Population Genetics

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for *Cambridge Companion to the Philosophy of Biology*, edited by D. Hull and M. Ruse,
Cambridge University Press

1. Introduction

Population genetics is a subfield of evolutionary biology that aims to represent mathematically the changes in the genetic variation of populations (specifically, sexually reproducing populations with Mendelian heredity) over time. The mathematical models of population genetics provide a theoretical basis for experimental studies of laboratory populations and studies of natural populations. Our primary focus in this essay is on population genetics theory itself, rather than its applications, although towards the end of the essay we give some discussion of the latter.

Population genetics attempts to measure the influence of the causes of evolution, viz., mutation, migration, natural selection, and random genetic drift,[i] by understanding the way those causes change the genetics of populations. But how does it accomplish this goal? We begin in the next section, (2), with a brief historical outline of the origins of population genetics. In section (3), we sketch the model theoretic structure of population genetics, providing the flavor of the ways in which population genetics theory might be understood as incorporating causes. In sections (4) and (5) we discuss two specific problems concerning the relationship between population genetics and evolutionary causes, viz., the problem of conceptually distinguishing natural selection from random genetic drift, and the problem of interpreting fitness. In section (6), we briefly discuss the methodology and key epistemological problems faced by population geneticists in uncovering the causes of evolution. Section (7) of the essay contains concluding remarks.

We are focusing on the issue of causality in population genetics because we take this issue to be at the core of many of the contemporary philosophical debates in population genetics. However, it should be noted that population genetics raises other philosophical issues that this essay will not address. To give two examples, there has been much debate over the questions of whether population genetics describes any scientific laws (see, e.g., Ruse 1977, Beatty 1995, Waters 1998), and whether the models of population genetics have been reconciled with the "semantic conception" of theories (see, e.g., Beatty 1982, Lloyd 1988).

2. Origins of Population Genetics and the Evolutionary Synthesis

In the early part of the 20th century, Gregor Mendel's experimental work on pea plants was commonly perceived to be at odds with Darwinian natural selection; the former, it was argued, was evidence for discontinuous evolution (involving large changes from parent to offspring), whereas the latter required continuous evolution (involving small gradual changes from parent to offspring). However, no later than 1932, the field of theoretical population genetics emerged as a reconciliation between Mendelism and Darwinism. Most biologists at the time accepted the fact of evolution, or Darwin's "descent with modification," but Darwin's idea of natural selection as a cause of that modification was controversial. Indeed, lacking was any generally accepted account of genetic variation in populations (is the variation continuous or discontinuous?), evolutionary change (is change gradual or saltational?), and an understanding of the appropriate use of statistical methods for studying these. The emergence of theoretical population genetics, which addressed all of these issues, is typically associated with the work of R. A. Fisher, Sewall Wright, and J. B. S. Haldane. The foundational works that ushered in theoretical population genetics are Fisher's (1930), *The Genetical Theory of Natural Selection*, Wright's (1931), "Evolution in Mendelian Populations," and Haldane's (1932), *The Causes of Evolution*. What follows is a brief summary of the views of these three biologists.

Fisher (1890-1962) was an English biologist trained in mathematics at Cambridge University. In addition to his unsurpassed contributions to statistics, his initial contributions to evolutionary biology predate those of the other two theorists. Fisher's aim in *The Genetical Theory of Natural Selection* was to formally and mathematically demonstrate how the "vague" concept of natural selection (as it was then considered) could possibly work. And he does this by considering the theory of natural selection against the principles of Mendelian inheritance on an analogy with the

mathematical techniques of statistical mechanics. Fisher's view is typically understood as follows: *Evolution is driven primarily by natural selection, or mass selection, at low levels acting on the average effects of single allele changes (of weak effect) at single loci independent of all other loci*.

Wright (1895-1988) was an American biologist trained by William E. Castle at Harvard University in physiological genetics. Prior to his groundbreaking research in evolutionary theory, which he carried out at the Universities of Chicago and Wisconsin, Madison, he worked as a staff scientist for the US Department of Agriculture. Wright's views changed greatly over the years, but what Wright was looking for in his 1931 essay, "Evolution in Mendelian Populations," were the ideal conditions for evolution to occur, given specific assumptions about the relationship between Mendelian heredity and the adaptive value of gene complexes. Ideal conditions, for Wright, are those conditions that produce the fastest rate of evolution to the highest "adaptive peak." Wright believed that these conditions required that populations be subdivided and semi-isolated, and that selection along with random genetic drift, and migration operated in a "shifting balance" of phases. Wright's Shifting Balance Theory can be summarized: Evolution proceeds via a shifting balance process through three phases: Phase I: *Random genetic drift causes subpopulations semi-isolated within the global population to lose fitness;* Phase II: *Mass selection on complex genetic interaction systems raises the fitness of those subpopulations;* Phase III: *Interdemic selection then raises the fitness of the large or global population.*

Haldane (1892-1964) was an English biologist trained in mathematics, classics, and philosophy at Oxford University. Haldane began his work on evolutionary problems in 1922 with theoretical or mathematical inquiries into the consequences of natural selection in Mendelian populations. Haldane's 1932 *The Causes of Evolution* is an original and important contribution to the origins of theoretical population genetics with its critical analysis of extant empirical work against the background of his own and Fisher's and Wright's theoretical work. The appendix to *Causes* is a critical discussion of his own and Fisher's and Wright's achievements regarding the reconciliation of Mendelism with Darwinism. Haldane agrees with portions of both Fisher's and Wright's evolutionary theories. For instance, Haldane supported Wright's emphasis on epistasis and migration, and he supported Fisher's view on the importance of natural selection over random genetic drift. Haldane further thought that natural selection would proceed rapidly in large populations, which neither Fisher nor Wright believed. It is easy and fairly common to view Haldane as a popularizer of population genetics among biologists generally. But this is a mistake: Much of Haldane's work in the 1920s adumbrates ideas found in the work of Fisher and Wright.

