The structure and development of evolutionary theory from a Lakatosian perspective

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Thesis report

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Front cover: Imre Lakatos (1922 – 1974), a Hungarian mathematician and philosopher of science, best known for his methodology of scientific research programs.

Abstract

A research program consist of a hard core of static beliefs, and a protective belt containing all other knowledge. The protective belt is dynamic and adapts in such a way that observations can be explained without affecting the hard core. Changes to the protective belt are called problem shifts. Depending on their empirical implications, these shifts are classified as progressive, scientific, or degenerative. Progressive shifts lead to new predictions. Under Imre Lakatos' sophisticated falsificationism, research programs can be evaluated by the nature of their problem shifts. Evolutionary biology is a huge research program, that has given rise to many subprograms. In this treatise a Lakatosian analysis of evolutionary biology is performed. The aim of this work is to assess the applicability of sophisticated falsificationism to evolutionary biology, and to evaluate evolutionary biology and its subsidiary research programs. It is concluded that sophisticated falsificationism is largely applicable to evolutionary biology. Over the last one a half century, evolutionary biology has seen both progressive and degenerative shifts. Notable areas of progress have been the Modern Synthesis, kin selection, and the integration of neutral and selective evolution.

Table of Contents

Introduction

According to Imre Lakatos, scientists are working under gradually evolving research programs. A research program consists of a 'hard core' of basic convictions, a 'protective belt' of auxiliary hypotheses, and a 'heuristic': an approach for tackling research problems. The hard core is the central idea under which the researchers are working and does not appreciably change during the life of the research program. The protective belt, on the other hand, is constantly subject to revision as new (and sometimes anomalous) data is accommodated. According to Lakatos, the way in which new evidence is digested is indicative for the health of the research program. If the incorporation of new data leads to novel predictions, Lakatos speaks of a scientific or progressive problem shift. If, however, anomalies are reconciled with the program in an *ad hoc* fashion that does not increase the empirical content of the program, it is a degenerative problem shift.

As seen through the glasses of Lakatos' model, evolutionary biology is a research program. Remarkably, except for two papers over 30 years apart (Michod, 1981; Pievani, 2012), no serious attempts have been made to subject evolutionary biology to a Lakatosian analysis. The aim of this treatise is to perform the most extensive and detailed analysis to date, that can serve as a springboard for future work. In particular, I will attempt to answer two main questions:

1. Is Lakatos' model for scientific method applicable to evolutionary biology?

2. To the extent that it is applicable, how well do evolutionary biology and its subsidiaries perform in terms of progressive or degenerative problem shifts?

The first chapter will introduce Lakatos' views. A fruitful analysis of the evolutionary research program requires a clearly delineated hard core, which is the purpose of the second chapter. This chapter also features an overview of the history of evolutionary thought from antiquity to Darwin. The next three chapters focus on theories and subprograms that are concerned with the mechanisms of evolution. Chapter 3 deals with the rise of neo-Darwinism. Chapter 4 specifically discusses the empirical challenge of social and altruistic behavior. Chapter 5 examines the debate between neutralists and selectionists. Lastly I will state my conclusions as regards the above research questions.

This thesis is written in American English. Quotations from British English sources have been left unedited in this respect. The reader is asked to be forbearing regarding the resulting linguistic inconsistencies (such as the American 'programs' versus the British 'programmes').

Chapter 1

Lakatosian research programs

The usual picture of the scientific method, as encountered in science textbooks and popular presentations, is as follows. The scientist draws up a hypothesis regarding the explanation of some phenomenon. He then devises an experiment to test his hypothesis, and predicts what the outcome of the experiment should be if his hypothesis is correct. If the results correspond to the prediction, the hypothesis is corroborated (but not proven). If, on the other hand, the outcome conflicts with the prediction, the hypothesis is falsified and needs to be adjusted or rejected and replaced. An honest and responsible scientist should make risky predictions and must be prepared to discard his hypothesis if the data does not agree with it.

Although it is widely held, this is only one among several ideas of how science works. And while many would agree that testing predictions plays at least some role in the scientific method, it appears that the actual situation is much more complicated. In this chapter we will walk through the major views on the scientific method, from Bacon's inductivism, to Popper's falsificationism, to Kuhn's paradigm theory, to finally arrive at Lakatos' sophisticated falsificationism.

1.1 Inductivism

For several centuries, the dominant view has been that science follows the inductive method. Inductivism was first proposed in Francis Bacon's 1620 book *Novum Organum* ('new method'). Bacon argued against the medieval reverence for classical authorities, such as Aristotle, and against the then conventional method of gaining knowledge by mere logical analysis of already accepted dogmas. Instead, he argued, we should rise above the level of the classical philosophers. We should make our own observations of the physical world, and use those as the basis for our knowledge.

The inductivist researcher starts by carefully observing singular facts, ideally without any theoretical prejudice ('theory-free facts'). If these facts exhibit a certain pattern, he postulates a modest hypothesis or law that generalizes the pattern. If, for example, in every observed instance one phenomenon occurs in the presence of another phenomenon (say, fire always occurs together with heat), this may lead to the hypothesis that there is a causal relationship (such as: 'fire causes heat'). This step, moving from particular instances to a generalized claim, is called the inductive inference.

According to inductivists, this inference is warranted when a number of conditions are satisfied. First, generalized claims may only slightly exceed their empirical support. This means that the inductive inference requires many observations, none of which contradict the hypothesis. Also, the pattern must be observed under many different circumstances. Hence, Bacon stressed the importance of systematic experimentation, as this allows the generation of large quantities of evidence, under controlled but varying conditions.

1.1.1 Difficulties with inductivism

Intuitively appealing as it may be, there are several problems with the inductive approach. The first problem comes from the history of science. Inductivism is not a correct descriptive account of the way science has progressed – or at least not a complete account. Many scientific breakthroughs have not resulted from simply applying the inductive inference. The double helical structure of DNA, for instance, could not be inferred from a large number of observations. Rather, it required creativity and bold hypothesizing on the part of Watson and Crick. The rules of inductive inference, then, appear to be too restrictive and out of line with actual scientific practice.

Another criticism is that the ideal starting point for the inductivist, gathering facts without theoretical prejudice, is unrealistic for several reasons. First, observations are selected. Researchers must make a selection of the kinds of observations that they deem relevant, and this presupposes some theoretical background knowledge. For example, the law of constant proportions, which says that elements are always present in the same proportions by mass in any sample of a given chemical compound, could not be discovered (inductively generalized) before the difference between compounds and mixtures was illuminated. Only then could chemists select the right set of relevant observations on which to base this law (mixtures are not relevant to the law of constant proportions).

Second, theory-free factual statements do not exist – they are always theory-laden. This is a result of the scientific terminology involved. For example, even the simple statement "this is a plant of species X" uses the theory-laden concepts of 'plant' and especially 'species', and is therefore rife with presupposed theoretic background knowledge.

A third reason theory-free facts are problematic is that observations are often acquired using techniques that are highly theory-dependent. Suppose a molecular biologist performs a Western blot to detect a specific protein in a biological sample. The presence of the protein is visualized as a highlighted area on a photograph, taken by a CCD camera with emission filters which picks up a fluorescent signal given off by a reporter molecule, attached to a secondary antibody, attached to a primary antibody, attached to the target protein, attached to a nitrocellulose membrane that has received the proteins from a gel that has undergone electrophoresis to sort the proteins by size or structure. Trusting the results of the Western blot presupposes the acceptance substantial theoretical knowledge of the various physical and chemical mechanisms at work in the detection of the protein. The trustworthiness of observations depends on the reliability of observational theories, and consequently, observations are not theory-free.

1.1.2 The problem of induction

The most fundamental objection to inductivism has come to be known as 'the problem of induction'. A notable proponent of this objection was David Hume, but it goes back to at least the 2nd century philosopher Sextus Empiricus. The problem of induction concerns the difficulty of moving from a collection of particular observations to a universal statement. As explained by Sextus Empiricus, the universal statement is either based on a complete, exhaustive collection of all the particulars, or on a limited sample of the particulars. Observing all particulars is usually impractical or impossible (e.g. in order to infer the universal statement that opposite sides of magnets attract each other, we would have to observe all the magnets throughout the universe that have ever existed or ever will exist). On the other hand, inferring the universal from a limited sample could lead to errors, because we cannot logically exclude the possibility that some of the unobserved particulars would negate the universal statement. No attainable amount of empirical support for the universal statement that all ravens are black can guarantee that we will never encounter a white raven.

Another conception of the same problem concerns the lack of justification for inferring future patterns from past experiences. For example, in all experiments performed in the past we have observed that plutonium-239 has a half-life of 24,110 years. But that still does not guarantee that plutonium will decay in the same fashion in the future. For this we need the additional assumption of the uniformity of nature, as David Hume put it.

Both conceptions of the problem of induction boil down to the same issue: it is not logically valid to infer a universal statement from an incomplete collection of particulars. The universal statements are never justified, in a strictly logical sense. Formulations of natural laws are always underdetermined – they always go beyond the evidence we have for them.

A related problem is that one of the required conditions for making the inductive inference, namely that a pattern must be observed under many different circumstances before it can be generalized in a universal statement, can never be sufficiently satisfied. This is because the variety of circumstances under which experiments can be conducted is literally endless. It would make sense for physicists to test whether the decay rate of plutonium-239 depends on temperature or pressure, but who is to say that it could not also depend on the position of Saturnus, on the hair color of the experimenter, on who won the Super Bowl last year, or on any other imaginable or unimaginable factor? If these questions seem silly, this only goes to show how our theoretical prejudice determines which factors are deemed meaningful variables.

1.1.3 The legacy of the inductive approach

Regardless of these problems, inductivism has been of major importance for the development of the sciences. While scientific practice did not in actual fact follow the inductivist ideal, Bacon's ideas helped to get science going as a systematic endeavor. Even after being overtaken by falsificationism in the 20th century, the inductive inference is still an essential ingredient of scientific practice, since it is applied every time when a general statement or law is formulated from a limited number of observations. In fact, with the development of statistics inductive reasoning has become more powerful and precise than it has been until the 19th century. Bayesian statistics, which is applied in fields ranging from economics to phylogenetics, is a modern application of inductive reasoning.

1.2 Falsificationism

During the 20th century, Karl Popper (1902-1994) set out to save science from the problem of induction (Popper, 1959/2002). The problem of induction is that even huge numbers of singular observations are unable to prove a general statement. However, one single observation is enough to *disprove* it. Thus, says Popper, science should progress not by proving true theories (for that is impossible), but by disproving false ones. The scientists' task, then, is not to find large quantities of corroborating data, but to find those crucial pieces of data that *falsify* their theories. Hence, Popper's approach is called falsificationism (it is also sometimes called critical rationalism).

The core of the falsificationist method is a deductive argument of the form *modus tollens*: if hypothesis *H* is true, then we should observe *O*; we do not observe *O*; therefore, hypothesis *H* is false. This is a logically valid argument that leads to a secure conclusion (contrary to the logically invalid inductive inference).

Not only is falsificationism taken to solve the problem of induction, it simultaneously provides a principle of demarcation between scientific and non-scientific or pseudoscientific theories. According to Popper, a theory or hypothesis is scientific if it makes testable predictions regarding observations that have not yet been made. Scientific theories must be falsifiable. Unfalsifiable theories, on the other hand, are deemed unscientific.

Falsificationism leads to a methodology that is radically different from inductivism. The inductivist builds knowledge from the ground up, carefully proceeding from observations to hypotheses, with claims always being in proportion to the evidence. Under falsificationism, scientists have far more freedom. Falsificationism encourages bold hypothesizing that goes much further beyond the evidence, with hypotheses only being tested after they have been proposed. Inductivism is a bottom-up, observation-driven approach. Falsificationism is top-down and hypothesis-driven.

Falsificationism marks a break with the past in another respect as well. Originally, it was hoped that a methodology could be invented that would serve as a mechanical rule book for scientific discovery. Falsificationism offers no guidance whatsoever concerning the generation of hypotheses; rather, it is concerned with the evaluation of hypotheses that have already been postulated.

1.2.1 The provisional acceptance of theories

A difficulty with falsificationism is that while it purports to provide a method for eliminating hypotheses, it lacks guidelines for provisionally accepting them. Provisional acceptance of theories is important, because it allows scientists to build theories on theories (e.g. like current research in molecular biology presupposes atomic theory), and because eventually scientists will want to use theories for technological or medical applications. Eventually, theories about radioactivity will be used to construct a nuclear power plant, theories about aerodynamics will be used to build an airplane, et cetera. Falsificationism, however, does not tell us at what point, after how many successful tests, a theory is fit for practical application. For regardless how many attempts at falsification a theory has survived, no matter how often its predictions have been verified, under falsificationism one is never justified in regarding a theory as true, or even probable. To do so would be to apply the inductive inference, which is exactly what the falsificationist wants to avoid.

Falsificationism provides no stopping point for testing theories. Recall the problem with inductivism mentioned above, concerning the endless array of different circumstances under which a theory would

have to be verified. The same problem resurfaces for falsificationism: there are infinitely many circumstances under which a theory can be tested.

1.2.2 Is the problem of induction really solved?

Another criticism is that falsificationism does not really succeed in solving the problem of induction (Hoyningen-Huene, 2010, 6:28-11:42). Falsificationism holds that universal statements (hypotheses, theories, and formulations of natural laws) can be falsified by singular observation statements. But a falsifying experiment, to be acceptable to the scientific community, must be reproducible. As every experimental scientist knows, results should always be repeatable, to counter the danger of experimental error. This was famously illustrated by the 2011 anomalous measurements that seemed to show that neutrinos can travel faster than light (Reich, 2011). This observation did not falsify the theory of special relativity, as it was subsequently shown that the anomalous readings resulted from an improperly attached fiber optic cable (Cartlidge, 2012).

This need for reproducibility seems to undermine the idea that *truly singular* observation statements can refute a universal statement. Observation statements based on experimental data are actually generalizations or statistical inferences from numerous singular measurements. So have we really circumvented the inductive inference? Does this not mean that falsifying observation statements depend on *inductive* generalizations from a limited number of observations?

In defense of falsificationism, it can be pointed out that observation statements, even if they are based on a large number of observations, are still considered 'singular' statements, not universal statements. The statement "at times t_1, t_2, t_3, at places p_1, p_2, p_3, et cetera, we observed that *X* was followed by *Y*" is a singular statement, and not the result of an inductive generalization. (The inductive generalization would be: "*X* is always followed by *Y*.") Since a singular statement is all that is required to falsify a universal statement, falsificationists do not depend on the inductive inference.

It is still true, of course, that such singular observation statements are fallible, and that falsification is therefore never absolutely definitive. Also, the second conception of the problem of induction (the lack of justification for inferring future patterns from past experiences) remains untouched by falsificationism. We still require the principle of the uniformity of nature.

1.2.3 Rescuing theories by introducing auxiliary hypotheses

The falsification of theories is problematic for yet another reason. It is often the case that researchers refuse to acknowledge the refutation of their theories in spite of seemingly falsifying data. Popper himself recognized this, and mentioned several ways in which anomalous data can be dealt with to avoid falsification of a cherished theory (Popper, 1959/2002, pp. 60-61). The data could, for instance, be explained away as a measurement error. Or the reliability of the experimenter can be questioned. Or the discrepancy can be resolved by amending the theory with an auxiliary hypothesis that explains the data.

As an example of this behavior, take the response to the unexpected findings of soft tissue with traces of collagen in *T. rex* bones, dated over 65 million years old (Asara, Schweitzer, Freimark, Phillips, & Cantley, 2007; Schweitzer, Johnson, Zocco, Horner, & Starkey, 1997b; Schweitzer et al., 1997a; Schweitzer et al., 2007; Schweitzer, Wittmeyer, Horner, & Toporski, 2005). These findings were highly controversial, as it seemed incredible that soft tissue and biomolecules could be preserved for such a long time. But this did not lead to a reevaluation of the theories on which the dating of these bones was based. Instead, the veracity of the findings was questioned. Some critics attempted to explain it

away as contamination or misidentification (Buckley et al., 2008), while others postulated that the observed soft tissues were actually bacterial biofilms, rather than authentic *T. rex* tissue (Kaye, Gaugler, & Sawlowicz, 2008). Both the contamination and biofilm explanations have turned out to be untenable (Bern, Phinney, & Goldberg, 2009; Lindgren et al., 2011; Schweitzer, Zheng, Cleland, & Bern, 2013), and biomolecules have now been found in numerous other fossils from the Cretaceous and before (Cleland et al., 2015; O'Malley, Ausich, & Chin, 2013; Schweitzer et al., 2009). Eventually, the original discoverers proposed the auxiliary hypothesis that a hitherto unknown chemical mechanism (with iron atoms helping to cross-link and stabilize biomolecules) could have preserved the tissues for millions of years (Schweitzer et al., 2014).

When a proponent of a theory blames discrepant data on instrument error or the incompetence of the experimenter, the issue can usually be resolved by simply repeating the experiment. (This is not always the case – in archeological and paleontological research, for instance, an object can be excavated only once, and part of the evidence is thereby destroyed.) Inventing an auxiliary hypothesis, on the other hand, is a more philosophically interesting way of dealing with anomalous evidence, and also more problematic, from the perspective of falsificationism. It is problematic because it can immunize theories against falsification. By postulating auxiliary hypotheses, it is practically always possible to escape falsification. This seems to lead to the conclusion that theories are unfalsifiable.

Popper solves the problem by adding a methodological rule to the falsificationist approach. This rule disallows the utilization of auxiliary hypotheses *unless they increase the falsifiability of the system as a whole*. Hypotheses that lead to several new predictions are acceptable, and may even strengthen the theory. But purely *ad hoc* hypotheses, whose only function is to explain away some anomalous data, without furnishing additional predictions, are prohibited. A similar way of distinguishing between legitimate and illegitimate use of auxiliary hypotheses is found in the philosophy of Imre Lakatos, as described in Section 1.4.

1.3 Kuhn's paradigm theory

After Popper proposed falsificationism as a prescriptive model for scientific methodology, the American historian and philosopher of science Thomas Kuhn (1922-1996) offered a *descriptive* account of actual scientific praxis. According to Kuhn, the history of science in any given discipline goes through a certain succession of phases: the pre-normal phase, the normal phase, and the revolutionary phase (Kuhn, 1962/1996).

During the pre-normal phase, the field is still in its infancy. There are several competing schools of thought, and consensus is lacking even about what constitutes the proper subject matter for the field. Examples are the fields of physical optics before Newton, and electricity during the first half of the 18th century.

When a theory is proposed or (re)formulated that is persuasive enough to win over the majority of researchers, the field matures and enters the normal phase. Kuhn calls such a theory a *paradigm*. During its reign, the paradigm shapes the landscape of scientific research in its field. The paradigm is not questioned by the scientists working under it, rather, the paradigm itself defines the field and determines which research questions are being asked. The period of normal science is characterized by a certain degree of dogmatism: anomalous data is not treated as evidence against the paradigm, but rather as presenting open, unsolved research questions, and attempts will be made to explain it under the ruling paradigm. These explanations may consist of auxiliary hypotheses. Sometimes *ad hoc* or even far-fetched explanations are accepted because they rescue the paradigm from falsification.

When the paradigm is plagued by a large number of anomalies, the paradigm is said to be in crisis. The revolutionary phase ensues when a new theory becomes available that more successfully explains the observations that were anomalous under the old paradigm. This leads to a paradigm shift, in which the new theory replaces the old one as the ruling paradigm, setting in a new period of normal science. Archetypal instances of paradigm shifts were the rejection of geocentrism in favor of heliocentrism in de 17th century, the replacement of Newtonian by Einsteinian physics in the early 20th century, and the shift from a stationary view of the continents to plate tectonics from the 1920s through the 1950s.

1.3.1 Incommensurability

One aspect of Kuhn's outlook on science is that competing paradigms are to some extent incommensurable. This means that they are so conceptually different that it may be difficult to directly compare paradigms to each other. Some of the new concepts cannot be expressed in terms of the old ones. For instance, the wave function of quantum mechanics is not expressible in terms of the ether field of field theory. Also, paradigms may differ with respect to how hypotheses are evaluated. For example, in classical physics determinism was considered an important value, while quantum mechanics is open to probabilities. As a result, the shift from one paradigm to another is, in some sense, a leap of faith. It is not a purely rational choice.

