approximately restated as epochal evolution takes many steps when the K complexity of the target phenotype is high. For the 3 and 4 input cases, the properties of the starting genotype don’t seem to matter.

I am attaching a link to a Google Collab copy of a Jupyter notebook which shows how an epochal evolution takes an extremely large number of steps for a 3-input goal. From this example, we can infer some additional properties of epochal evolution to a low-redundancy high-complexity target.

Cell [18] shows epochal evolution starting from a circuit of the phenotype [0x0055] to a goal of [0x00b6] which succeeds after 157257 steps. Evolution goes through 4 epochs:

[0x0055] --> [0x0005] --> [0x00f5] --> [0x00bf] --> [0x00be] --> [0x00b6].

Table of redundancies and K complexity of epochal phenotypes:

|  |  |  |  |
| --- | --- | --- | --- |
| Phenotype | Log Redundancy | K complexity | steps |
| [0x0055] | 8.6 | 1 |  |
| [0x0005] | 8.2 | 1 | 1 |
| [0x00f5] | 7.9 | 2 | 2 |
| [0x00bf] | 7.7 | 2 | 96 |
| [0x00be] | 5.2 | 4 | 349 |
| [0x00b6]. | 3.3 | 6 | 156908 |

We see that redundancy decreases and K complexity increases as epochal evolution proceeds. The last epoch takes by far the most steps.

In cell [18] of the example notebook, the redundancy of the goal phenotype [0x00b6] is 1842 which is 1.8e-7 of the sum of the redundancies of all phenotypes. Each step of the final epoch does a mutation and checks to see if it is the goal. Assuming a random model, this should take 1/1.8e-7 = 5.6e6 steps. It succeeds in far fewer steps because of genotype correlations---a genotype is likely to have similar neighbors (Greenbury 2016). Thus, since the Hamming distance from 0x00be to 0x00b6 is 2, two corresponding genotypes are much more likely than random to be neighbors.

Why does increased K complexity imply many evolutionary steps? If the K complexity of the target is *k*, then any circuit that implements the target must include at least *k* active gates, and these gates must be inter-related to output the target phenotype. Thus, as *k* gets larger, there are more constrained gates. These seem to roughly correspond to constrained sequence positions for the RNA model.