The mathematical reconciliation of Mendelism with Darwinism achieved by Fisher, Wright, and Haldane began the historical period of evolutionary biology called the "Evolutionary Synthesis" (also known as the "Modern Synthesis"). Their theoretical achievements combined with early experimental work by such luminaries as Theodosius Dobzhansky (1937) set the stage for the integration of previously divergent fields such as paleontology, zoology, botany, systematics, and genetics. To be sure, there was considerable disagreement among the architects of the Synthesis. Fisher and Wright in particular were engaged in an initially friendly controversy that

rapidly became heated, from 1929 until Fisher's death in 1962, over how to interpret their mathematical theories. By the 1950s, as Stephen Jay Gould (1983) points out, the Synthesis would "harden", emphasizing natural selection as the most significant evolutionary cause.

To a large extent, the applications of contemporary population genetics are deeply rooted in the achievements of the period between 1918 and 1960. Indeed, there is, for instance, persistent controversy over the relative significance of Fisher's and Wright's population genetics theories (Skipper 2002). Since 1960, applications of molecular techniques to evolutionary problems has led to revisions in the interpretation of some of the basic assumptions of population genetics theory as well as of evolution at the molecular level. Moreover, advances in microbiology and developmental biology have led to challenges to the explanatory scope of population genetics.[ii]

3. Contemporary Population Genetics

The models of contemporary population genetics exemplify the generalized reconciliation between Mendelism and Darwinism using the now well-entrenched statistical methods introduced by the architects of the field. As such, population genetics defines "evolution" as change in gene frequencies, or more strictly, any change in the frequency of alleles within a population from one generation to the next. Differently put, population genetics aims to account for the dynamics of genetic variation in populations. And it does so by attempting to uncover the patterns of those dynamics via the causes of evolution, viz., mutation, migration, natural selection, and random genetic drift. Our goal in this section is to provide the reader with a

general sense of what the models of contempory population genetics are like; consequently, our discussion must take a slight technical turn.

Population genetics begins its task by specifying the conditions under which gene frequencies remain *un*changed from one generation to the next: the conditions under which evolution is *not* occurring. These conditions are captured by the foundational principle of population genetics called the "Hardy-Weinberg Principle." The Principle begins with a set of assumptions about the genetic system, mating system, and population structure: Assume a randomly interbreeding, large (mathematically, infinite) population of diploid organisms with one genetic locus and two alleles. In fact, these assumptions are fundamental to most standard presentations of population genetics. Given these basic assumptions, the Hardy-Weinberg Principle states that in the absence of evolutionary causes, i.e., mutation, migration, natural selection, and random genetic drift, the gene frequencies of the population will remain unchanged from one generation to the next; the population will be in "Hardy-Weinberg equilibrium."[iii] In Hardy-Weinberg equilibrium, when the two allele frequencies are equal, the distribution of genotype frequencies will map on to the Mendelian 3:1 phenotypic ratio.

The mathematical relation between the allele frequencies and the genotype frequencies is

$$AA : p^2 \qquad Aa : 2\,pq \qquad aa : q^2$$

where p^2, $2pq$, and q^2 are the frequencies of the genotypes *AA*, *Aa*, and *aa* in zygotes of any generation, p and q are the allele frequencies of *A* and *a* in gametes of the previous generation,

and $p + q = 1$. The chances of all possible combinations of alleles occurring randomly is $(p + q)^2 = 1$ so that we arrive at the famous equation describing the Hardy-Weinberg Principle, $p^2 + 2pq + q^2 = 1$. As long as the basic assumptions hold in the absence of the evolutionary causes, the allele frequencies p and q will remain constant and genotype frequencies will be in accord with the equation; in other words, there is no evolutionary change in a population in Hardy-Weinberg equilibrium.

Understanding evolution as change in gene frequencies, then, is understanding the ways in which populations deviate from Hardy-Weinberg equilibrium. Population geneticists may begin with assumptions about the genetic system, mating system, and population structure, and then proceed to modify the mathematical representation of the Hardy-Weinberg Principle by adding parameters for mutation, migration, natural selection, and random genetic drift.

Consider a simple case. First, consider that the assumptions above concerning genetic system, mating system, and population structure hold. Second, assume we want to understand how natural selection may cause a population to deviate from Hardy-Weinberg equilibrium; specifically, we want to understand a simple case of viability selection. The frequency of the genotypes in our population before selection is given by the Hardy-Weinberg equilibrium equation, $p^2 + 2pq + q^2 = 1$. Since we want to understand how natural selection causes a deviation from that equilibrium, we modify the equation to include a parameter that captures the "selective pressure" on the genotypes, or in other words, the probability of survivorship of the genotype. This parameter is called "fitness" (w) and is usually measured relatively so that the

fitness of one genotype is expressed relative to another genotype; the genotype that is the standard of comparison is assigned a fitness value of 1.