1.3.2 Paradigm theory vs. falsificationism

Kuhn's paradigm theory seems at odds with falsificationism. The dogmatic element of normal science runs counter to Popper's admonition that scientists should attempt to falsify their theories. During normal science, researchers are not trying to falsify their paradigm. Much to the contrary: they actively try to resolve discrepancies within the framework of the paradigm, working hard to avoid falsification. It is only during and after the revolutionary phases that old paradigms are criticized by the mainstream scientific community. And it is only then, after the fact, that anomalous data, which may have been well known for a long time, comes to be regarded as falsifying to the old paradigm.

1.4 Sophisticated falsificationism

Whereas Popper gave a prescriptive account of how science *should* work, Kuhn delivered a descriptive narrative of how science actually *does* work, and these two were at odds with each other. Popper's approach (at least as it is often simplified) requires scientists to ruthlessly reject falsified theories, but Kuhn has shown that scientists are very reluctant in rejecting the paradigm they are working under. Also, in Kuhn's view competing paradigms represent wildly different ways of looking at the data, making it very difficult to compare them to each other. This implies that paradigm shifts have an irrational component to them. Although this might not be entirely fair, Kuhn's theory could be understood to be emphasizing dogmatism and irrationality – two characteristics most philosophers would not wish to subscribe to science. The Hungarian philosopher of science and mathematics Imre Lakatos (1922-1974) proposed what he called sophisticated falsificationism to salvage the rational essence of science (Lakatos, 1980).

1.4.1 The failure of dogmatic and naïve falsificationism

Lakatos distinguishes three types of falsificationism: dogmatic, naïve, and sophisticated falsificationism. Dogmatic falsificationism, Lakatos argues, is a position mistakenly ascribed to Popper. According to the dogmatic falsificationist, theories must make testable predictions in order to be

scientific. When a theory fails a test, it is conclusively refuted and must be rejected. This rejection is final and should never be revisited. Under dogmatic falsificationism, disproof, refutation, and falsificationism are the same thing.

Lakatos rejects dogmatic falsificationism (ibid., pp. 14-19) on the grounds that definitive, incontrovertible refutation by falsifying 'facts' is impossible. As explained in Subsection 1.1.1, theory-free facts do not exist. Therefore, contrary to dogmatic falsificationism, facts are not 'harder' than theories, and cannot definitively refute theories.

But even if facts were harder than theories, dogmatic falsificationism would still fail to achieve its aspired goal of definitive falsification. Proper scientific theories are not mere descriptions, but attempts to explain our observations – that is, they describe cause-and-effect relations. It is through the nature of these relations that expectations (predictions) are generated. Suppose that a theory states that observation *O* is the result of cause *C*. This can be tested in an experimental setup where *C* is generated, eliminated or changed in some way. The theory predicts that *O* should change accordingly. But, unfortunately, this is not a hard, ironclad prediction of the theory. The prediction only holds on the condition that no other factor, "possibly hidden in some distant and unspecified spatio-temporal corner of the universe" (ibid., p. 17), has any influence on the outcome. But this means that theories are never tested in isolation. What is tested is always a conjunction of a theory and a so-called '*ceteris paribus* clause', which states that no other relevant factor is in play. In the event of a failed prediction, one can always choose to blame the *ceteris paribus* clause, rather than the theory. The *ceteris paribus* clause can be replaced by an auxiliary hypothesis regarding some hitherto unknown force, particle, entity, or mechanism, leaving the theory untouched. Dogmatic falsificationism is therefore untenable, since its ideal of conclusive refutation is logically unattainable.

Naïve falsificationism is in many respects similar to dogmatic falsificationism. According to the naïve falsificationist, theories are scientific if and only if they produce testable predictions. And if these predictions are contradicted by the evidence, the theory is falsified and must be rejected, and this rejection is final. The difference with dogmatic falsificationism is that the naïve falsificationist fully acknowledges that his scientific judgments are always fallible. But he adopts a form of *conventionalism* to cope with this problem: he holds that the truth or falsity of propositions cannot be proven from facts, but may be *decided by agreement* (convention) among scientists. The naïve falsificationist, therefore, separates falsification from refutation and disproof: hypotheses can be regarded as falsified, without being strictly disproven or refuted, because our decisions are fallible.

A researcher working under the methodology laid out by naïve falsificationism, must make a number of conventionalist decisions. When performing a test, he must decide which theory to treat as falsifiable, and which theories to relegate to the unproblematic background knowledge. If the test results are at odds with the predictions of the theory under consideration, then in order to finalize the falsification he must decide to accept the *ceteris paribus* clause and reject the theory, rather than *vice versa*. (Of course, the *ceteris paribus* clause can and should be tested and corroborated, but can never be proven.) And if statistics play a role in the testing of his theory, he must also decide which arbitrary level of significance (e.g. 0.05) is required for falsification.

As a metaphor of the naïve falsificationist approach, compare the theory to a nut that must be cracked (Figure 1). In a strict, logical sense, the theoretical knowledge that must be presupposed in order to falsify a theory, is not 'harder' than the theory under test. So the naïve falsificationist uses conventionalist decisions to 'harden' or 'fortify' both the hammer (the observation statement) and the

anvil (other background knowledge, including the acceptance of the *ceteris paribus* clause), so that the nut can be cracked.

Lakatos rejects naïve falsificationism because these 'decisions' are too arbitrary (ibid., p. 99). Also, the history of science does not bear out the approach prescribed by naïve falsificationism. Researchers have often challenged and revisited experimental falsifications (ibid., p. 30), contrary to the 'once and for all' attitude stipulated by naïve falsificationism.

Figure 1: Falsifying a theory can be likened to cracking a nut. The naïve falsificationist uses conventionalist decisions to 'harden' the hammer (the observation statement that is in conflict with the expectations of the theory) and the anvil (other background knowledge).

1.4.2 Sophisticated falsificationism

Sophisticated falsificationism differs in that it does not aim to isolate hypotheses in order to test them. Rather, the sophisticated falsificationist holds that we always test the whole of our knowledge (this is similar to a principle that was already known as the Duhem-Quine thesis). This means that he does not need the decision to relegate certain theories to the unproblematic background knowledge in order to test one particular theory in isolation. The theory of primary interest, the 'observational' theories, the *ceteris paribus* clause, and even the observation statement itself, are all lumped together and tested as a whole.

> It is not that we propose a theory and Nature may shout NO; rather, we propose a maze of theories, and Nature may shout INCONSISTENT. (ibid., p. 45)

Recall that observation statements result from applying the observational theories (e.g. optical theories in the case of telescopic observations, chemical theories in the case of a Western blot) to nature, by means of some measurement technique. Hence, nature influences the observation statement. If the observation statement conflicts with the predictions of the theory, we have not achieved a refutation of the theory, but an inconsistency within the whole of our knowledge. The fault may lie with the theory under consideration, or with the *ceteris paribus* clause, or with the observational theories, or with the observation statement itself (observational error). The scientist, then, is free to tentatively choose (rather than definitively decide) which of these he will change or replace in order to resolve the inconsistency. But, as we shall see shortly, sophisticated falsificationism places requirements on the kinds of changes that are allowed.

Of course, the more prominent a theory is, the more likely it is that the blame will be directed towards one of the other parts of our knowledge. (In fact, prominent theories usually are not tested at all – it is rather their lower-level auxiliary hypotheses that are subjected to tests.) This reality is captured in

Kuhn's paradigm theory. Lakatos also acknowledges this, and incorporates it in his concept of research programs.

1.4.3 Lakatosian research programs

According to Imre Lakatos, scientists are working under gradually evolving research programs (roughly comparable to Kuhn's paradigms). A research programs consists of a 'hard core', a 'protective belt', and a 'heuristic' (Figure 2). The hard core is a prominent theory or some central idea, to which a group of researchers is to some degree committed. The hard core is not questioned by the supporters of the research program, and it does not appreciably change over the years.

The protective belt, on the other hand, is constantly subject to revision. It essentially contains all other knowledge, such as auxiliary hypotheses and observational theories. *The protective belt functions to shield the core beliefs against the 'incoming' grenades of falsifying data.* When observations are inconsistent with their expectations, rather than abandoning it altogether, researchers will often choose to 'tweak' their research program by changing something in the protective belt – perhaps by replacing some expendable subhypothesis by a new one, so the new data can be accommodated without affecting the hard core.

Finally, the research program also has a heuristic. When a new idea is first proposed, it is often no more than a rough sketch. Whether it is heliocentrism, plate tectonics, or natural selection, the initial proposal is very simplistic compared to later versions of the theory, and usually the discoverer is aware of this. At first it is merely the core idea, without the detailed elaborations that come later. However, *the core idea offers directions for further research.* It provides research questions and unsolved puzzles, and may already anticipate an approach for filling in the details. For example, when Newton first applied his law of universal gravitation to the solar system, he used a model in which a single point-like planet revolved around a fixed point-like sun. He then upgraded this to a model in which both the sun and the planet revolved around their common center of mass. Then he added more planets, all interacting with the sun but not with each other. Then he changed all bodies from mass-points to mass-balls. Then he took spinning and wobbling effects into account, then added interplanetary forces, then allowed for bulging planets, et cetera (ibid., p. 50). All of this work could be foreseen at the outset: his core idea provided a heuristic, a direction for future work.

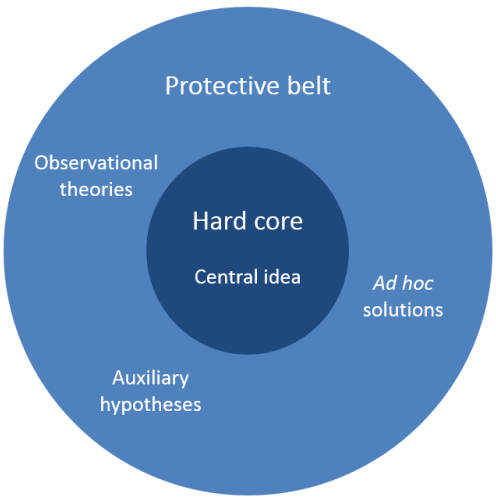

Figure 2: A research program consist of a hard core of static beliefs, and a protective belt containing all other knowledge. The protective belt is dynamic and adapts in such a way that observations can be explained without affecting the hard core.

So contrary to dogmatic and naïve falsificationism (and to popular conceptions, even among scientists, of the scientific method), prominent theories are not really refutable and are not even seriously tested. They become the hard core of a research program. According to Lakatos:

> But this hard core is tenaciously protected from refutation by a vast 'protective belt' of auxiliary hypotheses. And, even more importantly, the research programme also has a 'heuristic', that is, a powerful problem-solving machinery, which, with the help of sophisticated mathematical techniques, digests anomalies and even turns them into positive evidence. For instance, if a planet does not move exactly as it should, the Newtonian scientist checks his conjectures concerning atmospheric refraction, concerning propagation of light in magnetic storms, and hundreds of other conjectures which are all part of the programme. He may even invent a hitherto unknown planet and calculate its position, mass and velocity in order to explain the anomaly. Now, Newton's theory of gravitation, Einstein's relativity theory, quantum mechanics, Marxism, Freudism, are all research programmes, each with a characteristic hard core stubbornly defended, each with its more flexible protective belt and each with its elaborate problem-solving machinery. (ibid., pp. 4-5)

Every successive change in the protective belt of a research program effectually gives rise to a new theory ('theory' now becomes an all-encompassing term signifying the hard core plus the protective belt). Thus a research program is a series of theories, each theory being a refined version of its predecessor – unaltered with respect to the central idea, but different in some secondary aspect.

We saw earlier that sophisticated falsificationism bids us to test the whole of our knowledge, rather than isolated theories. We can now add a temporal dimension to this picture. Sophisticated falsificationism holds that we should not evaluate the strength of a theory at any particular moment in time (in temporal isolation), but instead we should appraise a research program by how it evolves over time.

1.4.4 Progressive and degenerating problem shifts

Changes in the protective belt are called 'problem shifts'. It is in the evaluation of these problem shifts that the rational nature of science comes into play. Lakatos specifies three kinds of problems shifts: scientific, progressive, and degenerating shifts. A problem shift is scientific if the new theory has *excess empirical content* over the old theory – that is, if it predicts novel facts that were not expected under the old theory. If these newly predicted facts are empirically confirmed, Lakatos regards the problem shift as not only scientific but also progressive: it constitutes scientific progress. If, however, the new theory does not predict novel facts, the problem shift is considered degenerative.

Research programs (series of theories) can attain the same evaluative labels (degenerative, scientific, or progressive) based on the types of problem shifts that they typically undergo.

> Thus, in a progressive research programme, theory leads to the discovery of hitherto unknown novel facts. In degenerating programmes, however, theories are fabricated only in order to accommodate known facts. [...] where theory lags behind the facts, we are dealing with miserable degenerating research programmes. (ibid., p. 5)

So rather than appraising theories in temporal isolation, Lakatos' approach is to consider the historical development of research programs. If a research program is characterized by progressive problem shifts, we have good reason to continue scientific effort in that direction. If, on the other hand, a

research program generally features degenerative adjustments, scientists have a rational basis for switching to another research program.

1.4.5 Lakatos' definition of falsification

These insights also change the meaning of falsification. Under dogmatic and naïve falsificationism, falsification is brought about by a discrepant observation. Under sophisticated falsificationism, falsification occurs when a new theory is proposed that explains the success of the old theory and on top of that possesses excess empirical content (i.e. produces new predictions), some of which is corroborated (see Table 1).

Table 1: Some key differences between dogmatic, naïve, and sophisticated falsificationism. Note that 'acceptance' here means 'acceptance as a scientific explanation' (as noted in Subsection 1.2.1, falsificationism does not have a criterion for accepting something as *true*).

	Dogmatic falsificationism	**Naïve falsificationism**	**Sophisticated falsificationism**
Criterion for acceptance	The theory makes testable predictions.	The theory makes testable predictions.	The theory explains the success of its predecessor, and has excess empirical content over its predecessor, some of which is corroborated.
Criterion for rejection	The theory is refuted (disproven, falsified) by a contradictory observation.	The theory is falsified by a *fortified* contradictory observation.	The theory is overtaken (falsified) by a new theory that satisfies the three criteria listed above.

So falsification and refutation are really two different things. A theory can be afflicted by hundreds of anomalies, but still remain unfalsified – until a better theory is proposed. Conversely, falsification can occur quite independently from any specific anomaly – all we need is the advent of a better theory. (It is immaterial whether this new theory is the next emanation of the same research program, or a whole new research program.)

1.5 Applying sophisticated falsificationism to evolutionary biology

In the mid-20th century, during most of the careers of prominent philosophers such as Popper, Kuhn, Lakatos, Quine, and Feyerabend, the philosophy of science was mostly focused on physics. The approaches of Popper, Kuhn, and Lakatos have also been applied to economics (Blaug, 1992). But scant attention was given to biology. This has since changed, and the philosophy of biology is now a respected subfield of the philosophy of science. Yet, to my knowledge, nobody to date has undertaken to critically analyze evolutionary biology using the criteria that Lakatos set forth (but see Michod (1981) for a Lakatosian analysis of Neo-Darwinism).

In this thesis I aim to show that sophisticated falsificationism can be usefully and profitably applied to biology. The evolutionary account of the origin and development of life is a research program, and in the following chapters I will chart its structure and the way it has developed over its history. As will be seen, the terminology of sophisticated falsificationism (hard core, protective belt, progressive and

degenerative problem shifts, *ceteris paribus* clauses, auxiliary hypotheses, heuristic), is quite applicable to the field of evolutionary theory.

1.5.1 A hierarchy of research programs within research programs

Some ideas in science are more ingrained than others. To some theories scientists are deeply committed, while others are held more loosely. Also, about certain questions there exists almost universal consensus, while others are highly contentious and have divided the scientific community in different camps. But even supporters of different schools do usually agree on some more fundamental issue. For instance, in the 1920s Harlow Shapley held that our own galaxy encompassed the entire visible universe, while Heber Curtis argued that spiral nebulae lay outside our galaxy and are in fact independent galaxies – but both of course agreed about the heliocentric model that had been established centuries earlier. This implies that there are research programs on different levels. Two groups of researchers can be working on competing research programs that are both located in the protective belt of an overarching research program on which both groups agree. Scientific knowledge, then, may be ordered as a hierarchy of research programs within research programs. Lakatos has not explicitly written about a hierarchy of research programs, but he did acknowledge that "science as a whole can be regarded as a huge research programme" (Lakatos, 1980, p. 47), which means that particular scientific research programs (such as Newtonian physics, or Big Bang cosmology) are lower-level research programs *within* science; so presumably he would have agreed with the idea of research programs on different levels.

One of my objectives, therefore, will be to map the structure of evolutionary biology in terms of subordinate research programs within the protective belt of the overarching evolutionary program. This will be the subject of the next chapter.

Chapter 2

The macrostructure of the evolutionary research program

If we look at evolutionary biology as a Lakatosian research program, then how is it structured? Which beliefs make up the hard core, and which theories and hypotheses belong to the protective belt? And which of these theories have attained the status of a (subsidiary) research program for themselves?

2.1 Criteria for distinguishing the hard core

Unfortunately, Lakatos did not lay out criteria for determining which propositions and assumptions belong to the hard core. In this study, I will use two criteria for distinguishing the hard core beliefs from those belonging to the protective belt.

First, there is the internal criterion that the core convictions are more fundamental than the peripheral ideas within the program. This criterion has a logical, a historical, and a psychological element to it. Logically, the content of the protective belt is always optional – it is expendable and can be sacrificed, refuted, rejected, without necessarily affecting the hard core. Rejection of a hard core conviction, however, will effectually mean a departure from the program, and will largely remove the motivation for developing the protective belt. Historically, the core is markedly more static than the protective belt. Psychologically, researchers are likely to be more committed to the hard core than to the theories in the protective belt, and they may even find it more difficult to consider or evaluate alternatives to their hard core (in accordance to Kuhn's incommensurability thesis).

Second, I will use the external criterion that the hard core must be formulated such as to set the program apart from competing research programs.

2.2 The long history of the evolutionary research program

Lakatos has remarked: "The actual hard core of a programme does not actually emerge fully armed like Athene from the head of Zeus. It develops slowly, by a long, preliminary process of trial and error." (Lakatos, 1980, p. 48, note 4) This is also true for the evolutionary hard core. Most people associate the rise of evolutionary biology with the work of Charles Darwin, and it is true that Darwin did more than anybody to formulate a robust and biologically informed account of evolution. But Darwin's ideas did not develop in a vacuum. Forms of evolutionary thinking had been around much longer. It preceded Darwin, not by decades, but by millennia.

The pre-Darwinian history and development of evolutionary theorizing is important, because it can teach us which are the program's most fundamental tenets. So in order to apply the first criterion, mentioned above, I will first do a brief survey of the history of evolutionary thought up to Darwin.

2.2.1 Evolutionary ideas in antiquity

Several of the classical Greek philosophers held, to a greater or lesser degree, to a materialistic philosophy: matter was the fundamental substance of reality, and it developed independently of supernatural causation. Accordingly, they formulated origins theories that, however crude and mythological, reflected this perspective. As early as the 6th century B.C. Anaximander of Miletus already speculated that life arose in mud, and that land animals, including mankind, derived from fish (Hippolytus, Refutation of All Heresies, 5). In the 5th century B.C. Empedocles of Agrigentum also argued that life had arisen spontaneously. Interestingly, he proposed that selection played a role in the formation of lifeforms. What arose spontaneously were not complete animals, but parts of animals – heads without necks, arms without shoulders, et cetera. These body parts joined together to form all kinds of different combinations, but only some of these combinations were viable, while the others became extinct. Thus, Empedocles envisioned a sort of trial-and-error process reminiscent of natural selection.

Another notable materialistic philosopher was Democritus, a contemporary of Socrates. He is most famous for advancing the notion that matter is composed of indivisible and eternal particles called atoms. As far as we know he did not write extensively about biological origins, but Deborah Gera notes: "Democritus seems to have discussed the evolution of society and culture and he *may* have included an analysis of the origin and development of language as well" (Gera, 2003, p. 167, italics in original). It was probably under the influence of Democritus that the Greek historian Diodorus Siculus, writing in the 1st century B.C., voiced very modern-sounding ideas about cultural evolution in his *Bibliotheca historica* (I.viii.1-8). He speculated that humans originally lived as foragers, lacking agriculture, clothes, and the ability to use fire. Over time, they learned to take shelter in caves and to store food supplies for the winter. As they started to live in groups for mutual protection against wild animals, they gradually developed speech, as well as the arts to enhance their social lives.

