

Speciation Via Meiosis — Research Report

Purpose: The objective of this research was to explain the inconsistency between the *Speciation* paper and accepted evolutionary models — specifically the evolutionary convergence exhibited in the bimodal seed random mating experiment.

Background: In the speciation paper, the researchers explore how sexual selection can help induce sympatric speciation in a population. In order to observe population dynamics over many generations, the researchers created a simulated island inhabited by a population of finches. Each individual finch had a specific beak size and could only consume seeds that corresponded to that beak size. If the individual survived, it would mate with another individual on the island and produce an offspring who's beak size was the average of the beak sizes of the parents, plus a gaussian-random value to account for mutation. The most startling conclusion from this experiment was that given a bimodal seed distribution, a population that used sexual selection during mating would diverge to cover all available niches while a population that mated randomly would converge and only cover one. This result goes against conventional wisdom, as a species is highly incentivized to take advantage of all available niches in its environment. The convergence exhibited in the bimodal seed random mating scenario is known as bottlenecking, and typically only occurs in small, declining populations. To see bottlenecking occurring in a large, healthy population suggests that there's a lurking oversimplification in the simulation.

Hypothesis: The cause for the population convergence in the bimodal seed random mating simulation was due to the oversimplification of genetic inheritance. Averaging the beak sizes of the parents radically inhibits a population's ability to maintain genetic diversity, which leads to population collapse in multi-niche environments.

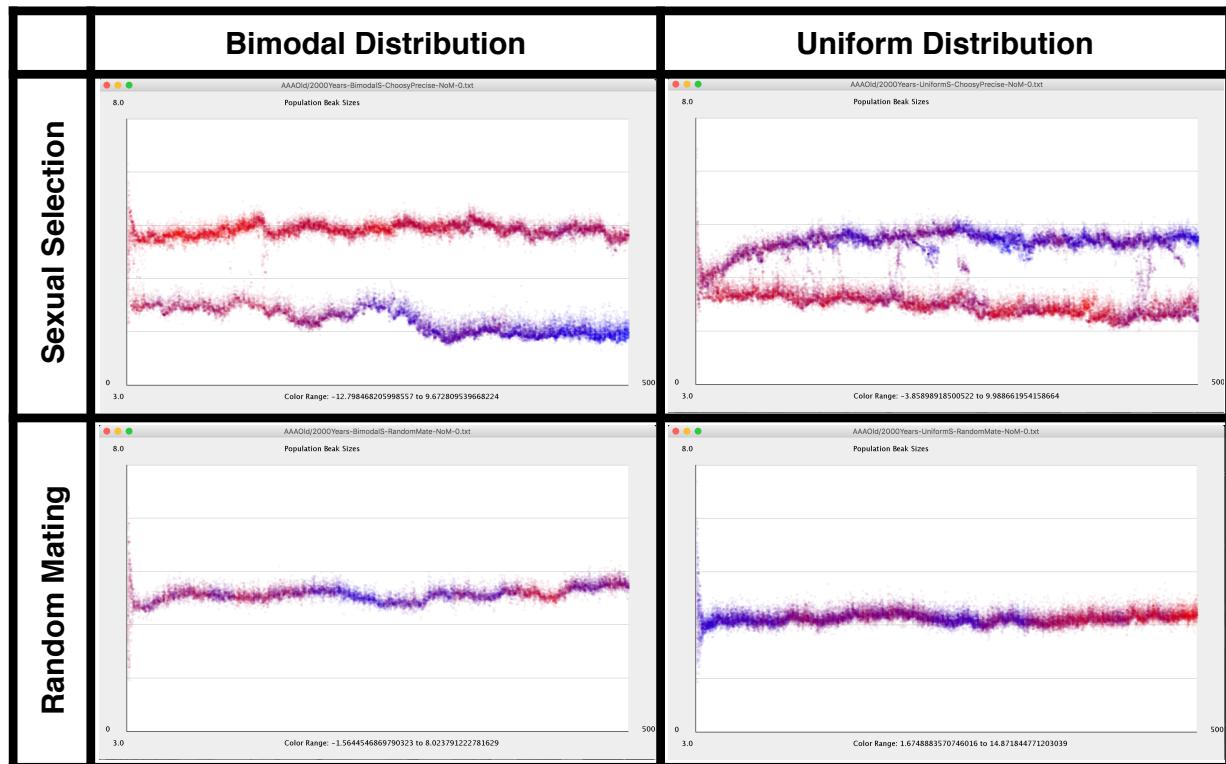
Experimental Design: In order to bring this experiment into line with the natural world, the simulation needs to be adapted to account for biologically accurate rules of genetic inheritance. Rather than a single numeric value, each finch is equipped with two sets of genes, one from each parent. Each gene contains an array of sub-genes, represented by a floating point value between zero and one. When mating, the genes undergo simulated meiosis. For each gene, the program randomly selects between the two sets and adds the chosen gene to the corresponding set in the child. After this process, the child will have two copies of each gene, one from father and one from the mother. During meiosis, each sub-gene also has a small chance to mutate, which randomly assigns the sub-gene a new floating point value between zero and one. For this experiment, a single gene was used to determine the beak size of the individual. This choice was made because a single gene, Bmp4, is responsible for most of the variation in beak sizes in real darwinian finches. To determine the beak size of the individual, the program generates a phenotype for each of the two genes by taking the sum of each of the sub-genes. The larger of these two phenotypes was assigned to the child as its beak size. This choice was designed to mimic complete dominance. Incomplete dominance and co-dominance were also coded for and achieved similar results. Finally,