Given the fitness parameter, if the frequencies of the genotypes *AA*, *Aa*, *aa* before selection are p^2, $2pq$, and q^2, respectively, then the frequencies of the genotypes after selection are p^2w_{AA}, $2pqw_{Aa}$, and q^2w_{aa} by incorporating the fitnesses of the genotypes in the computation of their post-selection frequencies. Indeed, the sum of the frequencies of the genotypes after selection equals the average fitness for the population, i.e., $p^2w_{AA} + 2pqw_{Aa} + q^2w_{aa} = \overline{w}$. And we have as the mathematical relation between the allele frequencies and the genotype frequencies:

$$AA : \frac{p^2 w_{AA}}{\overline{w}} \qquad Aa : \frac{2pqw_{Aa}}{\overline{w}} \qquad aa : \frac{q^2 w_{aa}}{\overline{w}}$$

We may then compute the post-selection frequencies of *A* and *a*, which are designated as p' and q' respectively:

$$p' = \frac{p^2 w_{AA} + pqw_{Aa}}{\overline{w}} \qquad q' = \frac{pqw_{Aa} + q^2 w_{aa}}{\overline{w}}$$

From these equations, the outcome of selection can be deduced: For instance, if $p > p'$, where $p = [(p^2 + 2pq) / 2]$, then selection is acting to decrease the frequency of allele *A* in the next generation.

The previous example is not intended to provide a primer on the statistical methods of population genetics let alone an understanding of them. Rather, it is intended to provide the flavor of the way in which evolution as change in gene frequencies is approached using a version of those tools: Starting from a mathematical statement about the distribution of allele frequencies in the absence of evolutionary causes, one may understand the ways in which those causes change that distribution by modifying the mathematical statement with parameters measuring the influence of those causes. Indeed, mutation, migration, multiple modes of selection, and random genetic drift are treated in more or less the same ways, i.e., by modifying and extending the basic mathematical statement of the Hardy-Weinberg Principle. Moreover, the basic tools roughly introduced here can be expanded to cover evolution for alternative assumptions regarding the genetic system, mating system, and population structure. Further, the theoretical apparatus can be made more powerful and expressive by introducing models which allow population geneticists to represent the probabilities of a range of possible results, rather than simply predicting a single result as in the model described above. (Biologists call models that predict one specific value *deterministic* models; this should not be confused with the Laplacean or philosophical sense of determinism, which generally refers to a property of the world rather than a property of a model. Models that provide a probability distribution for a range of results are called *stochastic* models. Deterministic and stochastic models will be discussed further in the next section).

4. Population Genetics Theory and Evolutionary Causes

As Michael Ruse has documented, Charles Darwin construed natural selection as a cause (or, more precisely, a *vera causa*) in order to conform to the predominant philosophies of science of

his time (Ruse 1979, Chapter 7). Contemporary population genetics, as we have seen, incorporates not just natural selection, but also mutation, migration, and random genetic drift. Is natural selection still construed as a cause? And are the other phenomena causes as well?

As we have seen, population geneticists define "evolution" as "change in gene frequencies." For selection, drift, mutation, and migration to be causes of evolution, they must be able to bring about such changes – at least theoretically, if not in reality as well. Unfortunately, ever since David Hume's skeptical challenge to cause-effect relationships, philosophers have been unable to agree on a definition of "cause," or even whether we can legitimately infer the existence of causes at all. Assuming, however, that there are such things as causes and that we can develop a satisfactory account of causation, it seems fair to say that in the context of population genetics, mutation, migration, selection, and drift are causes of evolution. For example, it is easy to see how mutation within a population will lead to a change in gene frequencies within that population. Similarly, migration into or away from a population also yields a change in gene frequencies in the population. (Selection and drift will be discussed further below).

The implications of the population geneticist's construal of evolution are threefold. First, the commonly held notion that evolution and natural selection are the same is false. Second, with four possible causes to consider, the equations can become quite complex. This is because, unlike the simplified scenarios above, these causes can act in combination, as is implied by Richard Lewontin's suggestion that,

> …population genetic theory is a descriptive theory that provides the mapping of causal processes as genetic outcomes. It says, '*if* mutation rates are such and such, *if* the mating pattern is such a one, *if* there are five genes affecting the character with the following norms of reaction, *then* the trajectory of the population in time, or the equilibrium state, or the steady state distribution of gene frequencies will be such and such' (Lewontin 1985, 10).[iv]

Third, even though the causes can act in concert, they are considered to be *distinct* causes. The most difficult case of distinguishing between the causes of evolution is that encountered in distinguishing selection from drift. Thus, we pay special attention to that case here. However, our discussion here will of necessity be relatively brief; for further discussion, see Millstein (2002) and earlier works (Beatty 1984, Hodge 1987).

The problem in distinguishing selection from drift arises at least in part as a result of ambiguities in the models of population genetics. This will require an exploration of three different aspects of population genetics. We will argue that it is a mistake to characterize selection and drift in terms of the first two of these aspects; the proper characterization of selection and drift derives from the third aspect.

Consider first the model of natural selection discussed in the previous section. Although the fitness value (the w in the equations) is generally understood to be a probability, namely, the probability of survivorship of the genotype, the equations themselves will not generate a range of possible future genotype frequencies. Rather, they will generate one specific genotype frequency

for each of the genotypes. That is, the model of natural selection is "deterministic," in the sense described above.

On the other hand, according to the standard presentation, models become stochastic and generate a range of possible genotype frequencies, when – and, according to some authors, only when (see, e.g., Brandon 2005; but cf. Millstein 2005) – the assumption of infinite population size is relaxed. To understand this, imagine an urn filled with red and green balls where balls are sampled without respect to color. If a large sample of balls were taken, we would expect the frequencies of colored balls in the sample to be very close to the frequencies in the urn. On the other hand, if we only take a small sample of colored balls, our sample may very well have different proportions of colored balls than the urn does. In the same way, if our population (the "sample" that is taken with each generation) is infinite, then we expect (with a very high probability) that descendant generations will have genotype frequencies very close to those of the parent generations. However, if the population size is finite, then the sample may not be representative; that is, the genotype frequencies of the descendant generation may diverge considerably from that of the parents. But in which direction will they diverge? For example, will the frequency of *AA*s increase or decrease? And by how much? We cannot say for certain; we can only predict the *probability* of various divergences, just as we would not be able to say for certain whether a small sample of balls would have a smaller or greater (or equal) percentage of green balls as compared to the urn, only the probabilities of drawing various numbers of green balls. So, the introduction of finite population size yields a stochastic model, i.e., a model that generates a probability distribution of future outcomes.