These lines of thought found continuation in the philosophy of Epicurus. This highly influential philosopher lived in the 4th and 3rd century B.C., but he fostered a loyal following that would carry his ideas well into the 2nd century A.D. and beyond. Like Democritus, the Epicureans were atomists and materialists, and while they did believe in the existence of gods, they denied divine providence (Russell, 1948, p. 235). The primary Epicurean text is the lengthy poem *De Rerum Natura* ('on the nature of things'), written in the 1st century B.C. by the Roman poet Lucretius. The following passage nicely captures the Epicurean outlook on natural history:

> Certainly the atoms did not post themselves purposefully in due order by an act of intelligence, nor did they stipulate what movements each should perform. As they have been rushing everlastingly throughout all space in their myriads, undergoing a myriad changes under the disturbing impact of collisions, they have experienced every variety of movement and conjunction till they have fallen into the particular pattern by which this world of ours is constituted. This world has persisted many a long year, having once been set going in the appropriate motions. From these everything else follows. (Lucretius & Latham, 1994, p. 35)

The poem also propounds the evolutionary views of Empedocles (ibid., p. XXX). While this is still far removed from a theory of biological evolution, the relevant observation here is Epicureanism's anti-teleological conception that nature has developed autonomously; that everything that exists has come about by unguided, natural processes – an outlook that would later be shared by the modern thinkers that developed the theory of evolution. Lucretius' poem is of special significance, because it was the reemergence of this text at the onset of the renaissance that brought Epicurean thought back to the attention of natural philosophers.

2.2.2 The return of Epicureanism and the rise of methodological naturalism

During the 3rd century, Epicureanism was eclipsed by Neo-Platonism, which in turn gave way to (and was partly subsumed under) Christianity. During the Late Middle Ages, Aristotelianism was the dominant philosophy in Europe. Aristotelianism was highly teleological: besides material causes, things also have *final causes*, that is, they have a purpose. This applies to both organic and inorganic entities: everything exists and happens for some goal, or *telos*. As a result, the behavior of inanimate objects was often ascribed to their *volitions* rather than their involuntary obedience to natural regularities. Celestial objects follow a circular motion because of their love for the perfect shape of the circle, and stones fall because of their intrinsic longing for the center of the earth. According to some authors, the influence of Aristotle's excessively teleological view of nature was an important impediment to the rise of science (Jaki, 1974, p. 104).

Medieval authors referred to Epicurus' ideas sporadically, and their knowledge about it appears to have been mostly based on secondary sources (Johnson & Wilson, 2007, p. 132). This changed when *De Rerum Natura* returned to the limelight in the 15th century. During the Renaissance and thereafter, the poem was read by, and influenced the thinking of, many eminent scholars, such as Gassendi, Bruno, Bacon, Boyle, Newton, Hobbes, Milton, Kant, and Diderot. It generated renewed interest in materialistic and non-teleological perspectives on nature, and helped atomism to stage a spectacular comeback. As Johnson and Wilson (2007, p. 131) point out: "Thanks in large measure to their compelling presentation in Lucretius' poem, Epicurean ideas effectively replaced the scholastic-Aristotelian theory of nature formerly dominant in the universities."

Initially, these Epicurean ideas were met with skepticism, because they were associated with atheism. But theistic scientists such as Pierre Gassendi, Robert Boyle and Isaac Newton harmonized atomism with a Christian worldview by arguing that atoms are not eternal, but have been created by God. Eventually, atomism gained wider acceptance as it was incorporated into a theistic framework.

More importantly for our present purposes, various forms of materialism gained much traction, especially in the 18th century. The roots of this development are diverse – it was not just Epicureanism. Already in the 13th century, Johannes de Sacrobosco argued that the universe operated as a huge machine (in his words, a '*machina mundi*'). Later, Rene Descartes regarded animals and the bodies of

humans as complex machines, behaving according to the rules of nature (Russell, 1948, p. 506). Meanwhile, Descartes' dualism severed the spiritual realm from the physical. The view that the physical world operates independently, according to its own rules, was bolstered by the success of Newtonian physics – even though Newton himself was a staunch believer in God's continued involvement in creation. The new way of thinking turned out to be widely acceptable. For theists, dualism reconciled the mechanical nature of the physical world with the existence of God and the immaterial soul. For deists, God was the 'First Cause' who stood at the beginning of an otherwise independently operating universe (such a non-interventionist God is very much in line with Epicureanism). And for atheists, of course, the independency of the physical universe fit their worldview perfectly. Eventually, these views morphed into what will here be called *methodological naturalism*: the perspective that science studies only the natural world, not the supernatural.

A good example of this trend towards positing physical explanations for the origin of the world or aspects of it, while still preserving a role for Divine direction, is provided by Immanuel Kant. When Kant published his nebular hypothesis of the origin of the solar system in 1755, he admitted that "Lucretius' theory or that of his predecessors, Epicure, Leucippus, and Democritus, has much in common with mine" (Kant & Watkins, 2012, 1:226). But he completely rejected the Epicurean denial of a divine purpose and direction, and argued that the fact that the law-like behavior of matter compels it to develop into a beautiful and orderly whole, is a strong indicator of the existence of God (ibid., 1:226-8). Later writers were less concerned with preserving a role for God (e.g. Laplace, who came up with his own version of the nebular hypothesis). The important point here, however, is that as methodological naturalism came into vogue among theists, deists and atheists, so did evolutionary scenarios.

2.2.3 Evolutionary ideas from 1700 to Darwin

If naturalism is to be fully embraced (whether this is for ideological, esthetic, or practical reasons), it follows that one should also search for naturalistic explanations for the origin of the living world. It should come as no surprise, then, that the period from Newton to Darwin was rife with speculations about the natural origin of man, animals, and other lifeforms. By 'evolutionary ideas' I do not refer merely to the discredited notion of spontaneous generation (the notion that maggots spontaneously arise in rotting flesh, et cetera) – though belief in spontaneous generation during this period certainly did bolster confidence in the plausibility of a purely materialistic, atheistic worldview (Gregory, 2007, p. 80). Rather, by 'evolutionary ideas' I refer to more substantive *historical scenarios* about the origin of man and other species, usually by some gradual process of descent from more primitive species.

For most of this period, 'evolution' was not the term of choice. In Germany, one spoke of 'metamorphose' (Nisbet, 1986). In France, it was called 'filiation', 'transmutation', or 'transformisme', while in England, it went by such names as 'doctrine of derivation', 'Lamarckian theory', and 'development hypothesis' (Osborn, 1894/1908, p. 15).

One of the earliest modern writers who expressed evolutionary ideas was the French mathematician and philosopher Pierre Louis Maupertuis (1698 - 1759). During this period the observation that creatures seem to possess precisely those characteristics that they need for their lifestyles, was seen as an argument for design. Maupertuis proposed a selection mechanism very similar to that of Empedocles as an alternative to design. Perhaps, he reasoned, chance has produced a large number of individuals with different combinations of organs and body parts. Only a small fraction of those individuals obtained the body parts required for their survival and reproduction, and these gave rise to extant species, while the others died out (Maupertuis, 1768, pp. 11-12).

Another notable author was the French diplomat Benoît de Maillet (1656 - 1738), whose famous book *Telliamed* was published *post mortem* in 1748. This work narrates a conversation between a missionary and an Indian philosopher called Telliamed (the author's name in reverse), who voices de Maillet's own views. Most of the book deals with geology and defends the idea that the earth's rocks have a subaqueous origin and continents have appeared as a result of the sea's diminution. In the final chapter, Telliamed contends that humans and terrestrial animals have descended from aquatic lifeforms. He mentions Lucretius and agrees with his rejection of the divine creation of man (De Maillet, 1748/1797, p. 232).

Telliamed supports his theory with extensive argumentation and numerous examples, which he himself deems utterly compelling. Some of his arguments still hold today. For example, he argues for the reality of biological change from the fact that fish of the same species differ from sea to sea. He also concludes that freshwater fish have descended (with modification) from saltwater fish that entered the rivers (ibid., p. 233). Some of his other arguments are rather fantastical. He documents a large body of anecdotal evidence for the existence of mermaids and what he calls 'sea men', of whom we supposedly descended (ibid., pp. 239-260).

His most interesting class of evidence concerns the similarity of terrestrial and avian species with aquatic species. This appears to anticipate the homology argument that was to be used by later evolutionists. However, most of the similarities he cites, such as the similar movement of fish through water and birds through the air (ibid., p. 234), would today be attributed to convergent evolution, rather than common ancestry. Lacking the current perspective of a single tree of life, de Maillet attempted to establish that different species of reptiles, mammals, and birds evolved from aquatic ancestors independently. Also, he believed that terrestrial mammals descended from aquatic or semiaquatic mammals, rather than the reverse.

At around the same time, Denis Diderot (1713 - 1784) also wrote in support of a materialistic origins of lifeforms. Diderot was the chief editor of the famous *Encyclopedie*, a 28 volume work that resulted from a collaborative effort by numerous writers, artists, and technicians, that came to be seen as an important representation of Enlightenment thought. Following Lucretius and the Epicureans, Diderot believed that matter is continually in motion – constantly rearranging itself in different combinations. Living beings, then, are fortuitous combinations of atoms. Many of the forms thus produced are 'monsters', but those few without serious deficiencies managed to survive and reproduce (Gregory, 2008, p. 122). In Thought XII of his *Thoughts on the Interpretation of Nature*, he seems to have hinted at the possibility of universal common ancestry, citing Maupertuis as a proponent of this view (Diderot & Adams, 1999, pp. 40-41).

It is worth noting that these French authors should not be regarded as isolated oddities. As already explained, their evolutionary ideas developed within the larger context of a move towards (methodological) naturalism. Of course, some thinkers, such as these French materialists, wanted to push the limits of the independent operation of nature further than others. Speculations about the naturalistic development of life were part of a multifaceted debate that included discussions on whether humans have immaterial souls, whether animals have souls, whether apes could be taught to speak, and whether nature possesses the power to produce life (Gregory, 2008).

After the French revolution the torch of evolutionary thinking was carried by Jean Baptiste Lamarck (1744 - 1829), arguably the most famous, or infamous, among the French proto-evolutionists. Lamarck was a thoroughgoing materialist, raised with Enlightenment ideals (Gould, 2002, p. 172). He believed that complex lifeforms have developed from lower forms, through a combination of two mechanisms.

The first mechanism is a 'complexifying force', that results from the flow of fluids through the body, carving out evermore complex canals between tissues. The second mechanism results from pressure on organisms to adapt to their environment. According to Lamarck, whose views on geology were strictly uniformitarian, the environment changes slowly but steadily. As their habitat changes, organisms change their behavior accordingly. Their behavior, in turn, modifies their physical characteristics: the use of certain body parts strengthens and enlarges them, while disuse leads to their deterioration. Finally, these modifications are inherited by their offspring. Today, Lamarck is mostly remembered for this second mechanism, often summarized as 'the inheritance of acquired characteristics'. It has come to be called Lamarckism, and is often contrasted with Darwinism or selectionism: the view that organisms vary randomly and are then selected for their degree of adaptation.

While most biologists and philosophers rejected his proposed mechanisms, the significance of Lamarck's work must not be underestimated. During the early 1800s transmutationism received enough attention in intellectual discourse to prompt Charles Lyell to devote four chapters criticizing specifically Lamarck's version of it in volume 2 of his *Principles of Geology* (Lyell, 1832). Though it was intended as a refutation of Lamarckism, the effect was the wide dissemination of transmutationism in England. Lyell's treatment of transmutationism inspired Robert Chamber's evolutionary ideas (see below), and was read by young Charles Darwin during his Beagle voyage.

2.2.4 Immanuel Kant on mechanistic explanations and teleology

Evolutionary ideas were also being discussed in 18th century Germany (ref Darwin's Ghosts?). The most prominent German scholar to wrestle with evolutionary ideas was none other than Immanuel Kant (1724-1804). In his *Critique of Judgement* (1790), Kant stated that we should pursue mechanistic explanations as far as can plausibly be done:

> Therefore, it is reasonable, even praiseworthy, to try to explain natural products in terms of natural mechanism as long as there is some probability of success. Indeed, if we give up this attempt, we must do so not on the ground that it is intrinsically *impossible* to find the purposiveness of nature by following this route, but only on the ground that it is impossible *for us* as human beings. (Kant & Pluhar, 1987, § 80, p. 303, italics in original)

Intriguingly, as Kant contemplated where the pursuit for a mechanistic explanation for life would lead to, he came surprisingly close to a modern picture of natural history:

> It is commendable to do comparative anatomy and go through the vast creation of organized beings in nature, in order to see if we cannot discover in it something like a system, namely, as regards the principle of their production. […] For there are [some facts in this area] that offer the mind a ray of hope, however faint, that in their case at least we may be able to accomplish something with the principle of natural mechanism, without which there can be no natural science at all: So many genera of animals share a certain common schema on which not only their bone structure but also the arrangement of their other parts seems to be based; the basic outline is admirably simple but yet was able to produce this great diversity of species, by shortening some parts and lengthening others, by the involution of some and the evolution of others. Despite all the variety among these forms, they seem to have been produced according to a common archetype, and this analogy among them reinforces our suspicion that they are actually akin, produced by a common original mother. For the different animal genera approach one another

> gradually: from the genus where the principle of purposes seems to be borne out most, namely, man, all the way to the polyp, and from it even to mosses and lichens and finally to the lowest stage of nature discernible to us, crude matter. From this matter, and its forces governed by mechanical laws (like those it follows in crystal formations), seems to stem all the technic that nature displays in organized beings and that we find so far beyond our grasp that we believe that we have to think a different principle [to account] for it. (ibid., § 80, p. 304)

In this passage we encounter not only the idea of descent with modification, but also a theory of common descent, backed up by comparative anatomy. He then goes on to argue that the earth could have given birth to lifeforms, which in turn parented forms that were better adapted to their surroundings, and so on until the formative power was exhausted. However, Kant reasons, if we were to accept this view of natural history, we would still "have to attribute to this universal mother [that is: the earth] an organization that purposively aimed at all these creatures, since otherwise it is quite inconceivable [how] the purposive form is possible that we find in the products of the animal and plant kingdoms." (ibid., § 80, p. 305) In other words, we would only have managed to push back, but not eliminate, the *final cause*.

2.2.5 Erasmus Darwin's anticipation of evolutionary theory

Turning to England, one of the most interesting figures in the history of evolutionary thought is Charles Darwin's grandfather, Erasmus Darwin (1731 - 1802). He was a medical doctor, botanist, inventor, and one of the last writers of 'philosophical poetry' in the tradition of Lucretius. He personally knew James Hutton (Stott, 2012, p. 170), who is still well-known for his advocacy of uniformitarian geology and 'deep time'.

Erasmus Darwin was a materialist with respect to the workings of nature. But he also believed, with the deists, that God was the 'First Cause' who set everything in motion. Like Gassendi before him, he argued that a proper understanding of atomism should not lead to atheism (E. Darwin, 1794/1803, XXXIX.12.6, p. 441).

That Erasmus Darwin was an evolutionist can be gleaned from his most important work, *Zoonomia*, published in 1794. He rejected species fixity and stated that animals have 'acquired' their traits by adapting to their environment over many generations:

> Beasts of prey have acquired strong jaws or talons. Cattle have acquired a rough tongue and a rough palate to pull off the blades of grass, as cows and sheep. Some birds have acquired harder beaks to crack nuts, as the parrot. Others have acquired beaks adapted to break the harder seeds, as sparrows. Others for the softer seeds of flowers, or the buds of trees, as the finches. Other birds have acquired long beaks to penetrate the moister soils in search of insects or roots, as woodcocks; and others broad ones to filtrate the water of lakes, and to retain aquatic insects. All which seem to have been gradually produced during many generations by the perpetual endeavour of the creatures to supply the want of food, and to have been delivered to their posterity with constant improvement of them for the purposes required. (ibid., XXXIX.4.8, p. 396)

He also thought that "the strongest and most active animal should propagate the species, which should thence become improved" (ibid., XXXIX.4.8, p. 396). And he even speculated that all animals might have descended from one common ancestor:

> From thus meditating on the great similarity of the structure of the warm-blooded animals, and at the same time of the great changes they undergo both before and after their nativity; and by considering in how minute a portion of time many of the changes of animals above described have been produced; would it be too bold to imagine, that in the great length of time, since the earth began to exist, perhaps millions of ages before the commencement of the history of mankind, would it be too bold to imagine, that all warm-blooded animals have arisen from one living filament, which THE GREAT FIRST CAUSE endued with animality, with the power of acquiring new parts, attended with new propensities, directed by irritations, sensations, volitions, and associations; and thus possessing the faculty of continuing to improve by its own inherent activity, and of delivering down those improvements by generation to its posterity, world without end? (ibid., XXXIX.4.8, p. 397)

Erasmus Darwin is particularly relevant, because he (together with Lamarck and Lyell) brought 18th-century French proto-evolutionism into the consciousness of 19th-century English naturalists. He forms one of the links in the sequence of influences running from the ancient Greeks, through Renaissance and Enlightenment thinkers, right down to Charles Darwin's own pedigree.

In 1844 Robert Chambers anonymously published his book *Vestiges of the Natural History of Creation*. This book presents a full-fledged naturalistic narrative of the world, discussing the origin of the solar system, the earth, the first life, and the subsequent development of all species, including large-scale common descent. There is much to be recognized for a post-Darwinian reader familiar with the typical arguments for evolution. The book appeals to homologies, rudimentary organs, and embryonic recapitulation (Chambers, 1844, p. 193ff). It also states that the powers that once created life may no longer be in existence, or may now be weaker than before (ibid., p. 176). This idea already existed in antiquity (Lucretius & Latham, 1994, p. 66), and is mirrored in some modern theories that life originated at a time when conditions were more favorable because the early earth had a reducing, rather than oxidizing, atmosphere (Orgel, 1998). *Vestiges* became very popular and went through 10 editions in 10 years. It strongly influenced Alfred Russell Wallace (Slotten, 2004, pp. 33, 95), the co-discoverer of natural selection. Darwin believed that *Vestiges* paved the way for the acceptance of his theory after the publication of *On The Origin of Species* in 1859.

2.2.6 Reflections on the pre-Darwinian history of evolutionary thought

The purpose of this historical excursus is not to provide a list of interesting trivia, nor is it meant to be an exhaustive inventory of all of Darwin's precursors. Rather, I aim to establish that there exists a continuity of thought, flowing from the pre-Socratic philosophers, via Lucretius, to modern thinkers and finally to the founder of the modern theory of evolution. All of the authors here cited were aware of at least some of their forerunners and were influenced by them, often with regard to both specific hypotheses and the underlying philosophy. A convenient timeline is provided in Figure 3.

The common themes one encounters in these sources are materialism (or methodological naturalism), transmutationism, descent from lower lifeforms, common ancestry, and a form of selectionism as an alternative to design. Of these, the first three are almost ubiquitous, while common ancestry and selectionism occur less frequently.

