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### **Sex as an Algorithm, the Theory of Evolution under the Lens of Computation**

In their 2016 article, authors and professors Adi Livnat and Christos Papadimitriou attempt to shed light on some of the questions that remain regarding the theory of evolution. Namely, the mechanisms of genes and the role of sex in evolution. To accomplish this, they look at computational models of evolution, beginning with the genetic algorithms proposed by John Holland in the 1970s. They began their research with the aim of understanding why heuristics utilizing asexual reproduction dominate in optimization problems, while asexual reproduction in nature is extremely rare and transient.

One issue with sex that algorithms must overcome (using a method called elitism) is that recombination is inevitable, and so even the greatest genotypes will be lost in the very next generation. The authors investigated this seemingly flawed mechanism using an equation which describes how genotype frequencies change over generations and found that while in asexual evolution the best combination of alleles always prevails, natural selection in sexual evolution favors “mixable” alleles, which perform adequately across a wide variety of different combinations. When viewed as a randomized algorithm, sexual evolution is very efficient, since in order to evaluate an allele it may insert the allele once and sample from all possible genetic combinations after only  $\log n$  generations, where  $n$  is the number of genes interacting with the allele.

In order to identify the quantity that genes are optimizing in sexual evolution, the authors present evolution as playing a coordination game. They found that genes use what is known in computer science as the multiplicative weights update algorithm to assign probabilities to alleles according to their mixability. Thus, sexual evolution seeks not to produce the greatest individuals, but rather a good overall population. The authors also discovered that mutation rates are not exactly random, but are in fact adaptive and context-dependent. Additionally, they found that evolution takes the interaction between genes into account when calculating fitness, in order to preserve the diversity of the population.

In the years following this article, the authors continued their work with the help of others to further develop the idea that sexual reproduction allows selection to favor mixable genes. They then extended their research to demonstrate the power of randomization in haploid and multilocus models. A more recent paper from Livnat's lab found that a malaria resistance mutation occurred more often in genes and populations where it was advantageous, providing important evidence of non-random mutation. These and other contributions continue to use the tools of computer science to uncover the fascinating mechanisms of evolution in nature.

I (Wyatt Miller) found presenting this article to be difficult on account of its length and technical details. I tried to cover as much of the material as possible within the time constraints, and while a script helped me to cover much of the article, it also resulted in a stale and non-interactive presentation. In hindsight, I would resolve this by reducing the amount of content and focusing on the salient points in a more engaging way.

### Works Cited

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- Melamed, D., Nov, Y., Malik, A., & Livnat, A. (2022). De novo mutation rates at the single-mutation resolution in a human HBB gene region associated with adaptation and genetic disease. *Genome Research*, 32(3), 488–498.