If one were to try to understand what selection and drift are from a literal interpretation of these models, one might be tempted to conclude that natural selection is the achievement of the predictions of the models. That is, one might be tempted to conclude that natural selection is when genotype frequencies are exactly those that the fitness values lead us to expect. One might be further tempted to label the introduction of finite population size into the models as the introduction of drift; again, reading literally from the models, drift then becomes any deviation from the expectations of selection. On this view, selection is deterministic, but drift is stochastic (in the senses described above). This is, in fact, one way of distinguishing selection from drift, but, as we shall argue below, it is not a very good way. The thing to notice at this point is that on this interpretation of population genetics, selection and drift are distinguished by the *outcomes* that are produced (agreement with fitness predictions and divergence from fitness differences, respectively).

Now let us consider a second aspect of population genetics. In discussing whether selection or drift predominates in a particular population, biologists will sometimes rely on the following "rule of thumb": natural selection has prevailed if $4N_e s >> 1$, whereas random drift has prevailed if $4N_e s << 1$, where N_e is the effective population size (i.e., the number of individuals in a population who contribute offspring to the next generation) and s is the selection coefficient (Futuyma 1986, 173). In other words, when the effective population is large and/or the selection coefficient is high, selection tends to prevail. When the effective population size is small and/or the selection coefficient is low, random drift tends to prevail.

If you were to take this second aspect of population genetics on its face, you probably would come to a very different conclusion than before. Namely, you would conclude that natural selection and random drift are not entirely distinct; instead, it would appear that selection and drift are on a continuum. With a low selection coefficient and a small population size, you have drift, but increase the selection coefficient and/or the population size and eventually you will have selection. With an intermediate selection coefficient and an intermediate population size, however, it is unclear on this view whether the population is undergoing selection or drift. Although it might not appear so, the conclusion that there is a continuum between selection and drift is also reached by a consideration of outcomes. The question is, which contributes more to the genotype frequency produced – the achievement of fitness expectations or the deviation from them? The idea is that when there is a low selection coefficient and small population size, the effects of drift (the effects of sampling) swamp the effects of selection, but when there is a high selection coefficient and large population size, the effects of selection swamp the effects of drift.

Thus, the literal reading of these two aspects of population genetics has led to a conundrum; two different aspects of the models of population genetics yield different conclusions about whether drift and selection are distinct concepts. On the first view, they *are* distinct concepts; selection is the achievement of fitness expectations and drift is any deviation from that expectation. On the second view, the two concepts are *not* distinct; rather, there is a continuum between drift and selection.

There is, however, a third alternative, which takes an altogether different approach. This is the approach that one of us has endorsed (e.g., Millstein 2002). Rather than literally interpreting the

models in isolation, we derive our concepts from *phenomena* that the models are intended to represent.

Interestingly enough, the presentation of the phenomenon of natural selection in population genetics textbooks generally does not deviate much from the Darwin's own presentation. In order for selection to occur in a population, 1) there must be heritable variation among individuals, 2) the variation must confer a differential ability to survive and reproduce in the given environment, and 3) and more offspring are produced than can survive in the given environment (i.e., there is, to use Darwin's phrase, a "struggle for existence"). But from these conditions Darwin did not conclude, as the selection equations discussed above seem to imply, that organisms having advantageous variations would necessarily be the ones with greater reproductive success. Instead, Darwin claimed, "if variations useful to any organic being do occur, assuredly individuals thus characterized will have the *best chance* of being preserved in the struggle for life" ([1859] 1964, 127; italics added. See also e.g., pp. 61, 81). In other words, we expect that the fittest organisms will be the most successful, but that does not always happen; perhaps, for example, the fittest organism fails to find food or is crushed by a falling boulder. In fact, unless one were to whiggishly claim that Darwin, in acknowledging that the expected may not happen, had a notion of drift, one is left with the conclusion that the phenomenon that Darwin called natural selection – arguably, the same phenomenon that the models are attempting to represent – is not "deterministic" at all, but rather "stochastic."

What phenomena, then, are the drift models purportedly representing? There are at least seven different kinds of drift phenomena (Millstein 2002). Here, we mention only two: indiscriminate

gamete sampling and indiscriminate parent sampling (see Beatty 1984). Gamete sampling is the process in which some – but not all – gametes are successfully united in zygotes, whereas parent sampling is the process in which some – but not all – organisms successfully reproduce and become parents. But there is a tempting rejoinder, which goes something like the following: "But *why* is it that some gametes become joined together in zygotes and others do not? Perhaps the successful gametes are fitter in some way; perhaps the sperm swim faster or the eggs are more robust. And *why* is it that some organisms survive to become parents when others do not? Again, perhaps they are just fitter." This rejoinder puts its finger on the difference between the phenomenon of selection and the phenomenon of drift. *If* some gametes *were* fitter, or *if* the individuals *were* fitter, then we would *not* be describing drift at all; we would be describing selection (i.e., *discriminate* sampling). The point behind discussing drift is that there may *not* be any fitness differences (although there may be physical differences that do not confer any fitness benefits), and yet some gametes or individuals may still be more successful than others. To use Hartl and Clark's example, imagine shellfish that "produce vast numbers of pelagic larvae that drift about in the sea" (1989, 70). Although Hartl and Clark do not elaborate, the image is of virtually identical larvae, subject to the vagaries of tides and predators (i.e., *indiscriminate* sampling).