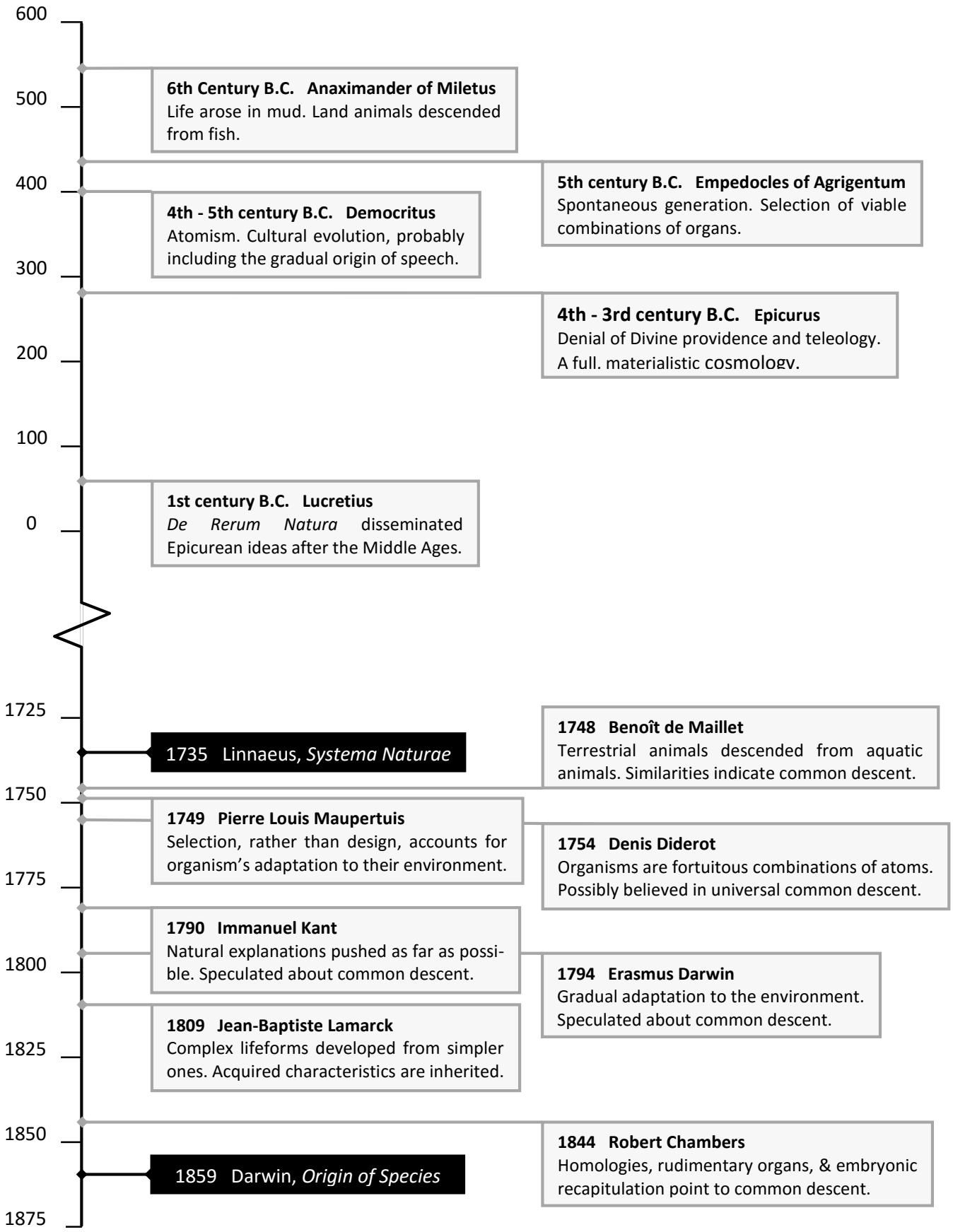

Figure 3: A timeline of pre-Darwinian evolutionary thought. The period between the works of Linnaeus and Darwin, arguably the two most important biological publications in the 18th and 19th centuries, gave rise to a significant amount of evolutionary speculation.

I think it is fair to conclude that many, or perhaps all, major aspects of Darwin's theory were anticipated by one or another author in the preceding centuries. Before the end of the 18th century, however, evolutionary thought amounted to nothing more than a collection of disjointed suggestions and hypotheses. It was not until Lamarck and Erasmus Darwin, and especially Charles Darwin, that these speculations developed into a substantive body of thought that served as a springboard for systematic further research, i.e. a mature research program.

2.3 Formulating the hard core

Having surveyed the history of thought that gave rise to the evolutionary research program, we are now in a better position to distinguish the hard core by applying the criteria mentioned earlier. There are a number of concepts that can be seen as candidates for placement in the hard core:

1. Methodological naturalism, or the origin of all lifeforms through *purely natural* mechanisms.
2. Descent with modification.
3. Common descent of all species from one or a small number of ancestors.
4. Selectionism.

Note that this selection intentionally limits the extent of the research program here discussed to the theory of evolution proper – the development of life *after it had already come into existence*. It could be argued that the theory of evolution is really just a part of an even larger research program, which includes cultural evolution, the origin of life, the birth of the solar system, and the development of the cosmos itself. As Dobzhansky has stated:

> Evolution comprises all the stages of the development of the universe: the cosmic, biological, and human or cultural developments. Attempts to restrict the concept of evolution to biology are gratuitous. Life is a product of the evolution of inorganic nature, and man is a product of the evolution of life. (Dobzhansky, 1967, p. 409)

And indeed, in light of our historical survey, in which we have encountered speculations on the origin of the solar system, the origin of life, and cultural evolution right alongside hypotheses on biological evolution, it appears these are all part of a grand, naturalistic metanarrative. Nevertheless, while I do not presume to disagree with Dobzhansky, I will here restrict myself to evolutionary biology because this is today a reasonably well-delineated scientific discipline. I will neglect cosmological and cultural evolution, and the origin of life will only be discussed to the extent that this is necessitated by a proper treatment of the notion of common descent.

I will now for each of these four candidates discuss whether they should be included in the formulation of the hard core of the evolutionary research program. Recall that I will use the two criteria specified in Section 2.1: the *internal criterion* that the content of the core must be more fundamental than the content of the protective belt, and the *external criterion* that the formulation of the core must set the research program apart from rival programs.

2.3.1 Naturalism

Naturalism, as here defined, is the principle that explanations must be naturalistic, or materialistic, in order to be acceptable or scientific. Note that this is a *methodological* principle – it does not require one to embrace *metaphysical* naturalism, the position that nature is all that exists. A theist or deist can be a naturalist in this methodological sense, even though he believes in the existence of God.

It is my contention that the pre-Darwinian history of evolutionary thought inescapably leads to the conclusion that naturalism lies at the heart of the evolutionary research program. The desire to explain origins materialistically is seen in virtually all major contributors to the program up to Darwin. Naturalism was in many cases the motivation to entertain evolutionary views in the first place.

To some extent, this also applies to Darwin himself. During the first half of the 18th century, naturalism had not yet conquered biology, but it had by and large conquered geology. Lyell and the uniformitarians had successfully supplanted diluvial geology with uniformitarianism, which is very much a naturalistic system. Darwin read Lyell and learned to apply uniformitarianism in geology. Neil Gillespie describes how this set Darwin up to accept a 'positivist' approach to science. By 'positivism', Gillespie means what is here meant by 'naturalism' (Gillespie, 1979, pp. 8, 159, note 121). According to Gillespie:

> Sometime between the spring of 1836 and the fall of 1838, when he was probably irreversibly committed to a belief in speciation by descent with modification (with whatever lingering doubts), Darwin realized that creationist explanations in science were useless. Once this had been decided, transmutationism was left as virtually the only conceivable means of species succession, certainly the only one that could be investigated. Hence, as Howard Gruber has pointed out, the descent theory provided Darwin with a system of laws organizing life – or, to be more accurate, with the problem of identifying those laws – long before he had any idea of its explanation. When Darwin began to consider the problem of species extinction, succession and divergence, he did so as an evolutionist because he had first become a positivist, and only later did he find the theory to validate his conviction. The well-known evidence gathered on the *Beagle* voyage – the similarity of living and fossil species in South America, the distribution of species on the Galapagos Islands, and so forth – became evidence, and its explanation a problem, only because Darwin had grown accustomed to positivistic explanations as a result of bending his mind to geology. (ibid., p. 46)

In other words, according to Gillespie it was naturalism that created the research questions that Darwin set out to answer. If he is right, then even for Darwin naturalism was a fundamental precept underlying his evolutionary research program. This weighs in favor of placing naturalism in the hard core.

Some might object that naturalism is not only an assumption of the evolutionary program, but of science as a whole, and that it is therefore not necessary to explicitly mention naturalism when formulating the hard core of the evolutionary research program. However, it is not at all clear that naturalism is a necessary condition for science. The Belgian philosopher Maarten Boudry has persuasively argued that methodological naturalism is only a *provisory* feature of science since it has grown out of the historical successes of naturalism. After all, "if supernatural explanations are rejected because they have *failed* in the past, this entails that, at least in some sense, they *might* have succeeded" (Boudry, Blancke, & Braeckman, 2010, p. 230). The notion that methodological naturalism is an *intrinsic* feature of science must therefore be rejected – it is entirely possible that, at some point in the future, a non-naturalistic theory or research program might arise that is more successful than its naturalistic competitors.

Nevertheless, many authors are adamant, contrary to Boudry, that methodological naturalism is a required feature of science (Lewontin, 1997; Pine, 1984, p. 10; Young & Strode, 2009). If this position is accepted, then science as a whole must be seen as a massive research program with methodological

naturalism as one of the hard core assumptions: the purpose of science is to explain as much as possible by naturalistic causes. Then evolutionary biology is a research program within the broader program called science. Under this view, naturalism does not need to be mentioned in the hard core of the evolutionary program.

I will here adopt that position, and exclude methodological naturalism from the hard core. However, we should not ignore the long history of proto-evolutionary theorizing, which shows that the motive to come up with a naturalistic or at least a non-teleological explanation for life was present with most proto-evolutionists. If will therefore add a non-teleological clause to the hard core of the evolutionary program. The addition of such a clause also assures that the external criterion is satisfied. It sets the program apart from other ideas about the origin of biodiversity: creation science and intelligent design, which pose, after all, teleological explanations for life.

2.3.2 Descent with modification

Descent with modification, or transmutation, as it was often called before Darwin, is what today would be called evolution. It is the idea that species change over time (Reece et al., 2011, p. G13). Since the Modern Synthesis, some authors define it as 'a change in gene frequencies'.

It goes without saying that this is an indispensable ingredient of evolutionary theory and should therefore be placed in the hard core, in conformance with the logical element of the internal criterion.

2.3.3 Common descent

By 'common descent' I refer to the notion that many current species have descended from a smaller number of common ancestors. Before considering its placement in the hard core, it should be noted that there are several gradations of common descent. A limited form of common descent may hold that only allied species share a common ancestor, like tigers and lions, or horses and donkeys. Even those who believe in special creation accept common descent in this limited sense. The other extreme is universal common descent: all species share a common ancestor. This is currently the majority view. Finally, there is also the possibility that all lifeforms have descended from not one, but a few common ancestors.

Does common descent belong to the hard core, and if so, which gradation of common descent? Common descent was explicitly embraced by some, but certainly not all, of the pre-Darwinian thinkers discussed above. However, Darwin himself accepted common descent and it formed an integral part of his theory as presented in the *Origin*. Ever since Darwin it has been a standard feature of evolutionary thinking, going largely unchallenged for more than 150 years. It appears that common descent is one of the foundational doctrines of the program.

The gradation that I will include in the hard core is not universal common descent, but rather 'large-scale common descent': all species have descended from *one or a few* common ancestors. This leaves open the question whether all life has descended from a single ancestor, or from a small number of independent ancestors.

Today, *universal* common descent is almost unanimously accepted, so why would this not be a part of the hard core? This is because universal common descent does not satisfy the internal criterion, while large-scale common descent does. Recall that the hard core is static: it does not change during the life of the research program. Also, the hard core beliefs are foundational, not optional. Universal common descent fails on both counts. Charles Darwin ended the *Origin* with these words: "There is grandeur in

this view of life, with its several powers, having been originally breathed into a few forms or into one …" (C. R. Darwin, 1859/1979, p. 459). Darwin clearly advocated large-scale common descent, and for him it was an open question to how many independent ancestors life could be traced back. Evolutionary biologists now believe that life can be traced back to a single universal ancestor, but that is a later development within the evolutionary research program.

The current acceptance of universal common descent is the result of empirical studies that showed that all life shares the same biochemistry. But it did not have to be this way. It is entirely conceivable that we would have observed two or three domains that differ radically from each other. Evolutionary biologists would then have concluded that life arose at least two or three times, and that these domains have evolved independently – and the evolutionary research program would not in any way have suffered from this. The program would have been substantially the same, save for the notion of common descent. Whether all life has evolved from one, two, three or a few more independent ancestors is not specified in the hard core. It is a free parameter in the protective belt that can be adjusted to fit the data. If a new lifeform were some day to be discovered that is unrelated to us, this would be unproblematic for the evolutionary research program because the hard core does not forbid such an observation. That there is large-scale common descent is one of the central tenets of the evolutionary research program. The more specific claim that all life descended from a single ancestor belongs to the protective belt.

2.3.4 Selectionism

The final candidate for placement in the hard core is selectionism. Selectionism is here used as a broad term encompassing all hypotheses that postulate some kind of selection process as a major mechanism for evolution. This includes Darwin's hypothesis of natural selection, the Modern Synthesis (or Neo-Darwinism, which combined natural selection with Mendelian genetics), and all their subvarieties and subsidiaries, such as sexual selection and kin selection.

Nobody can deny that natural selection is one of the most important facets of evolutionary biology. It was probably Darwin's most significant contribution. It is hard to even imagine where evolutionary biology would be today, had natural selection never been proposed.

Notwithstanding the importance of selectionism, a strong case could be built against placing it in the hard core. It is not a fundamental part of the program, because natural selection is just one out of a number of possible naturalistic mechanisms by which species may have originated. Perhaps *Lamarckism* is the driving force behind evolution. Or maybe the true cause of evolution is *saltationism*. Or perhaps *neutral evolution* is the dominant mode of biological change.

Each of these alternative mechanisms, (Neo-)Lamarckism, saltationism, and neutral evolution, have at some point been in serious competition with natural selection. Lamarckism and saltationism (the theory that evolution proceeds in large jumps) competed with selectionism in the decades before the advent of the Modern Synthesis, roughly from the 1880s to the 1920s. Neutralism holds that evolution, at least on a molecular level, is predominantly driven by neutral mutations, rather than beneficial mutations that are fixed by natural selection. Neutralism rose in the 1960s (Kimura, 1968) and is still defended today (Nei, Suzuki, & Nozawa, 2010). Thus, we see that selectionism is an optional part of the evolutionary research program. Both logically and historically there are and have been alternative mechanisms.

On the other hand, since the rise of the Modern Synthesis there has been a massive and sustained effort to explain biological phenomena in terms of selection processes. Selectionism could therefore

be recognized as an individual research program, with its own hard core, heuristic, and protective belt. Moreover, while it may have started out as a subsidiary research program that was located in the protective belt of the overarching evolutionary research program, the selectionist program has been so successful (especially compared to Lamarckism and saltationism) that it is now difficult to envision the theory of evolution without it. The selectionist program has become so important, that *it has moved towards* the hard core of the evolutionary research program.

2.3.5 The formulation of the hard core

Combining all this information, we arrive at a hard core that includes descent with modification, large-scale common descent, a commitment to non-teleological explanations, and possibly selectionism. I will utilize the following formulation of the hard core:

All species have originated by descent with modification from one or a few common ancestors, through non-teleological processes such as natural selection.

This formulation satisfies both criteria outlined in Section 2.1. It captures the fundamental, non-negotiable axioms of evolutionary biology, without feigning a commitment to ideas that are really only optional. At the same time, it is specific enough to distinguish evolutionary biology from rival programs such as Intelligent Design.

2.4 The protective belt

Now that we have formulated the hard core, determining the contents of the protective belt is easy. The belt contains everything else. We have already relegated Neo-Darwinism and universal common descent to the protective belt (although selectionism is moving into the hard core), but it also contains all other theories and hypotheses that have been developed within evolutionary biology: all ideas about the mechanisms of evolution, all hypotheses about specific taxa or events in the history of life (such as endosymbiosis), all explanations of anomalies, and even all background knowledge that is in any way involved in evolutionary theorizing (this includes observational theories and *ceteris paribus* clauses).

Figure 4 is a rough sketch of the macrostructure of the evolutionary research program. Here, the protective belt is divided into four quadrants. This is merely an arbitrary method of grouping similar things together – the division of these quadrants only partly corresponds to reality, since there is much overlap between them. For instance, 'background knowledge' plays a role everywhere.

The protective belt of the figure has been populated with hypotheses for illustrative purposes – this is, of course, by no means a complete picture. Items that are listed side by side are not necessarily (but may be) in competition with each other. The way in which a number of these concepts relate to each other will become apparent in the following chapters. Selectionism is marked as a subprogram within the protective belt of the overarching evolutionary program, that has moved towards the hard core of the overarching program. As will be seen in the next chapter, since the rise of the Modern Synthesis selectionism has been a tremendously successful subprogram that has given new impetus to the larger evolutionary research program.

Figure 4: The structure of the evolutionary research program.

Chapter 3

From Darwin to neo-Darwinism

Of the evolutionary mechanisms listed in Chapter 2, saltation and neutral evolution could, theoretically, have played a role in speciation (the splitting of a lineage into two lineages) and/or phyletic evolution (biological change within a single lineage), but not in adaptation. Lamarckism and selectionism are (or rather, were) the candidates for explaining adaptation. Of these, selectionism has achieved a full victory over its rival. It has given rise to the Modern Synthesis, or neo-Darwinism: a subprogram so successful that it has almost come to be equated with evolutionary biology itself (hence its move towards the hard core in Figure 4). This chapter traces the development of ideas from the 1870s to the reign of neo-Darwinism. Where applicable I will draw connections to Lakatos' methodology of scientific research programs.

3.1 The demise of Lamarckism

After the publication of the theory of natural selection by Charles Darwin and Alfred Russel Wallace in 1858 (C. R. Darwin & Wallace, 1858) and more extensively by Darwin in 1859 (C. R. Darwin, 1859/1979), Lamarckism did not immediately disappear from evolutionary discourse. Quite the opposite happened: while many biologists accepted Darwin's thesis of common descent, his proposed mechanism, natural selection, was met with skepticism. Even Darwin himself came to doubt the strength of selectionism, and resorted to a form of Lamarckism to explain biological change.

3.1.1 Early problems with selectionism

Selectionism seemed to be plagued by several problems. For one thing, natural selection was thought to be much too slow to account for the diversity and complexity of life within the available timeframe. During the second half of the 19th century, estimates of the age of the earth ranged in the tens of

millions of years. The highly respected physicist William Thomson, better known as Lord Kelvin, had calculated the age of the earth to be between 20 and 100 million years – the time required for the originally completely molten earth to cool to its present temperature (Lewis, 2002, pp. 34-36). (At the time, radioactivity and mantle convection, both of which produce additional heat within the earth, were unknown.) It was not until the advent of radiometric dating in the 20th century that estimates for the age of the earth in the billions of years gained general acceptance. For Darwin, however, it seemed he needed a faster mechanism than natural selection.

Also, many of Darwin's contemporaries more or less held to the notion of 'blending inheritance': the idea that an offspring's characteristics are a fusion of those of its parents, like a mixture of red and white paint will result in pink paint. If this is how inheritance works, then new (beneficial) varieties will quickly disappear. They will diminish by each passing generation and blend back into the population average faster than natural selection can increase their numbers. Obviously, some other theory of inheritance was needed.

3.1.2 Pangenesis

These were serious problems for selectionism. One author even goes so far as to say that, by this time, a good Popperian would have regarded Darwin's theory as "falsifiable but falsified" (Lee, 1969, p. 296). What happened next, however, is more intelligible when viewed through the spectacles of Lakatos' sophisticated falsificationism, than under dogmatic or naïve falsificationism.

As noted in the previous chapter, selectionism is an optional part of the overarching evolutionary program. (At least conceptually; of course, in light of current knowledge we could say that it is empirically the only feasible mechanism for adaptation, and therefore no longer 'just optional'.) It is entirely understandable, then, that Darwin attempted to salvage the hard core of his program by postulating another hypothesis in the protective belt – another mechanism than natural selection.

The mechanism he (provisionally!) articulated was pangenesis, a form of Lamarckian inheritance (C. R. Darwin, 1875, pp. 369-399). If an organism's acquired characteristics are inherited by its offspring, one could justly inquire by what mechanism this is achieved. The pangenesis hypothesis entailed that cells from all tissues secreted tiny particles called gemmules (or pangenes, or granules) that accumulated in the reproductive cells. In this way, information can be carried from all parts of the parent's body to its offspring, and the use and disuse of body parts in the parent can influence the development of those parts in its descendants.

