

Unraveling the genotype-phenotype map of evolving digital organisms

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Digital evolution is a form of evolutionary computation in which self-replicating computer programs—digital organisms—evolve within a user-defined computational environment. This experimental tool provides a unique framework to explore the structure of a genotype-phenotype map. In this map, the sequence of instructions constitutes the genome of digital organisms and defines its genotype. In addition to produce an offspring, a digital organism may be capable of computing one or more logic operations (tasks) by executing the instructions of its genome. We call the number and identity of the tasks it can perform as the organism's phenotype. The ability to preserve the phenotype under genetic mutations (robustness) leads to the existence of genotype networks (i.e., a continuous network of genotypes—in which two genotypes are connected if one can be converted into another by a single point genetic mutation—having all the same phenotype). Indeed, genotype networks are indispensable for evolutionary innovations because they allow the exploration of novel phenotypes while preserving the old ones. This ongoing project will show that only the rare and complex phenotypes allow substantial innovation, and even those are constrained to a few common, simple and robust novel phenotypes.

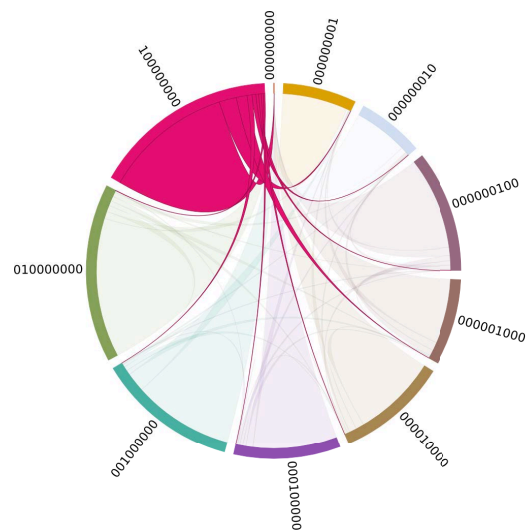


Figure 1: **Subset of the phenotype space.** Phenotypes are represented as a sequence of ones and zeros that indicate the logic function performed by the organisms with that phenotype (ordered clockwise following the complexity of the logic function performed, starting from the top). The arc length corresponding to each phenotype depicts the sum of the transition probabilities from that phenotype to the others (which are highly asymmetric). Transition probabilities of the most complex phenotype are highlighted. Only a few phenotypes are likely to be discovered from a given one, while most of them are unlikely to be encountered.