Thus, examination of the phenomena, prior to any representation by the models, yields a third way of understanding the difference between selection and drift. Selection, on this view, is a discriminate sampling process in which physical differences between biological entities (gametes, organisms, etc.) are causally *relevant* to differences in reproductive success. Drift, on the other hand, is an indiscriminate sampling process in which physical differences between

biological entities are causally *irrelevant* to differences in reproductive success.[v] Note that unlike the first two attempts to spell out the difference between selection and drift, the distinction is made by identifying selection and drift as different types of *processes* rather than different *outcomes.* In other words, selection and drift are different kinds of causal processes. In using the term "causal process," we mean to suggest that selection and drift are *physical* processes occurring in nature and in the laboratory; furthermore, they are to be distinguished from pseudo processes such as the movement of a shadow (Salmon 1984). Finally, in using the term "causal process" to describe selection and drift, we mean to suggest that selection and drift consist of a series of states occurring *through time*, where the states are generated causally.[vi] The *outcomes* of these processes, on the other hand, refer to one state (e.g., the genotype frequencies of a population) at a particular point in time.

Not only are selection and drift different kinds of causal processes, they are different kinds of causes, both of which can lead to evolution. Considering selection first, if the individuals whose variations confer on them a greater ability to survive and reproduce do in fact reproduce in greater numbers than individuals who lack these variations, then the gene frequencies of the second generation have changed from those of the preceding generation. Now there exists a greater proportion of individuals with "advantageous" variations; evolution has occurred. Natural selection has caused evolution. But if there is a change in the proportions of types from one generation to the next, but that change is *not* due to physical differences between individuals, then it is drift that has caused evolution. Each is a different cause because each is a different kind of causal process.

There are at least three advantages to this view over the other two.

First, we think it is a mistake to interpret models literally. The models of population genetics are highly idealized meta-mathematical structures that, at best, are understood as bearing a similarity relationship to the real world systems they describe. And precisely how to understand the extent of similarity between the models and the real world is no easy task (Wimsatt 1980). At any rate, the models were developed subsequent to understanding the phenomena they are trying to capture. It seems backwards, therefore, to try to understand the phenomena via the models.

Second, confusion arises in distinguishing selection and drift in large part because population geneticists sometimes speak of selection and drift as causal *processes* (as in the quote from Lewontin above), yet at other times they speak of selection and drift as *outcomes*, or effects (thus, e.g., drift is sometimes referred to as the "Sewall Wright Effect"[vii]). A moment's reflection will show, however, that population geneticists cannot have it both ways. If, for example, selection is identified with its outcomes, then selection is when organisms having a greater ability to reproduce as compared to their conspecifics do in fact enjoy greater reproductive success. However, this is just evolution, i.e., a change in gene frequencies from one generation to the next. It would not make sense for selection in this sense to be a *cause* of evolution; selection, considered as an outcome, is one *form* of evolution. But, as we discussed above, biologists commonly construe selection as a cause of evolution. This makes sense on the view of selection as a process, but not on the view of selection as an outcome.

And third, further confusion arises because the outcomes of the different processes often cannot be distinguished. To see this, first consider a population where physical differences between organisms do *not* confer any differences in survival or reproductive ability (a population undergoing drift, on our account), so that the relative values of different types may fluctuate from generation to generation. Now, consider a second population where physical differences between organisms *do* confer differences in survival and reproductive ability (a population undergoing selection, on our account). Suppose that the environment of the second population is fluctuating. Because of the fluctuating environment, different types may be favored in different generations, producing a fluctuation of types over the generations that produces a pattern that is indistinguishable from that of drift. If selection and drift are understood as purely outcomes, then either both the populations are undergoing drift or both the populations are undergoing selection. We are skeptical that any biologist would, when presented with this scenario, actually take either of these positions, because the two populations are biologically very different. Characterizing drift and selection as processes instead of outcomes captures, rather than glosses over, that difference.

We should emphasize that the claim here is that the *concepts* of natural selection and random genetic drift can be distinguished from one another, and that that distinction should be based on the kinds of processes they are, and not on the kinds of outcomes, as a literal interpretation of the models would suggest. However, that is not to suggest that selection and drift can be easily distinguished *empirically*. That, unfortunately, is much more complicated problem, which we present in a more general fashion below.

5. Causes, But Not All of the Causes

Even though population genetics models the causes of evolution, it is not clear that population genetics tells a complete causal story of evolution. That is, the question arises as to whether there are causes involved in the process of evolution that are not captured by the models of population genetics. Here we will focus on just one area: the concept of fitness. There is an extensive body of literature on the concept of fitness, especially on the propensity interpretation of fitness (Brandon 1978, Mills and Beatty 1979). However, although we acknowledge our intellectual debt to the propensity interpretation, we do not intend our discussion here to be a defense of this or any other interpretation of fitness. Rather, in this section we seek only to explore some issues of causality that the concept of fitness raises.

Above, we argued that natural selection is a cause of evolution.[viii] Yet natural selection is a causal process in two senses: it is itself a cause (of evolution), and it is made up of causes. It is to this latter sense, the causality *within* the process, that we now turn.

Prima facie, it makes sense to invoke fitness as a causal concept in a colloquial description of natural selection. After all, what makes one organism fitter than another organism in a given environment is its physical characteristics. And those physical characteristics cause the organism to have superior survival and reproductive success in the given environment. That is, the organism's superior fitness, under auspicious circumstances, causes its superior reproductive success. The identification of "fitness" as a cause of reproductive success seems so trivial as to be tautological.