3.1.3 Weismann's critique of Lamarckian inheritance

The most outstanding critic of Lamarckian inheritance in the late 19th century was August Weismann. A strong proponent of selectionism, this German biologist argued for a clear division between germ cells (gametes: egg and sperm cells and their progenitors) and somatic cells (which make up all other tissues, e.g. muscle cells, skin cells). According to his germ plasm theory, it was only through the germ line that hereditary information was carried to the next generation (Weismann, 1893). Somatic cells make no contribution. It is therefore impossible that changes in somatic tissues, resulting from use or disuse during the lifetime of the parent, affect the traits of its offspring.

Weismann criticized Darwin's pangenesis, on the grounds that evidence was required for the existence of gemmules, unknown and hypothetical entities (Weismann, 1889, pp. 78, 81), but no such evidence had come to light. Furthermore, he found it inconceivable that gametes should contain gemmules not only from every part of the body, but also from every stage of development:

> What an incomprehensible number of gemmules must meet in a single sperm- or germ-cell, if each of them is to contain a representative of every molecule or group of molecules which has formed part of the body at each period of ontogeny. […] One and the same part of the body must be represented in the germ- or sperm-cell by many groups of gemmules, each group corresponding to a different stage of development ; for if each part gives off gemmules, which ultimately reproduce the part in the offspring, it is clear that special gemmules must be given off for each stage in the development of the part, in order to reproduce that identical stage. And Darwin quite logically accepts this conclusion in his provisional hypothesis of pangenesis. But the ontogeny of each part is in reality continuous, and is not composed of distinct and separate stages. (ibid., pp. 324-325)

Weismann also provided examples of adaptations that could not possibly have originated from practice. For instance, butterflies (Weismann specifically refers to *Vanessa levana*) lay their eggs in such an orientation as to optimize their protection. They lay eggs only once in a lifetime, so they cannot learn or improve their egg-laying skills over their life. Likewise, the protective cocoons of the pupae of many insects are highly complex, but are produced only once in the lifetime of an individual, and therefore cannot be improved by practice. The origin and perfection of these adaptations, therefore, cannot be explained by the inheritance of acquired characteristics. They can only be explained by natural selection (ibid., pp. 94-96).

In addition, Weisman attacked the empirical support that was traditionally used to defend the inheritance of acquired characteristics. One such class of evidence was the degeneration of unused organs, such as the loss of functional eyes in animals that have lived in caves for many generations. Weismann argued that this can be explained apart from Lamarckian inheritance: “it is merely due to the cessation of the conserving influence of natural selection” (ibid., p. 88).

Another class of evidence for Lamarckism was the alleged observation that mutilations are inherited. To dispel this argument, Weismann performed an experiment in which the tails of mice were removed in five consecutive generations (ibid., pp. 431-433). None of the 901 newborn mice were born without a tail, or even with a smaller tail. Lamarckism could, of course, be rescued from such disconfirming results by claiming that tails are less prone to hereditary effects than other organs, or that mice have weaker hereditary powers, or that it takes more than five generations for the mutilations to take effect (ibid., pp. 433, 435). But these would all be ‘conventionalist stratagems’ on the part of the Lamarckist. It saves Lamarckism in exactly the way the Lakatos forbids: the evidence is explained away after the fact, without any independent evidence for the auxiliary hypotheses, and without leading to new predictions. The Lamarckian program was clearly in a degenerative state by this time.

With selectionism under pressure, and Darwin’s appeal to Lamarckian inheritance exposed as a degenerative problem shift, the theory of evolution found itself without an agreed upon mechanism. A strict Popperian might have demanded the repudiation of evolutionary theory at this point. But since the notion of common descent so elegantly explained both embryological data and comparative anatomy, scientists were not prepared to jettison the evolutionary research program. This tenacity (or stubbornness) in retaining a paradigm or research program in the face of difficult challenges fits a Kuhnian or Lakatosian model much better than a dogmatic or naïve falsificationist model. Lee aptly comments: “The scientist, like the gambler, may be more tempted by the prospect of possible future gains than disheartened by present loss” (Lee, 1969, p. 301). And indeed, the early 1900s would bring redemption, both in the form of higher estimates for the age of the earth, and the rediscovery of a powerful theory of inheritance: Mendelian genetics.

3.2 Gradualism vs. saltationism

During the latter part of the 19th century biologists were unaware of the existence of discrete units of inheritance (genes). They still held to the 'blending' view. It is in part due to this lack of a robust theory of inheritance that a controversy broke out between gradualists and saltationists.

Gradualism was defended by Darwin (hence, it is also called Darwinism), and later by Karl Pearson and Walter Weldon (Provine, 2001, pp. 26-35). The gradualists believed that evolution is *continuous*: it proceeds by small, incremental steps. According to the gradualists, it was the small differences observed between individuals within populations that were the raw material for evolution. Natural selection worked on these small variations.

Saltationism was initially advocated by Darwin's friend Thomas Henry Huxley and Darwin's half-cousin Francis Galton (ibid., pp. 11-12), and later by William Bateson (bid., pp. 41-43). Huxley and Bateson were skeptical about gradualism, because they believed selection to be too weak and the individual variations too small to amount to anything significant in the long run. Galton was critical of gradualism because he thought any directional change wrought by selection would quickly be undone by 'regression to the mean' of the population (Gillham, 2001, p. 91; Provine, 2001). So instead they proposed that evolution is *discontinuous*: it progresses by large, sudden leaps, which Huxley called saltations (Provine, 2001, p. 12).

3.2.1 Biometricians and gradualists vs. Mendelians and mutationists

Around the turn of the century, the main representatives of the gradualist camp were the biometricians, a group of highly influential biologists that endeavored to apply statistical methods to biological problems. The leaders of this school were Walter Weldon and Karl Pearson. Their most vocal detractor was William Bateson, who vigorously defended the discontinuous view. William Provine (ibid., pp. 25-89) describes how the disagreement about the mechanism of evolution led to a bitter controversy that raged for several years, featuring heated exchanges, personal attacks, and political power plays. Provine laments the fact that this conflict delayed the development of the neo-Darwinian synthesis (ibid., p. 25). On the other hand, as we will see, some of the arguments advanced in this debate now allow us to detect the kinds of progress that conform to Lakatos' methodology of scientific research programs.

In 1900 Hugo de Vries, Carl Correns, and Erich von Tschermak rediscovered Mendel's laws of inheritance. Mendelian inheritance entailed that heritable traits do not blend, but are carried from parent to offspring by discrete units of inheritance, called genes. Each individual possesses two versions of each gene, called alleles; one is received from each parent. During reproduction, the alleles segregate, so that only one allele of a gene is transmitted to each offspring. Alleles of different genes segregate mostly independently, so that a large amount of observable (phenotypic) variation is possible within a population, on account of each individual possessing a different combination of alleles. For some genes, one allele can be dominant while another is recessive. If an individual carries these two alleles (i.e. the individual has a heterozygous genotype for this gene), only the dominant allele is expressed in the phenotype, while the recessive trait lies dormant. Only if both alleles are of the recessive type (i.e. the individual is homozygous for this gene), is the recessive allele expressed in the phenotype. This explains why certain traits can sometimes 'skip' a generation.

Mendelian inheritance, which came to be called 'genetics' by Bateson, presented both a solution and a new problem to evolutionary thought. On the one hand, it solved the problem of beneficial traits disappearing because of blending or regression. On the other hand, it explained individual variations

in terms or *preexisting* alleles. This means that individual variations do not constitute something new. All we observe is new combinations of traits already in existence in preceding generations. Evolution requires the generation of truly *novel* variation. Hugo de Vries solved this problem by proposing that new variation is generated by large, abrupt mutations (de Vries, 1901). These mutations would be distinct from ordinary individual variations, and would represent large, discontinuous jumps. This put de Vries in the camp of the saltationists.

Not surprisingly, Mendelism was immediately seized upon by William Bateson, who saw in it a powerful argument for discontinuous evolution. The biometricians, for their part, regarded Mendelism as a threat to continuous evolution. Moreover, Karl Pearson was a staunch advocate of positivism, and the invisible Mendelian 'genes' seemed metaphysical to him (Grattan-Guinness, 2002, p. 1337). The incompatibility between gradualistic (Darwinian) evolution and Mendelism was one of the few things Bateson and Pearson agreed on. Thus, the debate between gradualists and saltationists morphed into a debate between biometricians and Mendelians.

3.2.2 Progressive shifts within the Mendelian program

From a Lakatosian perspective, it is highly revealing to explore the anomalies that initially confronted Mendelism, some of which were eagerly pointed out by the biometricians. For instance, Weldon called attention to the fact that certain characteristics are inherited differently from male and female parents – contrary to Mendelian expectations (Weldon, 1903, p. 290). He also asserted that sex determination itself was hard to explain under Mendelism (ibid., p. 293). Another class of anomalous data concerned heritable traits that did not segregate independently: they appeared to be inherited *jointly* more often than expected on Mendel's law of independent segregation.

But within a decade, these puzzles were spectacularly solved by a series of discoveries by researchers working within the Mendelian program. In 1902 Walter Sutton and Theodor Boveri established the link between Mendel's genes and intracellular structures called chromosomes (Avise, 2014, p. 19). Genes are located on the chromosomes. Somatic cells of higher life forms possess two sets of corresponding chromosomes; one set is inherited from each parent. For the production of gametes (egg and sperm cells) the two sets are mixed and randomly divided into two new sets, and each gamete is given one such newly created set of chromosomes, a process called meiosis. As sperm and egg fuse, a zygote is produced which once again possesses two sets of chromosomes. This mechanism was recognized as the physical basis for Mendel's laws. Each chromosome contains many genes. Genes that are located in close proximity to each other on the same chromosome are less likely to be split up during meiosis. They are *linked* to each other, and hence do not segregate independently. Linkage explained the exceptions to the law of independent segregation (Morgan, 1911).

As it turned out, even genes on the same chromosome can be split up by a process that came to be called crossing-over: the exchange of genetic material between the two corresponding chromosomes during meiosis. The further two genes are apart, the bigger the chance that crossing-over occurs between them. By determining the amount of linkage, the relative distance between two linked genes could be worked out. So not only did the illumination of the role of chromosomes solve the non-independent segregation anomaly, it even led to the development of a method for determining the order of, and quantifying the relative distances between, genes on chromosomes. All of this progress was facilitated by the Mendelian theory of inheritance and Mendel-style breeding experiments. To top it off, over twenty years later crossing-over as a mechanism for exchanging genes between chromosomes, until then only a Mendelian theoretical construct, was demonstrated to be a cytological reality (Creighton & McClintock, 1931).

With the identification of chromosomes as the carriers of genetic information, the road was free to work out the relationship between heredity and sex. In 1901 Clarence McClung had already proposed the existence of sex-determining chromosomes (McClung, 1901, 1902). A few years later, Thomas Morgan found that a mutation causing white eyes in fruit flies was linked to the sex-determining factor (it was on the X chromosome), and that this trait was inherited in a Mendelian fashion once it was assumed that males are heterozygous for the sex-determining factor while females are homozygous (Morgan, 1910). Thus, the aforementioned anomalies regarding sex-determination and the unequal inheritance of traits through maternal and paternal lines was solved, and in the process important things were learned about sex-linked disorders and the distinction between sex-chromosomes and autosomes.

In his work on the methodology of scientific research programs, Lakatos approvingly states that Newtonian physicists managed to turn "one counter-instance after another into corroborating instances" (Lakatos, 1980, p. 48). Looking at the early history of Mendelian genetics, the same pattern is observed. This is not to deny, of course, that real examples of non-Mendelian inheritance were also found. In 1909 Erwin Baur and Carl Correns discovered that certain traits were only transmitted from mother to offspring, and correctly concluded that the carriers of these heritable traits must reside in the egg's cytoplasm (Avise, 2014, p. 27). It was later found that they had been looking at chloroplastic traits, and that the same applies to mitochondrial traits. Subsequently, several other forms of non-Mendelian inheritance have been uncovered, such as epigenetics. But these findings, while limiting the scope of the Mendelian system, in no way overturned Mendelian inheritance in those numerous instances where it does apply.

3.2.3 The Hardy-Weinberg principle

One other example of progress within the Mendelian program cannot go unmentioned. In 1908 Godfrey Hardy and Wilhelm Weinberg independently recognized an important consequence of Mendel's laws (ibid., p. 23). This consequence, which is now known as the Hardy-Weinberg principle, entails that the frequencies of two alleles of the same gene will, under certain (hypothetical) conditions, result in predictable genotype frequencies. Suppose that in a population there are two alleles of a certain gene, *A* and *a*, which have allele frequencies *p* and *q*, respectively. If $p = 0.6$, then $q = 0.4$. The Hardy-Weinberg (HW) principle states that the three possible genotypes (*AA*, *Aa*, and *aa*) will, *when they are in equilibrium*, have the frequencies p^2, $2pq$, and q^2, respectively (see Table 2).

The genotypic frequencies will be in HW-equilibrium if the following conditions are obtained: the population is infinite, the gene does not mutate, mating is random, and there is no selection. (No selection means that *AA*, *Aa*, and *aa* have identical fitness – there are no differences in reproductive success.) Moreover, under these circumstances the frequencies should remain stable over the generations. In natural populations, these conditions are never satisfied, if only because populations are not infinite. Nevertheless, for large populations in which mating is reasonably random, the predicted frequencies should be approximated if there is no selection. Reversely, significant deviations from the HW-equilibrium can be interpreted as evidence for the operation of disturbing factors, such as active selection for or against one of the genotypes.

Table 2: The frequencies of the three possible genotypes under HW-equilibrium, given that the frequency *p* of allele *A* is 0.6, and the frequency *q* of allele *a* is 0.4.

Genotype	Frequency under equilibrium	Example if $p = 0.6$ and $q = 0.4$
AA	p^2	0.36
Aa	$2pq$	0.48
aa	q^2	0.16

HW-equilibrium has been observed in real populations. For instance, Michael Ruse (1982, p. 90) recounts a study of M-N blood groups in England. Given the selective neutrality of these blood groups, the ratios were expected to be in HW-equilibrium. This is indeed what was found in a sample of 1279 people (see Table 3).

Table 3: The predicted (based on HW-equilibrium) and observed M-N blood group ratios among 1279 English people.

	M	MN	N
Predicted frequencies	28.265	49.800	21.935
Observed frequencies	28.38	49.57	22.05

Observations like these neatly illustrate the strength of the Mendelian program. (Note, however, that these results only count as a corroboration of the HW-principle because there are *independent* reasons to believe these traits to be selectively neutral. After all, the principle only predicts HW-equilibrium under the aforementioned conditions, so that deviations from the HW-equilibrium are not taken as evidence against the HW-principle, but as evidence for disruptive influences. Mendelians would therefore only *predict* HW-equilibrium if there are good grounds for thinking the conditions are met, to a reasonable degree.)

The Hardy-Weinberg principle has been of great importance for the subsequent development of evolutionary population genetics. Ruse draws an analogy with Newton's first law, which states that an object will remain at rest or will retain its velocity and direction as long as no forces act upon it. "By adopting this law, the Newtonian has a firm base from which to work. He can introduce factors for change, knowing that they will not be swallowed up in an already-existing, unstable state" (Ruse, 1973, pp. 37-38). Similarly, the HW-principle supplies the geneticist with a stable baseline, facilitating the analysis of factors that bring about deviations from this baseline.

3.2.5 Towards a synthesis of Mendelism and selectionism

It is important to note that during the first decade of the 20th century, Mendelism was associated with mutationism and saltationism, while biometry and gradualism were associated with selectionism. It is not that mutationists and Mendelians *denied* the operation of natural selection or its role in evolution, but they deemphasized selection as an inventive and directional force, and emphasized mutation as the engine of evolution. From the early stages, however, the seeds of a synthesis between Mendelian inheritance of discontinuous characters and Darwin's selection of small variations could be found in the writings of Mendelian researchers. Reginald Punnett, a prominent geneticist, stated in the second edition of his work titled *Mendelism*:

> A cursory examination of the horticultural literature must convince anyone, that it is by selection of mutations, often very small, that the gardener improves his varieties. Evolution takes place through the action of selection on these mutations. Where there are no mutations there can be no evolution. (Punnett, 1907, p. 74)

Over the following years, as the experimental evidence for Mendelian inheritance accumulated, the supposed tension between Mendelism and Darwinism abated. This culminated in the development of the Modern Synthesis.

3.3 The advent of neo-Darwinism

The Modern Synthesis, also called neo-Darwinism, refers to the synthesis of Mendelism's inheritance of discontinuous traits with Darwinism's gradualistic evolution by means of natural selection. A number of developments in the early 20th century led up to this synthesis. First, biologists found that most mutations are deleterious and are therefore unlikely to significantly contribute to evolution (Nei, 2013, p. 39). Clearly, mutation pressure by itself is wholly inadequate to account for evolution. Second, mathematician Henry Norton showed (in a book by Punnett) that natural selection was surprisingly adept at influencing gene frequencies (Punnett, 1915, pp. 154-156). For example, according to Norton's figures, the frequency of a dominant mutant allele with a 10 percent advantage over the wild type (unmutated) allele, will increase from 0.009 to 0.5 in just 53 generations. And finally, in 1918 Ronald Fisher demonstrated that continuous variation within a population (such as variation in height among humans) could be explained under Mendelism by positing a large number of genes that each have a small effect on a trait (Fisher, 1918).

These results opened the door for a stream of publications, in which mathematical and statistical tools were employed to model the effects of natural selection on gene frequencies in populations. Important contributions to the neo-Darwinian Synthesis were made by Ronald Fisher (Fisher, 1930), John (J.S.B.) Haldane (Haldane, 1932), and Sewall Wright (Wright, 1931, 1932), among many others. Due to the work of these mathematicians, neo-Darwinism became the dominant research program about the mechanism of evolution, a position it has maintained until the present day. At the core of this program lies the persuasion that evolution consists of change in the relative frequencies of alleles (that have been produced by mutations), mostly under the influence of natural selection.

3.3.1 Theoretical models and the heuristic of population genetics

Recall from Subsection 1.4.3 that research programs have a heuristic. The program generates research questions, as well as an approach for engaging with these research problems. Lakatos gave the example of the stepwise increase in sophistication of Newton's model for the solar system: Newton started out with a single point-like planet revolving around a fixed point-like sun, then he had both the sun and planet revolve around their common center of mass, then added more planets, then changed all bodies from mass-points to mass-balls, et cetera. This is remarkably similar to the work of the early neo-Darwinians (Michod, 1981).

The earliest models of population genetics were, of course, quite unsophisticated. These models calculated how allele frequencies changed under the influence of natural selection given certain fitness values of the 'competing' alleles. Haldane reminisces how his early models, concerning a single gene with just two alleles, made numerous simplifying assumptions (Haldane, 1964):

- One of the alleles is completely dominant.
- The population is infinite, so sampling effects play no role.
- Generations do not overlap.
- Mating is entirely random.
- There are no complicating factors, such as mutations or gametic selection.
- Fitness values remain constant over time.

These assumptions greatly simplify the mathematics, but are false for most actual biological situations. Of course, at the time, population geneticists were well aware of the assumptions they were making. In a 1924 paper, Haldane stated:

> It is proposed in later papers to discuss the selection of semi-dominant, multiple, linked, and lethal factors, partial inbreeding and homogamy, overlapping generations, and other complications. (Haldane, 1924, p. 40)

And indeed, over the subsequent decades population geneticists developed models that incorporated many of these other factors, such as incomplete dominance, inbreeding and assortative and disassortative mating (Wright, 1921), overlapping generations (Haldane, 1962), simultaneous allele substitutions at multiple loci (Haldane, 1957) et cetera. This progressive development of ever-more-complex algorithms for modeling shifts in gene frequencies strongly resembles the pattern Lakatos describes.

3.3.2 Empirical confirmation of population genetics models

This work by population geneticists was highly theoretical. Naturally, their models were *informed* by empirical data, but how much was fed back into the empirical branches of biology in the form of testable predictions? Some experimentalists, such as Ernst Mayr, criticized the theoreticians for not anticipating anything that was not already known from observation (Provine, 1977). For instance, writing about "the mathematical theory of evolution", Conrad Waddington asserted: "Very few qualitatively new ideas have emerged from it" (Waddington, 1957, p. 60).