to ensure that the changes in the results are purely due to inheritance rather than the new gene structure, the program also has a control method called pseudo-meiosis. During pseudo-meiosis, the genes from each set are averaged rather than randomly selected.

Results: The first step in this experiment was to ensure that the pseudo-meiosis control method maintained the results in the original experiment. These results are as follows:

- 1.) BSAM: Population divergence filling both niches.
- 2.) USAM: Population branching with high levels of hybridization.
- 3.) BSRM: Population converges around one niche.
- 4.) USRM: Population converges and wanders over time.

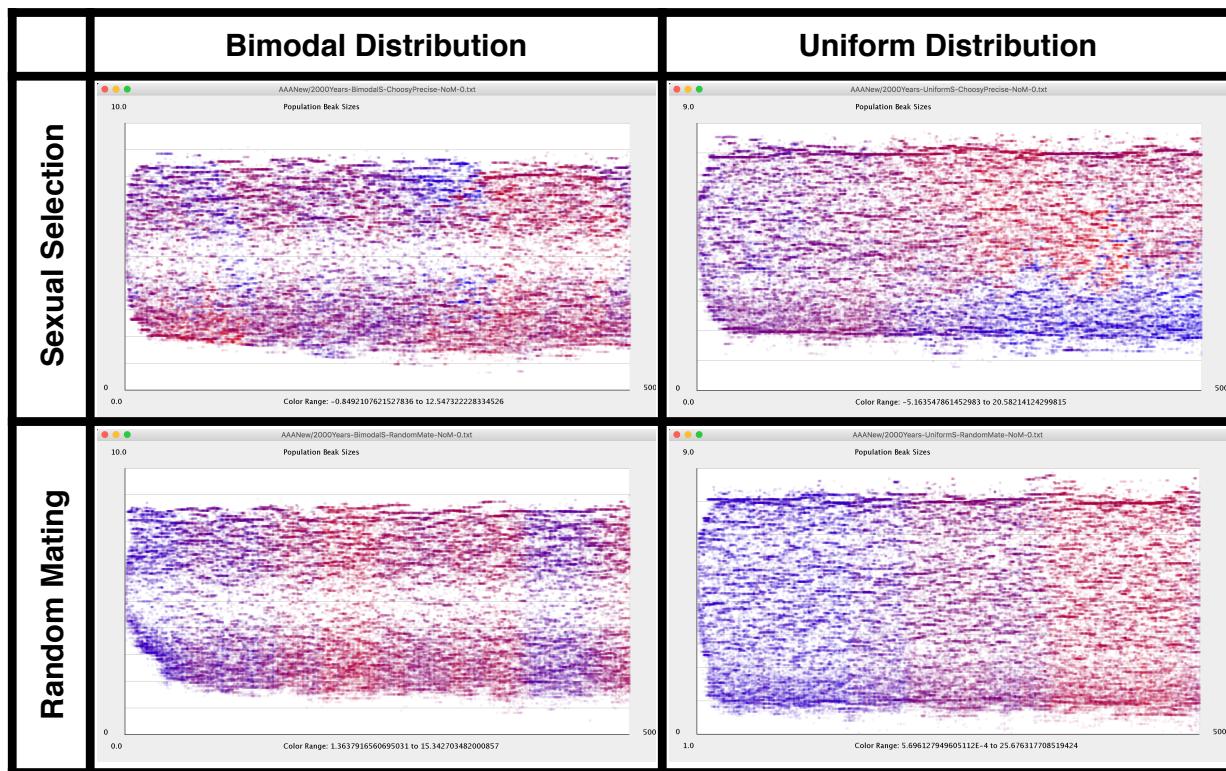
The results from the pseudo-meiosis method strongly reflect the results from the initial paper. These results are illustrated in the following graphs (Note that the scale for the y-axis begins at 3.0 and ends at 8.0).