However, as Elliott Sober (1984) has pointed out, the situation is not as simple as the colloquial story makes it appear. After all, in population genetics, fitness (the "*w*" in the equations described above) does not represent just one physical trait. That is, the fitness of a finch is not just the shape and size of its beak, not just its ability to avoid predators and disease, and not just its ability to find a mate and reproduce; its fitness is *all* of those things together. Sober argues that whereas any of those elements individually may cause or prevent reproductive success, they generally do not *all* cause or prevent reproductive success in any given instance. Thus, according to Sober, fitness is "causally inert."

It should be noted, however, that population genetics models typically subdivide fitness traits into two broad components: an organism's ability to survive (viability), and an organism's ability to reproduce (fecundity). Yet this gross distinction does not address the different kinds of abilities that fitness encompasses. Consider fecundity. In the models of population genetics, fecundity encompasses at least three different kinds of abilities: 1) an organism's ability to produce various numbers of offspring, 2) an organism's ability to attract mates, and 3) an organism's ability to fight for potential mates.

For Darwin, on the other hand, the latter two abilities were in a distinct category. In fact, Darwin considered these traits to be the basis of *sexual selection*, which for Darwin was a different type of cause than natural selection. This is because natural selection, which would involve viability as well as fecundity in the first sense, would tend to produce organisms which are adapted to their environments: finches with beaks of a certain shape and size, for example. Sexual

selection, on the other hand, would involve primarily fecundity in the second or third senses, which would mean that the traits that were produced would not tend to be those that were adaptive. Instead, we find sexual selection yielding traits like the inefficient-but-beautiful tail of a peacock (as a result of the second sense of fecundity) or antlers of a male deer (as a result of the third sense of fecundity). If sexual selection and natural selection truly are different kinds of causes, as Darwin thought, then they are causes that population genetics models do not distinguish between (in the sense that they are not treated any differently – although of course sexual selection is explicitly discussed in most population genetics textbooks), and this is in part a result of not distinguishing among different types of fecundity.

Further complicating matters is the fact that, as discussed above, population genetics uses *relative* fitness. That is, it is not an individual's ability to survive and reproduce that appears in the equation, but rather, its – or, more precisely, its genotype's – ability to survive and reproduce as compared to the abilities of others in the population.[ix] Of course, relative fitnesses are calculated from genotype fitnesses. But this is not simple computational convenience; the relative fitnesses are what really matter for the evolution of the population. If there are no fitness differences among genotypes, there will be no selection, and a population in which one genotype is twice as fit as its conspecific will evolve differently than one in which it is three times as fit. And yet, is relative fitness a causal concept? If it is, it does not seem to be a causal concept that adheres to any one individual. So, interpreting the causality of relative fitness is challenging.

Thus, it would appear either that population genetics fails to fully capture the actual causes that operate in a population undergoing selection, or that biologists and philosophers have yet to

provide an adequate interpretation of fitness. Given the numerous alternatives in the literature, the latter would seem to be the consensus view.

6. How Do We Find the Causes?

Thus far we have interpreted population genetics as a causal theory from the point of view of the theory, its structure. Our view may be expanded by considering how population genetics theories are related to real populations of organisms. What we want to explore, then, is how population geneticists credential empirical causal claims made about their models.

Elisabeth Lloyd (1988) has constructed a simple, broad framework for the confirmation of evolutionary and ecological models. On her view, empirical claims, or hypotheses, that some model is similar to some natural system are confirmed by way of (C1) fit between model and data, (C2) independent support for aspects of the model, and (C3) variety of evidence. Fit between a model and data is just evidence that demonstrates a matching between the model and the data. Since population genetics theories are embedded with numerous assumptions, e.g., that mating is random, that populations are large, etc., any independent empirical support for those assumptions will increase the confirmational standing of a model. Most important is that there are a variety of types of support for a model, i.e., a variety of instances of fit and a variety of instances of independent support for any assumptions. On Lloyd's view, standard statistical techniques for analyzing data, common across the biosciences, are used to analyze (C1)-(C3).

One of us (Skipper 2004) has argued that a constellation of experimental strategies forms the basis of Lloyd's confirmation framework. The idea here is that fit, independent support, and variety of evidence are all driven by experimental methodology. Thus, e.g., fit between model and data are at bottom driven by the practical procedures and techniques used to collect the data. There are a number of strategies, including (E1) experimental checks and calibration, (E2) reproducing artifacts known to be present, (E3) intervention, (E4) independent confirmation using different experiments, (E5) elimination of error, (E6) using the results to argue for their validity, (E7) using an independently well-corroborated theory of the phenomenon to explain the results, (E8) using an apparatus based on a well-corroborated theory, and (E9) using statistical arguments (cf. Rudge 1998). And they are used to justify experimental claims across the three main classes of experiment, i.e., natural experiments, or observations of evolution in action, field experiments, controlled manipulations of populations in the wild, and laboratory experiments, highly controlled manipulations of populations in the laboratory (Diamond 1986).[x]

As an illustration, consider the famous case of the Scarlet Tiger moth, *Panaxia dominula*, perhaps the longest running, at 60+ years, field study in ecological genetics, first studied by R. A. Fisher and the famed ecological geneticist E. B. Ford (1947). Fisher and Ford carried out a field experiment using the novel (at the time) capture and release protocol to determine whether natural selection or random genetic drift caused the fluctuations in the *medionigra* gene of the moth, responsible for a specific wing coloration phenotype. By capturing moths from an Oxfordshire field, marking them with a dab of paint, and recapturing them, Fisher and Ford could, over time, track the fluctuations in the *medionigra* gene via its phenotype, a particular wing coloration pattern. From data collected between 1939 and 1946, Fisher and Ford performed

statistical analyses (E9 above) that supported a fit with their selectionist model (C1 above) over a random genetic drift model. Note that Fisher and Ford inferred that selection controlled the fate of the *medionigra* gene and not that they had direct observational evidence of selection acting on the moths with this phenotype. Their statistical argument (E9) was that the fluctuations in the gene from year to year were too great to be due to drift and, so they must have been caused by selection.