A few reasons could be cited for the limited predictive power of the population genetics models. For one thing, natural populations are usually very large, making a good sampling impractical or impossible. And for small, seemingly isolated subpopulations it is often hard to quantify, and thus control for, migration (gene flow) from other areas. Also, selection processes are very slow compared to the human lifespan, and selection pressures so small that they are hard to measure (Provine, 1977, p. 22). Finally, in real-world situations, circumstances may vary from year to year, changing the fitness values of alleles and the direction of selection (Grant & Grant, 2002). Given these facts, it is no surprise that it is difficult to quantitatively predict the rate at which gene frequencies will change. A more fruitful approach for testing the mathematical models is to apply their predictions to organisms with short generation spans in controlled laboratory settings. The field of experimental evolution with bacteria and other microorganisms began to take flight in de 1980s.

Nevertheless, earlier in the 20th century there have been a few instances where the work of neo-Darwinian geneticists has led to otherwise unanticipated observations. One example concerns the phenomenon of heterozygous advantage, also called overdominance. In 1922, Fisher showed mathematically that if heterozygotes for a gene are fitter than either homozygote, selection will actively sustain both alleles in the population in what is called a balanced polymorphism (Fisher, 1922). This was taken to be one possible way in which genetic variation can be maintained in a population.

Heterozygous advantage, while strictly theoretical when Fisher proposed it, has since been observed to be a real phenomenon. Let me discuss just one example of this. In parts of West and Central Africa, a certain percentage of the population suffers from a genetic disease called sickle cell anemia, which is caused by a mutation in the hemoglobin gene. This mutation can be lethal when homozygous (genotype: *aa*), although life can be prolonged with treatment. People who are heterozygous for the mutation (*Aa*) do not suffer from the disease, but have some mild symptoms. Significantly, the heterozygotes have an advantage over either homozygote (*AA* and *aa*) in that they have increased resistance against malaria (Aidoo et al., 2002), an infectious disease with one of the highest death tolls in human history. Consequently, in areas where malaria is rampant the heterozygote genotype has the highest fitness. The result is a balanced polymorphism: neither allele will be driven to fixation (that is: attain a frequency of 1) – natural selection maintains both alleles in the population (Livingstone, 1971).

Perhaps somewhat less spectacular, but still interesting, is that in the same 1922 paper Fisher argued that the variation within a population of a continuous trait could be expected to reside in an equilibrium between the variation-increasing work of mutations and the culling effect of selection. All else being equal, then, the variance should be proportional to the population size. He therefore concluded that "a numerous species, with the same frequency of mutation, will maintain a higher variability than will a less numerous species" (Fisher, 1922, p. 324). This expectation was empirically confirmed in a 1926 study on variability of wing pigmentation in Lepidoptera. It was concluded that "[t]he data for 35 species presented with this paper thus seem to provide a decided confirmation of the conclusion arrived at on purely theoretical grounds" (Fisher & Ford, 1929, p. 374).

Besides the confirmation of specific predictions, neo-Darwinian population genetics can be credited for guiding and stimulating empirical research in other ways. The mathematical models provided a framework for the quantitative analysis of field, lab, and paleontological data. For instance, in his classic work *Tempo and Mode in Evolution*, George Gaylord Simpson makes extensive use of the findings of population geneticists, chiefly Sewall Wright, in his analysis of horse evolution (Simpson, 1944, esp. pp 30-69). Here, as in many other cases (Provine, 1977, pp. 18-20), the models lent significance to the data gathered by empiricists.

The mathematical models exemplify the type of positive heuristic that Lakatos describes as an element of scientific research programs. And while the generation of testable predictions based on these models was somewhat limited for most of the 20th century, there have been some notable successes. We will now turn to a specific challenge that has confronted selectionism: the evolution of non-selfish behavior.

Chapter 4

The selection of social and altruistic behavior

Neo-Darwinism entails that organisms have been fashioned by natural selection, which is the preferential multiplication of traits that promote reproduction. It seems surprising, then, to find numerous examples in nature of organisms that exhibit various kinds of non-selfish behavior that may even be harmful to their own reproductive chances. This ranges from alarm calls when spotting an approaching predator (by which the caller may direct attention to itself), sharing of food, eusociality (a division of labor in which non-reproducing individuals assist the reproducing individuals), self-imposed abstinence (or regulation) of reproduction, to any other behavior that costs energy while benefiting others, such as grooming among primates. How can natural selection create and maintain such behavior? This question also applies to more passive forms of social behavior: why do organisms not resort all-out aggression and selfishness to further their own chances of reproduction? Several hypotheses have been developed within the protective belt of the neo-Darwinian program to explain these phenomena, such as group selection (Wynne-Edwards, 1962), kin selection (Hamilton, 1964a, 1964b), reciprocal altruism (Trivers, 1971), and the handicap model (Zahavi, 1995). I will here only focus on group and kin selection.

4.1 Group selection

One of the proposed mechanisms by which social behavior at the cost of the individual could evolve is by selection at the level of groups. It stands to reason that groups of organisms that are willing to cooperate with each other (even though it may be costly for the individuals performing this behavior) will have a selective advantage over groups of more selfish organisms. This higher-level selection was already invoked in 1871 by Darwin to explain social behavior in man:

> When two tribes of primeval man, living in the same country, came into competition, if the one tribe included (other circumstances being equal) a greater number of courageous, sympathetic, and faithful members, who were always ready to warn each other of danger, to aid and defend each other, this tribe would without doubt succeed best and conquer the other. (C. R. Darwin, 1871, p. 156)

Of course, this raises the question how such behavior could arise in the first place:

> But it may be asked, how within the limits of the same tribe did a large number of members first become endowed with these social and moral qualities, and how was the standard of excellence raised? It is extremely doubtful whether the offspring of the more sympathetic and benevolent parents, or of those who were the most faithful to their comrades, would be reared in greater number than the children of selfish and treacherous parents of the same tribe. He who was ready to sacrifice his life, as many a savage has been, rather than betray his comrades, would often leave no offspring to inherit his noble nature. The bravest men, who were always willing to come to the front in war, and who freely risked their lives for others, would on an average perish in larger numbers than other men. Therefore, it seems scarcely possible (bearing in mind that we are not here speaking of one tribe being victorious over another) that the number of men gifted with such virtues, or that the standard of their excellence, could be increased through natural selection, that is, by the survival of the fittest. (ibid., pp. 156-157)

In other words, Darwin used group selection to explain the persistence of non-selfish behavior, but he did not think natural selection could explain its origin. For this he invoked reciprocal altruism, which resulted in non-selfish habits, which in turn became heritable. (The last step probably depended on Lamarckian inheritance.)

During the 20th century forms of group selection were postulated to explain certain phenomena by Sewall Wright (1945) and Vero Wynne-Edwards (1962). Wright made use of the insight that in small populations chance predominates over deterministic selective processes, so that selectively disadvantageous alleles can become fixed – a process called genetic drift. He argued that if a population were subdivided into numerous small subpopulations, a trait that is beneficial to the group but somewhat disadvantageous to the individual might become fixed within any given subpopulation by genetic drift. The success of this group compared to other groups might then facilitate the spreading of this trait throughout the population.

This scenario has been criticized for involving an unlikely conjunction of fine-tuned parameters (Williams, 1966, p. 112). For this process to work at multiple loci (which is required for more complex adaptations by group selection), there must be many such subpopulations and this situation must persist long enough. The subpopulations must be small enough to allow genetic drift, but large enough to prevent extinction. Migration between subpopulations must be rare enough to avert the danger of infiltration by 'selfish' individuals within 'unselfish' groups, but frequent enough to allow the exchange of fixed 'unselfish' trait between groups. John Maynard Smith, after analyzing a similar scenario, concludes that the model is "too artificial to be worth pursuing further" (Maynard Smith, 1964, p. 1146).

Williams has some further criticism in store for group selection (Williams, 1966, pp. 115-116). He argues that with individual selection, an allele could replace another allele at a rate of 0.01 per generation. A selection pressure of one percent is more than enough because most populations consist of so many individuals that selection overcomes the erratic effects of chance, and because many

generations are available for the substitution. For groups, however, this rarely seems to be the case. The number of populations within a species is usually so small that, as far as competition between groups is concerned, chance is a far more important factor. Group selection is in all probability too weak to drive a trait with a 0.01 advantage to fixation. The turnover rate of groups (i.e. the extinction and replacement of groups) is also extremely slow as compared to the rapid succession of generations. As a result, for group selection to be an important factor in evolution, we either need an extremely large number of groups, or immensely high selective pressures, neither of which seems likely.

In defense of group selection, Charles Goodnight and Lori Stevens (1997) pointed out that Williams only took additive gene effects into account. They contend that group selection turns out much more efficient if non-additive effects are factored in:

> Aggressive interactions, or any other form of genetically based interactions among individuals, are nonadditive genetic effects that cannot contribute to a response to individual selection but can contribute to a response to group selection. (ibid., p. S67)

Williams' analysis (carried out firmly within the framework of the neo-Darwinian program), as well as Goodnight's and Stevens' response, could be taken as a helpful indication of the conditions under which group selection might be expected to operate. It seems to me that neo-Darwinian population genetics tentatively predicts that if group selection is observed to operate, it will involve a large number of groups, high selection differentials, rapid turnover rates of groups, limited migration between groups, non-additive gene effects, or preferably a combination of these. This prediction appears to have been confirmed by experiments on group selection.

4.1.1 Progress in group selection research

From the late 1970s onward group selectionists have published experimental results to support their theory (Goodnight & Stevens, 1997). I will here mention three of these experiments and offer some brief comments.

The first to test group selection experimentally was Michael Wade (1977). He used red flour beetles (*Tribolium castaneum*) to select for both large and small population size. In red flour beetles, population size mainly depends on cannibalism rate, so the selected trait is strongly related to interactions between individuals. In each experimental treatment, he had 48 populations that were founded by 16 individuals. After 37 days he used the largest populations to found 48 new populations, when selecting for large population size, and he used the smallest populations when selecting for small population size. He observed a strong response to this mode of selection. After only nine generations, selection for large population size resulted in a mean size of 178 individuals, while selection for small population size resulted in a mean size of 20 individuals.

It must be commented that the design of Wade's study was very favorable to group selection. He implemented a huge selection differential – the strongest possible selection pressure that his experimental setup allowed. Furthermore, there was zero migration between populations. Even in founding new populations there was no mixing of previous populations: all founders came from the same mother population. This prevents the intrusion of highly cannibalistic beetles into populations with minimal cannibalism, thus eliminating one of the weaknesses of group selection. The effectiveness of group selection under these conditions is right in line with the expectations outlined above.

David Craig (1982) performed an experiment in which group selection and individual selection were pitted directly against each other. In 20 populations of confused flour beetles (*Tribolium confusum*) he applied group selection for emigration and individual selection against emigration. After 40 days, the tendency to emigrate was measured (by placing the beetles in a vial with medium for four hours, where they had the opportunity to travel up a thread into another vial) and selection was applied. Individual selection against emigration was implemented by eliminating 25 percent of the emigrants and returning the others to their mother population. Group selection for emigration was executed by selecting the five populations with most emigrants and founding four new populations from each of them, for a total of 20 new populations. This was repeated for 14 cycles. Craig observed a significant increase in emigration tendency. Group selection had overpowered individual selection.

This appears to be a resounding victory for group selection, but in this experiment, again, no migration between populations was allowed. Also, the two selection pressures were very different. Eliminating 25 percent of the emigrants may seem like a severe individual selection pressure against emigration, but it may still be an underestimation of casualties among emigrants in nature. Selecting the top five emigrating populations to found all 20 populations in the next round, on the other hand, is an unrealistically stringent form of group selection for emigration. It is essentially a form of truncation selection: all groups that do not make the top five (an arbitrary threshold) are artificially cut off from contributing anything to the next generation. In Craig's experiment, therefore, group selection for emigration was much more severe (75 percent of the groups were eliminated) than individual selection against emigration (only 25 percent of the emigrants were eliminated). One wonders whether group selection would still have been victorious if both parameters had been set to 50 percent.

William Muir (1996) reports a study on white leghorns (chickens) that are adapted to living in multiple-hen cages by group selection. Keeping leghorns in high density in battery cages stimulates aggression, which leads to high casualty rates. To prevent this, industrial producers sometimes resort to the less-than-humane practice of beak trimming. Muir observed a substantial decrease in mortality, owing to a decline in aggression, in response to group selection within five generations. His results indicate that "beak-trimming of the selected line would not further reduce mortalities, which implies that group selection may have eliminated the need to beak-trim" (ibid., p. 447).

Goodnight and Stevens note that all studies in group selection have focused on traits related to interactions between individuals, and cite this as the reason for the success of group selection as compared to individual selection in these studies. They refer to a series of models by Bruce Griffing (Goodnight & Stevens, 1997, p. S68 and references therein; Griffing, 1981) which show that individual selection often promotes aggression, whereas group selection alone is able to squelch this behavior.

How are we to evaluate these developments in the context of our analysis of evolutionary biology as a scientific research program? From a Lakatosian perspective, group selectionism can be regarded as a 'microprogram' within the selectionist program. It cannot be denied that some progress has been achieved: group selection has been shown to work in experiments and domestic breeding, and Griffing's models help us see why. It remains doubtful, however, whether the right conditions are ever actualized in nature. In their review of group selection research, Goodnight and Stevens give a rather optimistic appraisal of the situation, and it could be argued that they oversell the efficiency of group selection. They assert: "Laboratory experiments have established that group selection is very effective, that it can occur with weak selection differentials (S = 0.05) […]" (Goodnight & Stevens, 1997, p. S71). However, among neo-Darwinians a selection differential of 0.05 is regarded as gigantic. I believe this only serves to show that the findings of group selectionists confirm the expectations I expressed in the previous subsection: whenever group selection works, certain conditions must obtain, such as huge

fitness coefficients, limited migration, the selected traits are related to (social) interactions, et cetera. In other words: the mother-program (neo-Darwinism) accurately predicts the situations in which a subprogram (group selection) may be successful. Confirmed expectations count as progress, and the credits for this progress accrue to the neo-Darwinian program that generated these expectations. Besides intellectual satisfaction, progress in this area is also useful because it has important implications for domestic breeding strategies (Wade, Bijma, Ellen, & Muir, 2010).

4.2 Kin selection

The main rival of group selection is kin selection, the first comprehensive treatment of which was written by William Donald Hamilton (1964a, 1964b). The gist of the argument is that it may be selectively beneficial for an organism to make sacrifices for its kin, because it increases the chance that his genes will be propagated *through his family members*. To be more precise: the genes that drive an organism to behave altruistically towards his kin, are likely to also be carried by his kin. Such genes promote their own proliferation, because carriers help each other.

Altruism, like any behavior, is only advantageous if the benefits outweigh the costs. This reality is captured in what is now known as Hamilton's rule: Altruistic behavior that has evolved by kin selection will meet this requirement:

$$r \cdot B > C$$

Here, C is the cost to the altruistic individual, B is the benefit to the beneficiary, and r is the relatedness of the beneficiary to the altruist. The relatedness coefficient, r, was first developed by Sewall Wright over 40 years earlier in a study on domestic breeding (Wright, 1922), but now proved useful in a different context. Hamilton states one of the implications of his model:

> This means that for a hereditary tendency to perform an action of this kind to evolve the benefit to a sib must average at least twice the loss to the individual, the benefit to a half-sib must be at least four times the loss, to a cousin eight times and so on. To express the matter more vividly, in the world of our model organisms, whose behaviour is determined strictly by genotype, we expect to find that no one is prepared to sacrifice his life for any single person but that everyone will sacrifice it when he can thereby save more than two brothers, or four half-brothers, or eight first cousins… (Hamilton, 1964a, p. 16)

Of course, many cases of altruistic behavior are not quite as radical as sacrificing one's life, but the same principle applies: the measure of commitment, the price an organism is willing to invest, will depend on the benefit to, and the relatedness of the beneficiary.

Kin selection has been the dominant view since the late 1960s, thanks in part to Williams' endorsement in his 1966 book, and his repudiation of group selection. The gene-centered view of evolution, as exemplified in kin selection, has interesting implications. It lies at the heart of most hypotheses that aim to explain the puzzle of sex-ratios in social Hymenoptera (ants, wasps, and bees), where males are haploid so that sisters have a 75 percent relatedness (Meunier, West, & Chapuisat, 2008). Also, one of the fruits of kin selection was the development of an entire new field of scholarship, that will be reviewed in the next section: sociobiology.

4.3 Sociobiology

Sociobiology studies the way in which natural selection has shaped social behavior – that is: interactions between members of the same species. The core idea of sociobiology is that selection adapts the individual's behavior so as to optimize the propagation of his or her genes. It may be profitable to aggressively compete for access to food and the right to reproduce, but it may also profit to take a more passive, patient, and careful approach. Other key concepts in sociobiology are relatedness and investment. An organism is most related to itself (so selfish investments profit the proliferation of its genes), but is also related to its siblings, parents, and offspring (so investments in their reproductive success also profit its genes). I will briefly discuss some of the ideas developed within sociobiology, as well as two instances of empirical confirmation.

4.3.1 Hawks, doves, and evolutionary games

One might be tempted to think that natural selection promotes unrestrained aggression when it comes to acquiring food or ensuring the right to copulate. After all, genes that urge organisms to make every effort to reproduce tend to be represented in the next generation in higher numbers than genes that make organisms passively accept their fate as non-reproducers. However, aggression is not always the optimal strategy. Fighters run the risk of injury or death. Under many circumstances it may be better to avoid physical conflict, and live to compete another day. A certain piece of food, or even breeding rights at any particular moment, may not be worth the risk. In sociobiological parlance, an aggressive individual is referred to as a hawk, while passive or peaceful individuals are called doves (Maynard Smith, 1982, pp. 11-20).

Sociobiologists have theorized that the optimal strategy depends on the ratio of doves to hawks within the population. In a population in which every individual is a conflict-avoiding dove, it is highly profitable to be a hawk: you can always steal everyone's food without running the risks attached to fighting. Thus, in a population of doves, the genes for aggression will quickly spread. If there are many hawks, however, it is far less rewarding to be a hawk. The conquered extra resources may no longer be worth the injuries sustained in fights. In such a situation it is better to be a dove. In a population with many hawks, genes of doves will spread rapidly. The ratio of doves to hawks, therefore, may tend towards an equilibrium. Of course, this might just as well be an equilibrium between the chance that any given individual will behave as a dove and the chance he will behave as a hawk in a particular situation. This equilibrium ratio, if it is robust, is called an 'evolutionarily stable strategy' (ESS). That is "a strategy such that, if most of the members of a population adopt it, there is no 'mutant' strategy that would give higher reproductive fitness" (Maynard Smith & Price, 1973, p. 15). When a population is in equilibrium, both options (being a dove and being a hawk) will have identical fitness. The study of optimal and stable strategies is called game theory.

Game theory has also been used to explain ritualized combat. In many species, males compete for territory or access to females. Often, these conflicts are settled by ritualized battles that do not inflict serious injury to either party – even though these animals might be equipped with potentially deadly weapons. Why would they refrain from using lethal force? In one of the earliest game-theoretic models, John Maynard Smith and George Robert Price showed that natural selection could maintain the propensity to practice ritualized combat as the norm within a population, even if this population also contains individuals that do employ dangerous tactics. In their model, they included five behavioral types: 1) the 'Mouse', who always plays fair (that is, he uses ritualized combat) and immediately flees when his opponent cheats, 2) the 'Hawk', who always cheats and continues until he is wounded or his opponent retreats, 3) the 'Bully', who starts out cheating but retreats after his

opponent has cheated twice, 4) the 'Retaliator', who plays fair but retaliates if his opponent cheats, and 5) the 'Prober-Retaliator', who mostly plays fair but occasionally cheats. Given the values they assigned to the penalties for defeats and injuries and the rewards for victories, they found that the population "will come to consist mainly of Retaliators or Prober-Retaliators, with the other strategies maintained at a low frequency by mutation" (ibid, p. 16). In other words, ritualized combat will become the norm.

4.3.2 Empirical confirmation of a game-theoretic model

As stated before, Lakatos acknowledges model-building as part of the positive heuristic of scientific research programs. Models can illuminate which hypotheses or sets of assumptions might be fruitful in explaining natural phenomena. But eventually these theoretical models must generate empirically testable predictions, in order to determine whether the hypotheses on which they are based are progressive. I will here discuss one instance of an empirical test within the sociobiological research program.