The two biggest differences between the pseudo-meiosis method and the paper's results are that each population exhibits less variance and the USAM situation exhibits less branching. Both of these results are likely due to reduced mutation rates caused by the replacement of the gaussian-random value with random genetic mutations.

However, the fundamental behavior of each population remained the same. Thus, we can conclude that the changes in the population dynamics in the meiosis experiment were caused by the change in genetic inheritance, rather than due to a lurking variable. These results are summarized in the following graph (Note that the scale for the y-axis

begins at 0.0 and ends at 10.0).



By simply changing the genetic inheritance method, the simulation gives a radically different result. First, each population exhibits a much higher level of genetic variation. While pseudo-meiosis causes populations to collapse into thin bands, meiosis seems to encourage high levels of population diversity. Second, while sexual selection was critical to population divergence pseudo-meiotic populations, it has almost no effect on populations that reproduce via meiosis. For the meiotic populations, divergence occurred in bimodal seed distributions regardless sexual selection.

Analysis: Unlike meiosis, where genetic information is passed directly to the child, in pseudo-meiosis some genetic information is destroyed in the inheritance process. By averaging the beak sizes, you actually lose the genetic information that coded for the fringes of the population. Barring mutation, in pseudo-meiosis the largest beak in each generation is guaranteed to be larger than all the beaks of all successive generations. In other words, no matter who the largest beaked individual mates with, its children are guaranteed to have a smaller beaks than it does. This effect causes pseudo-meiotic populations to quickly coalesce around an equilibrium, hence the population collapse. This effect can be mitigated by using sexual selection to prevent distinct populations from interbreeding, but nevertheless these independent populations still exhibit internal population convergence. Meiotic inheritance avoids this issue entirely by passing genetic information directly to the child. Even in the case of incomplete dominance, where the genes of the parents are averaged, the actual information itself is unaffected. Hence, meiotic inheritance prevents the destruction of fringe genes, which allows the

populations to maintain extremely high levels of diversity, thus preventing population collapse.

Conclusion: This experiment demonstrates that the reason for the population collapse in the original experiment was averaging beak sizes during inheritance. This slight oversimplification inadvertently added a tendency for population convergence that is not exhibited in actual biological populations. When meiosis is taken into account, we see that populations actually exhibit very high levels of genetic diversity even without sexual selection. It remains to be seen if this effect remains true when individuals possess more than one gene, however it likely will due to the non-destructive nature of meiotic inheritance. While these results indicate that the *Speciation* paper's results may not be applicable to the biological world, the paper's findings are still useful in future biological research. The initial experiment illustrates that populations can maintain genetic diversity through speciation even when the population is strongly pressured to converge. While this convergence was unintentional in the initial experiment, population convergence occurs frequently in the natural world, typically in small, declining populations. Biologists hypothesize that during these bottleneck events, speciation can occur very rapidly, and sexual selection might provide insight on the mechanism for that speciation. This avenue of research exceeds the scope of this experiment but provides a promising lead into the hidden workings of the natural world and warrants further investigation.