Over the last 10-15 years, further field and laboratory experiments have revealed flaws in Fisher and Ford's experimental procedures, flaws that have been carried through the 60 years of field work on *Panaxia* (e.g., Goulson and Owen 1997). Fisher and Ford, as well as subsequent experimenters, failed to account for temperature fluctuations in the moths' environment during their experiment. The interpretation of Fisher and Ford's results hinge on performing this experimental check (E1), since temperature fluctuations affect the expression of the *medionigra* gene in the moth during the larval stage, turning the wing color darker in either the extremes of cold or hot. Affected moths with the *medionigra* gene would look more like the dominant form, f. *dominula*, and, thus, would be scored as such. The capture-mark-release census data would be skewed and, thus, the fit between the selectionist model and the data would be called into question. Because the check was not performed, a large portion of the experimental results on *Panaxia* are ambiguous. Ironically, Sewall Wright (1948) pointed out that Fisher and Ford's (1947) "argument by elimination" of drift to selection was not as strong as they believed. But Wright's critiques, now vindicated, were ignored.

The example of the Scarlet Tiger moth highlights the way in which we view how population geneticists (and ecological geneticists) credential empirical or experimental claims about evolutionary causes. The example also highlights the ways in which such claims can go wrong. The preceding has only been a sketch, but we think it is a plausible one. What, ultimately, can be claimed about the strength of such claims? Lewontin (2000) makes plain that the epistemological landscape of population genetics is a continuum from a "maximal inferential program" and a "minimal deductive program." The minimal program is tantamount to theoretical population genetics, or the program of providing the network of relationships between evolutionary causes and their outcomes at the genetic level. The maximal program aims to give a correct account of evolutionary causes that have led to any and all observed patterns of genetic variation in natural populations. The maximal program is epistemologically unrealistic because it requires that scientists know the apparently unknowable: all of the biological and natural historical details of any arbitrarily chosen species. The minimal program is entirely analytic, having "no truly epistemological problems, only questions of methodological ingenuity" (Lewontin 2000, 200). Somewhere between the two extremes is what Lewontin thinks is epistemic reality in population genetics. Indeed, Lewontin claims, "the best to which population geneticists can aspire is a formal structure that sets the limits of allowable explanation and a set of existentially modified claims about what has actually happened in the real history of organisms" (Lewontin 2000, 213). We agree.

7. Conclusion.

The problematic of population genetics is to account for the dynamics of genetic variation in natural populations via the causes of evolution, viz., mutation, migration, natural selection, and random genetic drift. The present essay has very briefly surveyed the historical development of population genetics, the current model theoretic structure of population genetics, key conceptual problems in understanding important evolutionary causes, and the problem of ferreting out those causes via theoretical and experimental work. We have here managed to pick away only at the very tip of the iceberg; there is much philosophical work to be done on the key theme of this essay – population genetics as a causal theory – as well as on other problems of the field. Moreover, it is important to note that while population genetics aims to understand the causes of evolution, it is generally understood as not contributing significantly or at all to our understanding of other evolutionary causes, such as the causes of speciation and extinction. That is, there is more to evolutionary studies than population genetics, in spite of the dramatic problems and progress of the field.

Acknowledgements

Thanks to John Beatty, Michael Dietrich, Jon Hodge, David Hull, Anya Plutynski, and Michael Ruse for helpful comments and discussion on an earlier draft of this essay. Remaining infelicities are our own.

References

Beatty, J. 1984. Chance and Natural Selection. *Philosophy of Science* 51: 183-211.

Beatty, J. 1982. What's Wrong with the Received View of Evolutionary Biology? in P.D. Asquith and R.N. Giere (eds.), *PSA 1980, Proceedings of the 1980 Biennial Meetings of the Philosophy of Science Association, Volume 2*. East Lansing, Michigan: Philosophy of Science Association.

Beatty, J. 1995. The Evolutionary Contingency Thesis. *Concepts, Theories, and Rationality in the Biological Sciences: The Second Pittsburgh-Konstanz Colloquium in the Philosophy of Science, University of Pittsburgh, October 1-4, 1993*. Edited by G. Wolters and J. Lennox, 45-81. Pittsburgh, PA: University of Pittsburgh Press.

Brandon, R. 1978. Adaptation and Evolutionary Theory. *Studies in History and Philosophy of Science* 9: 181-206.

Brandon, R. 2005. The Difference Between Selection and Drift: A Reply to Millstein. *Biology and Philosophy* 20: 153-70.

Darwin, C. [1859] 1964. *On the Origin of Species: A Facsimile of the First Edition*. Cambridge, MA: Harvard University Press.

Diamond, J. 1986. Overview: Laboratory Experiments, Field Experiments, and Natural Experiments. *Community Ecology*. Edited by J. Diamond and T. Case, 3-22. New York: Harper and Row Publishers.

Dobzhansky, Th. 1937. *Genetics and the Origin of Species*. New York: Columbia University Press.

Fisher, R. A. 1930. *The Genetical Theory of Natural Selection*. Oxford, UK: Oxford University Press.

Fisher, R. A. and E. B. Ford 1947. The Spread of a Gene in Natural Conditions in a Colony of the Moth, *Panaxia dominula* L. *Heredity* 1: 143-74.

Futuyma, D. 1986. *Evolutionary Biology*. 2nd edition. Sunderland, MA: Sinauer and Associates.