The female digger wasp (*Sphex ichneumoneus*) digs burrows with one or more brood chambers in which she stores paralyzed grasshoppers as food for her offspring. She then lays one egg in the brood chamber and closes the entrance with soil. She can then dig a new brood chamber in the same burrow, or dig a new burrow. Digging and hunting are time-consuming activities: it may take one to ten days per burrow. And the nesting season only lasts for six weeks, so time is a precious resource.

Occasionally, burrows are lost due to invasions by ants or centipedes. After the grasshoppers have been devoured, the burrows may become available again. This means there are empty burrows available. Thus, female wasps are presented with a choice: should they dig a new burrow, or look for an existing one? Using an existing burrow saves her much digging time. However, she might accidentally enter a burrow that is already in use by another wasp (she cannot detect whether or not a burrow is occupied). When two females are using the same burrow, they are both investing hunting time in collecting grasshoppers for the offspring of only one of them. When they meet, a fight will ensue, and the loser leaves the burrow permanently, while the winner lays the egg.

Brockmann, Grafen, and Dawkins (1979) investigated the possibility of an ESS concerning the ratio of choosing to dig a new burrow versus using an existing one. If the population currently is in equilibrium, both choices should be equally profitable (since there should not be a selective pressure in favor of either choice). Using data from a population of digger wasps in New Hampshire, they found that there was no significant difference between the success rates of the two possible decisions in terms of the numbers of eggs laid per 100 hours of work. This corroborates the notion of an ESS. The authors then devised a model to account for this equilibrium, and based on this model predicted the ratios of various combinations of decisions and outcomes. These predictions were spectacularly confirmed for the New Hampshire population (ibid., p. 491). This can be regarded as a victory for sociobiology and, by extension, for the neo-Darwinian program from which it was spawn.

However, the predictions failed for a population of the same species in Michigan. Interestingly, the authors try to account for the discrepancy by invoking various auxiliary solutions. Perhaps the environment has recently changed and the wasp's strategy is 'out of date', that is: not yet adapted to the new conditions. Or maybe there is a contagious disease affecting shared burrows, making it less profitable to enter existing burrows. Or perhaps there is gene flow from other areas, upsetting the balance of the Michigan population. This is reminiscent of Lakatos' description in Subsection 1.4.3 of the reaction of the Newtonian scientist to anomalous planetary movements: within the program there

is a range of available explanations for unexpected data. Basically, all assumptions underlying a model can be challenged, except for the core assumptions of the overarching research programs (in this case: the neo-Darwinian assumption that evolution consists of change in the relative frequencies of alleles, and the sociobiological assumption that selection adapts the individual's behavior so as to optimize the transmission of his or her genes to future generations). An auxiliary hypothesis is generated by simply rejecting a non-core assumption. Ideally, such auxiliary solutions should each be tested and a more sophisticated model should be worked out that more accurately fits the data.

4.3.3 Conflicts of interest within the family

Sociobiology has generated numerous interesting insights on conflict and collaboration among family members. Richard Dawkins (1976/2006, pp. 123-139) eloquently describes under which conditions siblings should selfishly compete with each other for food, and under which conditions they should help each other, so as to optimize the perpetuation of their genes – given the 50 percent relatedness between siblings. Dawkins also describes why selective pressures create conflicts between parents and offspring. Parents want to keep feeding their offspring until they can fend for themselves – after that point they want to shift investments towards a new or younger litter. The child, on the other hand, wants his parents to keep feeding him right up to the point where the cost to future or younger siblings would be twice his own benefit. During the period in between these two points the parents and child have conflicting interests. This is why in mammals the timing of weaning is often a matter of dispute between a mother and her offspring.

Conflicts are even more pronounced between parents. They are usually not related to each other, and their only real connection is their 50 percent relatedness to their common offspring. It profits the male if the female invest as much as possible in *his* offspring – and *vice versa*.

Especially in species where fertilization is internal, the initial investment in offspring by males is negligible compared to that of females. Males only provide sperm, while the mother provides the much larger ovum. She also nourishes her children, either because they grow inside her, or because she lays eggs that contain sizable quantities of food. This asymmetry in prenatal parental investment has far-reaching consequences for the types of selective pressures on males and females.

Because of her substantial investment, the female stands to lose more if her children die than the male does. The total number of offspring she could rear is very limited. The male, on the other hand, has only invested some sperm – he could do this a thousand times! He can afford to walk off and inseminate another female. As a result, selective pressure on females is to aim for quality, while for males selective pressure tends to be for quantity.

Dawkins describes two broad strategies that the female could follow: the 'domestic bliss' strategy and the 'he-man' strategy (ibid., pp. 149-162). If she follows the domestic bliss strategy, she attempts to involve the male as much as possible in feeding and protecting her young. Unfortunately, it is difficult to 'force' the male to cooperate. What is to prevent the male from just leaving her to raise the children on her own, while he goes off looking for another female to fertilize? Her only means of control is that she can be choosy in which male to copulate with. She can attempt to pick a faithful male that will help in the upbringing of their offspring. But she can only exercise this power *before* copulation. "Once she has copulated she has played her ace" (ibid., p. 149) – beyond that she has no control. What she could do, Dawkins theorizes, is demand that the male shows his loyalty by investing in her before mating – she can be coy. She could have him build her a nest, bring her food, or just insist on a long courtship

period. In this way, she forces the male to make a 'prenatal' investment as well, so he too will be committed to their offspring.

The 'domestic bliss' strategy will only work if enough females play the same game. If most females are coy, males will have little choice but to bow to their demands. Firstly, males who are willing to go through the courtship period will have a selective advantage over those who are not. Secondly, infidelity would mean having to pay the dowry again. And if there is a fixed breeding season, there might not even be the possibility of mating with other females. But if only a few females are coy, there will be little pressure on males to be faithful.

To see whether coy females can succeed in forcing males to cooperate, Dawkins works out a simple model with two types of females (coy and loose) and two types of males (faithful and philanderer). Coy females insist on a long engagement period, even though this is also costly to themselves. Loose females will readily mate with a male, without any prior demands. Faithful males are willing to pay the dowry and remain faithful after copulation. Philanderers are unwilling to invest in a courtship period and will desert the female immediately after copulation. Given the (arbitrary) scores Dawkins allots to the four possible match-ups, he concludes that all four types of behavior will be maintained in the population. (The population does not, however, converge on an evolutionarily stable equilibrium. As Dawkins explains in an endnote to the 1989 edition of his book, the ratios will keep oscillating unpredictably.) Dawkins' model is admittedly simplistic, but more complex analyses have been performed by Maynard Smith (1977).

If the female adopts the 'he-man' strategy, she assumes responsibility of rearing their children on her own. Instead of selecting a mate that will help her in the upbringing, she will attempt to mate with the healthiest, strongest, most attractive male. This gives her offspring, which will carry his *and* her genes, the best chance of becoming reproductively successful. The he-man strategy places selective pressure on males to increase their prowess in whatever quality females value.

One especially fascinating implication of this strategy is that it can lead to a self-perpetuating runaway selection process for the exaggeration of the male characteristic that females find attractive, such as the peacock's tail, This is because offspring will inherit both genes for the desired male characteristic and for the female's preference. This means that females with a preference for long tails will themselves also tend to carry genes for long tails. And males with long tails will also tend to carry genes for a preference for long tails. One can see the theoretical recipe for a positive feedback loop (Dawkins, 1986/1996, pp. 277-315). Once a species goes down this path, the process may continue until physical of physiological limits are reached, or until counteracting selective pressures start to come into play (such as selection against large tails in peacock's because of the associated clumsiness or vulnerability to predators).

4.3.4 Lakatosian assessment of sociobiology

The gene-centered, sociobiological approach appears to be a promising framework for explaining many types of behavior observed in nature. However, unless these explanations lead to testable predictions, they are of little scientific value.

> Yet, a recurrent criticism of current sociobiological theories is that they too often provide nothing more than a post hoc explanation of how existing phenomena could have arisen as a direct result of Darwinian selection. Because the theories have no empirical implications beyond what they were originally devised to explain, they cannot be put to any genuine test. (Freese & Powell, 1999, p. 1705)

Sociobiology is so flexible that it is able to explain seemingly contradictory behaviors. For instance, Richard Dawkins can think of reasons why males would want a long engagement period (to make sure his mate is not impregnated by other males), or why they would not want that (it costs time and energy). Dawkins has a story to tell when observing birds throwing out eggs containing their unhatched siblings (Dawkins, 1976/2006, pp. 134-135). But he can just as easily explain altruism between siblings.

Explanatory scope is of course not a negative feature of a research program. After all, both selfishness and altruism are observed in nature, so the ability to explain both is a virtue. But the *mode of explanation* is key in evaluating the program. If a program can explain two contrary phenomena, then neither could be *predicted* by the program – unless the explanations include details about under which conditions each phenomenon is to be expected. Applying this to the issue at hand: a good sociobiological explanation will identify under what circumstances we should expect selfish behavior and under which conditions we expect altruism. Fortunately, at least one prominent example of this can be provided.

4.3.5 An example of the predictive power of sociobiology

Kin selection and sociobiology have been of great importance for explaining the origin and maintenance of eusociality. In eusocial systems, such as encountered in termites, ants, and certain bees and wasps, only some individuals in the colony reproduce, while others are sterile. Usually there is a single reproducing female, the queen. The non-reproducing individuals, the workers, perform other tasks, such as building and defending the nest, gathering food, rearing the young, and taking care of the reproducing individuals. This, of course, raises the question of why the workers 'agree' with this arrangement. Should there not be a strong selective pressure in favor of genes that promote reproduction? Kin selection theory partially solves this puzzle by drawing attention to the fact that the workers are related to the queen and their reproducing brothers and sisters. Their genes are perpetuated through them. The eusocial system is an efficient way to propagate their genes.

Richard Alexander has proposed the contrary hypothesis that eusociality has not evolved because it increases the inclusive fitness of the sterile workers, but because it increases that of their parent. If he is right, then the *opportunity for parental manipulation of progeny* is the critical factor in the evolution of eusociality (Alexander, 1974). This implies that eusociality could only evolve under conditions that are conducive to parental manipulation. This insight, in turn, allowed Alexander to make a prediction as to under what set of circumstances eusociality would exist *if it would ever be encountered in vertebrates*.

Stanton Braude relates the story of how Alexander predicted the characteristics of a colony of eusocial vertebrates in a series of guest lectures in a number of North American universities in 1975 and 1976.

> Alexander predicted that a eusocial vertebrate's nest should be (1) safe, (2) expandable, and (3) in or near an abundance of food that can (4) be obtained with little risk. These characteristics follow from the general characteristics of primitive termite nests inside logs. The nest must be safe or it will be exploited as a rich food source for predators. It must be expandable so that workers can enhance the value of the nest. It must be supplied with safe abundant food so that large groups can live together with little competition over food or over who must retrieve it. The limitations of the nest characteristics suggested that the animal would be (5) completely subterranean because few logs or trees are large enough to house large colonies of vertebrates. Being subterranean further suggested that the eusocial vertebrate would be (6) a mammal and

> even more specifically (7) a rodent since many rodents nest underground. The primary food of the hypothetical vertebrate would be (8) large underground roots and tubers because the small grassy roots and grubs that moles feed on are so scattered that they are better exploited by lone individuals and would inhibit rather than encourage the evolution of eusociality. The major predator of the hypothetical vertebrate would have to be (9) able to enter the burrow but be deterred by the heroic acts of one or a few individuals. This would allow for the evolution of divergent life lengths and reproductive value curves between workers and reproductives. Predators fitting this description would include snakes. The eusocial vertebrate was also expected to (10) live in the wet-dry tropics because plants there are more likely to produce large roots and tubers that store water and nutrients to help them survive the dry periods. The soil would need to be (11) hard clay because otherwise the nest would not be safe from digging predators. These two characteristics further suggested (12) the open woodland or scrub of Africa. (Braude, 1997)

At one of these guest lectures, mammalogist Terry Vaughan pointed out to Alexander that a eusocial rodent does indeed exist: the naked mole-rat (*Heterocephalus glaber*). Moreover, the naked mole-rat, of which little was known at the time, turned out to closely resemble the hypothetical eusocial rodent described by Alexander. His prediction was spectacularly confirmed!

A criticism of this example is that many of these attributes could have been predicted purely on the basis of ecological considerations, without necessarily adopting a sociobiological or even a selectionist perspective. This predictive success should therefore mostly be credited to Alexander's keen ecological insights. Nevertheless, a sociobiological rationale behind some of the predicted properties (such as no. 3 and 9) is clearly present.

Chapter 5

Selectionism vs. neutralism

Since the early 20th century, selectionism has been the dominant view among evolutionary biologists. Yet, already in 1932 Sewall Wright noted that natural selection does not always reign supreme (Wright, 1932). He realized that in small populations not selection but genetic drift is the dominant mechanism of biological change. Genetic drift is the change in gene frequencies due to random sampling effects, quite apart from selection. Each generation only a portion of the population manages to reproduce, and some reproduce more than others. This is partly determined by chance. In sexual species, the random segregation of alleles in meiosis is an additional source of randomness. In large populations, these random effects are mostly (but not entirely) averaged out, so that beneficial alleles tend to increase in frequency while deleterious alleles decrease in frequency. In small populations, however, random effects can overpower selection so that the reverse may also occur.

Wright envisioned the 'fitness landscape': a metaphorical landscape where each coordinate represents a certain combination of genetic traits, while the elevation at that coordinate signifies the fitness of that combination of traits. The fitness landscape consists of hills and valleys. Natural selection drives populations towards peaks in the landscape. This means, however, that populations can get 'stuck' on a local fitness peak, frustrating further evolutionary progress. Wright believed that genetic drift could lower the fitness of small populations by increasing the frequency of deleterious mutations. He invoked genetic drift to explain a population's descent down the slope of a hill, so it can enter the zone of attraction of another peak.

Wright was primarily thinking of the genetic drift of deleterious alleles. A few decades later, biologists would use the old concept of drift in a new context: the fixation of selectively neutral mutations.

5.1 Haldane's dilemma and Kimura's solution

In 1957, Haldane published a paper in which he calculated the rate at which alleles could be substituted by natural selection. He built on the insight that selection processes require genetic deaths: individuals carrying the less fit alleles must die and be replaced by those carrying the more advantageous alleles. The rate of substitution is thus limited by the reproductive excess of fitter individuals. Every selection process incurs a cost, and this cost is paid in the form of reproductive excess. Haldane called this 'the cost of natural selection'. A related concept is 'genetic load' (Crow, 1958; Muller, 1950), which is a somewhat more nebulous way of quantifying the same thing. The speed at which these costs are paid (or the load is reduced) determines the rate of evolution.

The cost of natural selection and its equivalent, genetic load, apply to all types of selection (Kimura, 1960), be it the spreading of new beneficial mutations, the elimination of deleterious mutations, or the maintenance of alleles at certain frequencies (as is necessary for balanced polymorphisms and traits with frequency-dependent fitness, such as dove-hawk interactions).

Given his estimate of how much reproductive excess would be available to pay for substitutions, Haldane calculated that typically one new beneficial mutation could be driven to fixation every 300 generations, on average. According to Haldane, this figure "accords with the observed slowness of evolution" (Haldane, 1957, p. 524). Notwithstanding Haldane's satisfaction with this result, many biologists considered his rate of substitution to be too slow. The issue has since come to be known as 'Haldane's dilemma'.

In the late 1960s, Motoo Kimura noted that the number of nucleotide substitutions that must have taken place during evolution, given the observed differences between species, far exceeds Haldane's figure of one substitution per 300 generation (Kimura, 1968). Kimura offered a simple solution: most nucleotide changes that reach fixation are in fact *selectively neutral*, or almost so.

> Thus the very high rate of nucleotide substitution which I have calculated can only be reconciled with the limit set by the substitutional load by assuming that most mutations produced by nucleotide replacement are almost neutral in natural selection. (ibid., p. 625)

Neutral mutations do not affect the fitness of their carriers, and are therefore not helped along by natural selection. They increase and decrease in frequency by genetic drift, that is, *by chance*. Since selection provides no directionality to the changes in frequencies of neutral mutations, many neutral mutations disappear – their frequency drifts to zero. Some neutral mutations, however, just happen to be carried by individuals that, for whatever reason, are above average reproducers. These mutations get fixed without incurring the costs that are paid for traits that are selectively driven to fixation. (For those who prefer the terminology of genetic load: neutral mutations have zero effect on the genetic load. As given in Kimura's formula (2'), the substitutional load $L = 4N_e s \cdot \log_e(1/p)$, where N_e is the effective population, p is the starting frequency of the allele, and s is the selection coefficient. As s goes to zero, so does L.) The number of neutral mutations that can be fixed is therefore not limited by the cost of natural selection (or by the genetic load that the population can tolerate).

Then how fast can neutral mutations become fixed? According to Kimura, the probability of a newly mutated allele to establish itself in the population is about equal to its initial frequency. This means that in the long run the rate of neutral substitutions in the population per generation is equal to the number of novel neutral mutations that an average individual contracts in its haploid genome. If each newborn individual carries, say, 50 new neutral mutations in its haploid genome, then in the long run 50 mutations will be fixed in the population per generation. The real mutation rate is difficult to

determine (it varies between species and between genomic regions), but is likely to fall within the range of 30 to 90 per haploid genome (Conrad et al., 2011; Kondrashov, 2003; Nachman & Crowell, 2000; Roach et al., 2010). Most of these mutations are neutral. Whatever the exact number, the neutral substitution rate is bound to be far greater than one substitution per 300 generations. Thus, Kimura concluded that the vast majority of nucleotide substitutions that caused the differences between species must have been selectively neutral.

The prevalence of neutral changes in evolution also explained the large amount of variation that was observed in the genomes of animal species. Under selectionism, much of this variation was attributed to balanced polymorphisms (see Subsection 3.3.2). However, as noted above, selection costs reproductive excess, and this limits how much can be selected for. Kimura and Crow (1964) calculated that the total number of balanced polymorphisms that can simultaneously be maintained in the population is rather limited. In his classic book on neutral evolution, Kimura recounts:

> If these [polymorphisms] were generally maintained by overdominance at individual loci, it seemed to me that the total amount of segregation load […] or selective deaths involved must be intolerably large for higher animals. (Kimura, 1983, p. 27, in-text reference removed)

Shortly after Kimura's paper, King and Jukes (1969) joined him in the defense of neutralism. They pointed out that mutation rates are so high that most mutations must be occurring in non-functional parts of the genome. For if they occur in functional parts, too many will be deleterious, leading to extinction. They state that mammals are estimated to have no more than about 40.000 genes, which amounts to only about one percent of the mammalian genome. Consequently, the bulk of mutations occur in non-protein-coding regions and are likely to be neutral.

Soon after the publication of the neutral theory, a controversy broke out over the arguments for and against it. It is important to note that selectionists do not deny that some neutral evolution occurs, nor do neutralists deny the role of natural selection in the substitution of some mutations. The disagreement is over which mechanism predominates. Also, neutralists only challenge selectionism in the arena of molecular evolution. They claim that molecular change is mostly attributable to mutations and genetic drift, while selection primarily fulfills the conserving role of weeding out deleterious mutations. Both camps accept the importance of selection in phenotypic evolution. Neutral evolution can change organisms at the molecular level, but it cannot explain adaptation (but see Subsection 5.5.1!).

5.2 Neutralism's place within the macrostructure of the evolutionary research program

Neutralism is regarded as a rival of the Modern Synthesis (Pievani, 2012, p. 216). Yet, it was developed within the framework of population genetics, which had been established by neo-Darwinians. Neutralism's primary argument against selectionism relied on the concept of genetic load, which was a product of selectionism. If neutralism is to be considered a rival of neo-Darwinism, then the latter has given rise to its own challenger.

How should we classify neutralism? Richard Michod sees selectionism and neutralism as "two 'mini' research programmes within population genetics" (Michod, 1981, p. 22). So he agrees with my thesis that there are subprograms within programs (see Subsection 1.5.1 and Section 2.4), but categorizes the programs differently. He views population genetics as the overarching mother-program. In my classification, evolutionary biology is the mother-program of both selectionism and neutralism. This

may just be a matter of perspective. If evolutionary biology is our point of departure, as it is in this treatise, then evolutionary biology defines the hard core of the program, while genetics (Mendelism) is a development from another field that had to be accommodated (as in the Modern Synthesis) and now functions as an 'observation theory' or as 'unproblematic background knowledge'. If genetics were our starting point, it may have been the other way around. Whichever perspective is chosen, both evolutionary biology and population genetics are common denominators among selectionists and neutralists. Together they are the arbiter in the neutralist-selectionist controversy. I will return to the question of the status of neutralism at the end of this chapter.