Gould, S. J. 1983. *Hen's Teeth and Horse's Toes*. New York: W. W. Norton and Co.

Goulson, D. and D. Owen 1997. Long-Term Studies of the *medionigra* Polymorphism in the Moth *Panaxia dominula*: A Critique. *Oikos* 80: 613-7.

Haldane, J. B. S. 1932. *The Causes of Evolution*. London, UK: Longmans.

Hartl, D. and A. Clark 1989. *Theoretical Population Genetics*. Sunderland, MA: Sinauer and Associates.

Hodge, M.J.S. 1987. Natural Selection as a Causal, Empirical, and Probabilistic Theory, *The Probabilistic Revolution*. Edited by L. Krüger, 233–270. MIT Press: Cambridge, MA.

Lewontin, R. C., 1985. Population Genetics. *Annual Review of Genetics* 19: 81-102.

Lewontin, R. C. 2000. What Do Population Geneticists Know and How Do They Know It? *Biology and Epistemology*. Edited by R. Creath and J. Maienschein, 191-214. Cambridge: Cambridge University Press.

Lloyd, E. A. 1988. *The Structure and Confirmation of Evolutionary Theory*, New York: Greenwood Press.

Mills, S. and J. Beatty 1979. The Propensity Interpretation of Fitness. *Philosophy of Science* 46: 263-86.

Millstein, R. L. 2002. Are Random Drift and Natural Selection Conceptually Distinct. *Biology and Philosophy* 17: 33-53.

Millstein, R. L. 2005. Selection vs. Drift: A Response to Brandon's Reply. *Biology and Philosophy* 20: 171-5.

Rudge, D. W. 1998. A Bayesian Analysis of Strategies in Evolutionary Biology. *Perspectives on Science* 6: 341-60.

Ruse, M. 1970. Are There Laws in Biology? *Australasian Journal of Philosophy* 48: 234-46.

Ruse, M. 1979. *The Darwinian Revolution: Science Red in Tooth and Claw*. Chicago: University of Chicago Press.

Salmon, W. 1984. *Scientific Explanation and the Causal Structure of the World*. Princeton: Princeton University Press.

Skipper, Jr., R. A. 2002. The Persistence of the R.A. Fisher-Sewall Wright Controversy. *Biology and Philosophy* 17: 341-67.

Skipper, Jr., R. A. 2004. Calibration of Laboratory Models in Population Genetics. *Perspectives on Science* 12: 369-93.

Sober, E. 1984. *The Nature of Selection: Evolutionary Theory in Philosophical Focus*. Chicago: University of Chicago Press.

Waters, C. K. 1998. Causal Regularities in the Biological World of Contingent Distributions. *Biology and Philosophy* 13: 5-36.

Wimsatt, W. C. 1980. Reductionistic Research Strategies and Their Biases in the Units of Selection Controversy. *Scientific Discovery: Case Studies*. Edited by T. Nickles, 213-59. Dordrecht: Reidel.

Wright, S. 1931. Evolution in Mendelian Populations. *Genetics* 16: 97-159.

Wright, S. 1948. On the Roles of Directed and Random Changes in Gene Frequency in the Genetics of Populations. *Evolution* 2: 279-94.

[i] Biologists refer variously to “random genetic drift,” “genetic drift,” “random drift,” or simply, “drift.” These are all the same phenomenon.

[ii] See, in particular, chapter XXX of this volume on the challenge issued from "evo-devo."

[iii] There is some question here about what counts as an “assumption” and what counts as a “cause,” as well as concerning which assumptions are “basic.” Here we ignore these complexities and simply echo the most common way that population genetics models are presented.

[iv] Lewontin’s point here is actually to show the limitations of population genetics, an issue that will be discussed below; his quote also hints an even greater complexity to the causality of population genetics than is presented here.

[v] John Beatty has suggested to us (personal communication) that perhaps indiscriminate sampling phenomena ought to be seen as *causes* of drift rather than drift itself. On this view, drift should be seen as the analog to *evolution by natural selection*, not the analog to natural selection itself; the analog to selection (discriminate sampling) would be simply indiscriminate sampling. Here we must acknowledge that biologists do sometimes refer to indiscriminate sampling as drift and at other times refer to the effects (or outcomes) of indiscriminate sampling as drift. So, if we want to avoid confusion, we have to decide whether drift refers to the causal process or the outcome. Since biologists do sometimes speak of drift and selection as alternatives, and since they are both in a broad sense treated as causes of evolution in population genetics textbooks (where it is common to list selection, drift, mutation and migration as causes), we argue that it makes sense to have drift refer to the causal process. That is, it makes sense to

treat drift in the same way that selection is treated. However, it is probably true that in some sense it doesn't matter whether you call the causal process "drift" or the outcome "drift", *as long as it is clear when one is referring to the causal process and when one is referring to the outcome* (Millstein 2002).

[vi] Even though indiscriminate sampling is characterized by as a process where physical differences between biological entities are causally *irrelevant* to differences in reproductive success, it is still a causal process in this sense. For example, in gamete sampling, the uniting of gametes to form zygotes over time consists of many states that are the result of underlying causes.

[vii] One might easily object to the attribution of this phenomenon to Sewall Wright; our point here is only to emphasize how common it is for drift to be called an effect.

[viii] Even here a problem of interpretation presents itself: at what level (gene, organism, group, species) does this cause operate? But see (XXX) this volume.

[ix] Using the fitness of genotypes rather than the fitness of individuals may be another way in which population genetics does not capture a complete causal picture – assuming, that is, that the causal stories of individuals are part of the evolutionary story, which is not entirely clear.

[x] Diamond introduces his own experimental strategies as well.