5.3 Testing the neutral theory

In a chapter assessing the empirical strength of neutralism, Francisco Ayala states that the neutral theory is more amenable to empirical testing than selectionism:

> Since natural selection is not involved, environmental variations as well as other parameters that might affect selective values can be ignored. It is therefore possible to advance evolutionary models that include a very few parameters, notably mutation frequencies (which determine the rates at which allelic variants arise in a populations), population size (which determines the magnitude of the sampling errors from generation to generation), and time (for situations not in equilibrium). The presence of very few parameters makes it possible to derive precise predictions about evolutionary patterns. (Ayala, 1977, p. 183)

During 1970s, Ayala has performed various tests of the neutral theory in several species of fruit flies (genus *Drosophila*). In one instance, Ayala (1972) tested whether the pattern of genetic variation observed in populations of *Drosophila willistoni* in South America agrees with the predictions of neutralism. Under the neutral theory the frequencies of most alleles drift randomly. This means that different, isolated populations should differ greatly in their allelic frequencies. Contrary to this expectation, Ayala found that the allelic frequencies at most polymorphic loci (of soluble proteins) strongly correlated between different populations. A similar result was found in *Drosophila pseudoobscura* by Prakash, Lewontin, and Hubby (1969). In addition, Ayala found that the number of alleles per locus is approximately the same in different populations, even though neutralism predicts that larger populations should harbor higher numbers of alleles per locus.

These observations do not directly refute neutralism. The neutralist can accommodate the data by rejecting the premise that the populations are really isolated from each other (Kimura & Ohta, 1971). This is not unreasonable, since even with limited levels of migration different subpopulations will form a single, panmictic population. But then a new difficulty arises. A panmictic population of *D. willistoni* in South America would be truly gigantic. Under neutralism, the amount of genetic variation depends, among other things, on the effective population size. The theory predicts that the fraction of individuals that is heterozygous at any given locus ($\overline{H}_e$) will be:

$$\overline{H}_e = 4N_e \cdot \upsilon \,/\, (4N_e \cdot \upsilon + 1)$$

Where N_e is the effective population size and υ is the mutation rate. Ayala uses the neutral mutation rate estimated by Kimura & Ohta (ibid.), which is 10^{-7}. The effective population size is hard to determine. Ayala writes:

> The geographic distribution of this species extends over several million square kilometers. Throughout this enormous territory *D. willistoni* is often the most abundant drosophilid. An experienced collector typically obtains several hundred to several thousand individuals in two or three hours within a few hundred square meters. There is no indication that the removal of these individuals affects substantially the size of the population. Collections made in consecutive days in the same site yield approximately equal numbers of flies. (Ayala, 1972, p. 221)

Based on these considerations, Ayala estimates that the N_e cannot be lower than 10^9 (one billion). I believe this figure grossly underestimates the effective population of *D. willistoni* in South America's tropical rain forests, but let us accept it for the sake of the argument. The numbers imply that $\overline{H}_e$ = 400/401. In other words, the neutral theory predicts that there are so many neutral alleles drifting about, unchecked by selection, that at each locus practically 100 percent of the individuals is heterozygous. However, Ayala measured $\overline{H}_e$ to be 17.7 ± 03.1 percent, powerfully contradicting the neutralist prediction.

5.3.1 A degenerative shift in the neutralism program

How do neutralists respond? Kimura (1983, pp. 256-257) indicates that the appropriate mutation rate should be 10^{-8} per generation, because the rate estimated by Kimura and Ohta (1971) is 10^{-7} *per year*, and fruit flies can go through 10 generations per year. This is a valid point, although if we want to nitpick it could be pointed out that the rate of neutral mutation mentioned by Kimura and Ohta actually is $1.6 \cdot 10^{-7}$ per year, or $1.6 \cdot 10^{-8}$ per generation.

But more significant is Kimura's assertion that the effective population could actually be much smaller than 10^9. He argues that the above formula for predicting $\overline{H}_e$ only applies in equilibrium. If the population has recently expanded from smaller numbers, the equilibrium heterozygosity may not yet have been reached. Also, if the rate of extinction (and subsequent replacement) of local subpopulations is much greater than the rate of migration between subpopulations, the N_e of the panmictic population is drastically lowered. Combining these factors, Kimura boldly declares that the applicable figure for N_e could be as low as 10^7, a mere ten million. By positing that $\upsilon = 10^{-8}$ and $N_e = 10^7$, Kimura brings the expected heterozygosity down to 28.6 percent. This is still higher than the observed value of 17.7 percent, but, Kimura asserts, it is "close enough to make Ayala's criticism lose much of its force" (Kimura, 1983, p. 257). Note that replacing Kimura's value of υ by $1.6 \cdot 10^{-8}$ yields 39.0 percent, further widening the gap between the neutralist prediction and the observation, even if we accept Kimura's low population estimate.

This sequence of anomalous observations and neutralist attempts at rescuing their program is highly revealing from a Lakatosian perspective. The initial expectation was that different populations would display widely divergent allele sequences. Upon the finding that different populations actually have highly correlated allele frequencies, the neutralist hypothesized that migration morphs all those subpopulations into one panmictic population. This auxiliary hypothesis generated a new prediction: such huge population must maintain massive numbers of allelic variants, resulting in high levels of heterozygosity. When this prediction was negated as well, the neutralist rationalized the anomaly away by assuming that the population only recently expanded to current levels, and that local extinction dominates over migration between subpopulations. Thus, the neutralist explanation requires migration rates that are high enough to harmonize allele frequencies across subpopulations, but small enough to be overruled by local extinctions. And even granting this unlikely constellation of circumstances, the neutralist expectation ($\overline{H}_e$ = 0.390) does not match the evidence ($\overline{H}_e$ = 0.177).

5.3.2 Neutralizing neutralism

Ayala (1977) also compared the allelic frequencies at the same loci in different but related species. Under neutralism, the frequencies of most alleles drift randomly. Different species, therefore, are expected to diverge because the random changes that occur in one genealogy will often be different from those that occur in another genealogy. Since species are reproductively isolated from each other, this divergence cannot be countered by 'migration'. When a species splits into two different species, from that time onwards the frequencies of neutral alleles should drift apart. The occurrence of new mutations would also contribute to this divergence. This means that species that recently split apart will still share many of the same alleles, and in similar proportions. But species whose most recent common ancestor lived in the remote past will have drifted further apart: at many loci, very different allele frequencies are to be expected.

Ayala determined the allele frequencies at many different loci in five closely related species of fruit flies (*D. willistoni*, *D. tropicalis*, *D. equinoxialis*, *D. paulistorum*, and *D. nebulosa*), and analyzed whether the observed pattern agrees with the expectations of neutralism. If these alleles are indeed neutral, the pattern of divergence should reflect the order of speciation events. If, on the other hand, the allele frequencies are influenced by natural selection, we could observe a configuration inconsistent with the phylogeny (that is: the family tree of these species).

The allelic frequencies at the Acph-1 locus are shown in Table 4. Notice the conspicuous similarities between *paulistorum* and *nebulosa*. In both species, allele #108 is most common, with #112 and #106 at lower frequencies. The same alleles are rare or absent in the other species. Barring selection, these data strongly suggest that *paulistorum* and *nebulosa* very recently derived from a common ancestral population, from whom they inherited their allele frequencies. Not enough time has elapsed to allow for large shifts. The other species appear to be further removed, both from the *paulistorum*/*nebulosa* clade and from each other – they are so distant from one another that in each of them a different allele has come to dominate the population.

Table 4: Allelic frequencies at the Acph-1 locus among five species of *Drosophila*. The most important figures are emphasized. The frequencies do not always add up to 1, because very rare alleles haven been omitted. These data are taken from Ayala (1977, p. 187).

Allele #	*Willistoni*	*Tropicalis*	*Equinoxialis*	*Paulistorum*	*Nebulosa*
94	0.011	**0.959**	0.013	-	-
100	**0.969**	0.023	0.172	-	-
104	0.016	0.004	**0.811**	0.035	0.008
106	0.001	-	-	**0.050**	**0.096**
108	-	-	0.004	**0.671**	**0.619**
112	0.001	-	-	**0.224**	**0.272**

But these conclusions are strongly opposed by the data from another allele, Xdh (Table 5). There we find that allelic frequencies in *paulistorum* greatly resemble those in *willistoni*, and to a slightly lesser degree those of *equinoxialis*. This suggests that these three species share a recent common ancestor. The other two species appear to have split off earlier, and have undergone significant genetic drift since the speciation event.

Table 5: Allelic frequencies at the Xdh locus among five species of *Drosophila*. These data are taken from Ayala (1977, p. 192).

Allele #	*Willistoni*	*Tropicalis*	*Equinoxialis*	*Paulistorum*	*Nebulosa*
91	-	0.031	-	-	-
92	-	0.013	-	-	0.010
93	-	0.387	-	-	-
94	-	0.017	-	-	0.015
95	-	**0.524**	-	-	0.053
96	0.001	0.019	0.003	0.002	**0.730**
97	0.006	0.005	0.007	0.001	0.158
98	**0.113**	-	0.031	**0.194**	0.031
99	0.068	-	0.048	0.031	-
100	**0.467**	-	**0.687**	**0.404**	-
101	**0.322**	-	**0.218**	**0.312**	0.001
102	0.017	-	0.002	0.020	-

The situation only worsens when other loci are considered. Table 6 shows the data for two other loci. The Ao-1 locus supports the *equinoxialis*/*paulistorum* clade, but groups *willistoni* with the other two species. At the Adk-2 locus, yet another picture emerges: now it is *equinoxialis* and *nebulosa* that form a clade, and considerable time must have passed since the split with the other species.

Table 6: Allelic frequencies at two loci among five species of *Drosophila*. These data are taken from Ayala (1977, pp. 187-188).

Locus: Ao-1					
Allele #	*Willistoni*	*Tropicalis*	*Equinoxialis*	*Paulistorum*	*Nebulosa*
96	0.005	0.028	-	0.003	-
98	0.091	0.038	-	0.041	0.032
100	**0.733**	**0.849**	0.002	-	**0.774**
101	-	-	-	0.043	0.003
102	0.108	0.057	0.050	0.131	0.120
103	0.005	-	0.029	0.022	0.042
104	0.010	-	**0.796**	**0.655**	0.004
105	0.016	0.028	0.044	-	-
106	0.001	-	**0.072**	**0.200**	-
Locus: Adk-2					
Allele #	*Willistoni*	*Tropicalis*	*Equinoxialis*	*Paulistorum*	*Nebulosa*
96	0.011	0.033	0.003	-	-
100	**0.944**	**0.948**	0.038	**0.985**	0.003
104	0.019	0.019	**0.941**	0.015	**0.971**
108	0.005	-	0.007	-	0.023

Ayala's complete dataset covers 30 distinct loci. The data shows a disorganized checkerboard of similarities and differences, with different loci implying wildly disparate patterns of relationships. Under neutralism, no single phylogeny can be consistent with most of the data. The majority of Ayala's loci must have been influenced by natural selection in at least one species. To my knowledge, neutralists have never responded to this criticism.

5.4 Areas of progress for neutralism

Despite these difficulties, it would be a mistake to assume that neutralism has unequivocally been at the losing end of the neutralist-selectionist controversy. There have also been victories. One notable instance involves the neutralist prediction that "[f]unctionally less important molecules or parts of a molecule evolve (in terms of mutant substitutions) faster than more important ones" (Kimura & Ohta, 1974, p. 289). This prediction flows from the idea that functionally important parts are under stringent 'purifying' selection, while unimportant parts are less constrained.

In the translation from nucleic acids to proteins, three nucleotides (together called a codon) code for one amino acid. Most amino acids are coded for by two or more different codons. Because of this redundancy in the genetic code, nucleotide substitutions in protein-coding DNA sequences do not always change the amino acid (AA) sequence of the protein. Mutations that do not change the AA sequence are called silent or synonymous mutations. Synonymous mutations were believed to be neutral or nearly neutral. This led Kimura to expect that most changes in protein-coding sequences that have occurred during evolution would be of the silent type. Kimura found confirmation of his prediction in early sequence data. Comparisons between human and rabbit hemoglobin mRNA sequences, as well as between histone H4 mRNA sequences of two sea urchin species, showed that the vast majority of substitutions were synonymous (Kimura, 1977).

Today, the neutrality of codon choice is no longer a truism, as a substantial amount of evidence has been amassed that indicates that certain codons are preferred over others, and that selection exerts control over codon usage (Kober & Pogson, 2013; Lynn, Singer, & Hickey, 2002). Still, Kimura's suggestion that synonymous mutations have less of an impact on functionality remains reasonable.

5.4.1 The molecular clock

More interesting than the confirmation of Kimura's prediction, perhaps, is the support that neutralism provided for the then up-and-coming notion of the 'molecular clock'. This refers to the idea, first pioneered in the early 60s (Zuckerkandl & Pauling, 1962), that the timing of phylogenetic splits (such as the time of divergence of the human and chimpanzee lineages) can be calculated based on the differences in protein or nucleic acid sequences between species. The more time has passed since the last common ancestor, the more mutations will have been sustained. "If elapsed time is the main variable determining the number of accumulated substitutions, it should be possible to estimate roughly the period at which two lines of evolution leading to any two species diverged" (Margoliash, 1963, p. 677). The pattern of differences and similarities in sequences from different species can be used to construct a phylogenetic tree, and by counting the numbers of substitutions between the tips and nodes in the tree, the elapsed time since phylogenetic splits can be approximated.

The validity of the molecular clock is predicated on the assumption that there is some degree of constancy in the rate of substitutions. Selectionism provides no grounds for such an assumption, because it claims that genetic change is mostly governed by selection, and selective pressures vary in direction and intensity. The neutral theory of molecular evolution, on the other hand, can supply the rationale behind a constant substitution rate. This connection between the genetic clock and non-adaptive changes was realized by Emile Zuckerkandl and Linus Pauling even before Kimura articulated the neutral theory in 1968:

> It would then appear that the changes in amino acid sequence that are observed to be approximately proportional in number to evolutionary time should not be ascribed to vital necessities of adaptive change. On the contrary, the changes that occur at a fairly regular

> over-all rate would be expected to be those that change the functional properties of the molecule relatively little […] *There may thus exist a molecular evolutionary clock.* (Zuckerkandl & Pauling, 1965, p. 148, italics in original)

On the neutral theory, the long-term rate of substitution is roughly equal to the rate of neutral mutations per haploid genome per generation. So as long as mutation rates are approximately constant, the assumption underlying the genetic clock technique should hold true.

For perfectly neutral mutations, the substitution rate is also independent of population size. This is not the case for so-called 'nearly neutral mutations' (Ohta & Kimura, 1971). According to Tomoko Ohta, nearly neutral mutations constitute a sizable fraction of the substitutions in molecular evolution (Ohta, 1972, 1973). These mutations can behave *as if* they are neutral if $|s| < 1/4N_e$, where N_e is the effective population size, and s is the selective (dis)advantage of the mutant allele. This implies that the number of mutations that will behave as neutral is inversely proportional to the population size. In small populations many deleterious mutations may escape selection's attention, while this would not happen as much in large populations. From this it follows that substitution rates fluctuate with population size. So neutralism not only makes the relative constancy of molecular 'tick rates' intelligible, it also helps us understand under what circumstances the rates may vary:

> Many processes could affect the number of substitutions per unit time, primarily by changing the balance between the relative influences of selection and drift, either for specific genes or sites in genes, or across whole genomes. (Bromham & Penny, 2003, p. 218)

This "balance between the relative influences of selection and drift" can vary among genes and even among different sites of the same gene – both because some mutations are synonymous and because some amino acids are more critical than others. It can also vary over time: as a protein attains a new function, the selective pressure on its different constituents change. And if a gene is rendered non-functional (i.e. it becomes a pseudogene), its rate of substitution increases because subsequent mutations will now be neutral and will no longer be weeded out by selection. A fast substitution rate in a stretch of DNA indicates that its exact sequence is unimportant or even that it is dysfunctional. Conversely, conservation of certain sequences across taxa is can be regarded as an indication of selection and, accordingly, functionality.

5.4.2 Detecting positive selection

A notable result of the interplay between neutralism, the genetic clock, and phylogenetic reconstructions based on molecular data, was the development of methods to use the d_N/d_S ratio to detect natural selection. This is the ratio between non-synonymous (d_N) and synonymous (d_S) mutations, also signified by ω (Yang & Bielawski, 2000). In a non-functional DNA sequence, such as a pseudogene, all mutations are neutral and there should be no bias in favor of either synonymous or non-synonymous mutations. In that case, ω will be ~1. For most functional genes, synonymous substitutions will outnumber non-synonymous ones, so $\omega < 1$. If this is the case, the gene is said to be under 'purifying selection'. Selection maintains the AA sequence of the coded protein, but neutral, synonymous substitutions still occur. The most interesting situation is when non-synonymous substitutions outstrip the synonymous ones, so that $d_N/d_S > 1$. The gene is under 'positive selection': amino acid changes are actively driven to fixation by natural selection. This may indicate that the gene is (or was) being tuned for a specific function.

Of course, both purifying and positive selection may have occurred at different stages in the history of a gene, or at different locations in the same gene. As a result, a single value for ω for an entire gene may be too coarse. More refined methods calculate d_N/d_S ratios for different portions of genes; sometimes even down to the level of single codons (Cavatorta, Savage, Yeam, Gray, & Jahn, 2008; Suzuki & Gojobori, 1999). This is done by mapping the inferred mutations over the phylogenetic tree. To attain reasonable resolution, a large number of sequences from many different species is required, so that sufficient numbers of mutations per locus are observed.

These methods allow researchers to identify at which amino acids the crucial changes have taken place. The codons where $\omega > 1$ may have been important in adaptive evolution, even if other portions of the gene show evidence of purifying election. Paradoxically, one of the greatest virtues of neutralism may lie in pinpointing the places where it does not apply!

5.5 Neutral networks

It is generally understood that neutral evolution cannot explain the origin of adaptations. Surprisingly, this may not be entirely true. The neutral theory claims that most change at the molecular level is neutral, and that selection is primarily a guardian against deleterious mutations (purifying selection) rather than a guide towards higher fitness (positive selection). On this view, mutation pressure pushes evolution onward. However, even when only fulfilling the negative role of purging deleterious mutations, selection could, theoretically, influence the direction of neutral evolution. Whether this will happen depends on the topology of the fitness landscape.

Recall Wright's fitness landscape from the introduction of this chapter. The landscape metaphor can also be applied to single proteins. Here, each coordinate in the landscape (also called sequence space) represents a particular AA sequence, while the elevation at that coordinate indicates the fitness of that sequence. Coordinates that are adjacent to each other are separated by a single amino acid substitution (or deletion or addition).

Of all possible AA sequences, only a tiny minority yields functional proteins. Most of sequence space is dominated by a huge, flat plane – a massive desert of dysfunctionality. There are small pockets of functional sequences (hills), but these are relatively rare occurrences. Most random changes to functional proteins, therefore, are expected to reduce or even eliminate functionality. This conforms to observations. Still, an unexpectedly large proportion of mutations does not diminish protein functionality (Taverna & Goldstein, 2002). This surprising ability of proteins and other biological systems to withstand changes is called robustness (de Visser et al., 2003). Robustness can be considered an adaptive feature. And this 'adaptation' can be explained through neutral evolution.

5.5.1 Neutral networks may explain protein robustness

Robust proteins do not occupy sharp, isolated peaks in the landscape. Rather, they are located on wide plateaus. It has been suggested that these plateaus are surrounded by sizable areas of similar elevation, and perhaps even by 'networks' that connect different plateaus (Babajide, Hofacker, Sippl, & Stadler, 1997; Huynen, 1996). These plateaus and networks are high and flat, which means that mutational steps in these areas are selectively neutral. Thus, protein sequences can traverse the networks by neutral evolution.

Of course, the plateau will be bordered by downward slopes, or even steep cliffs. Each time a mutational step pushes a protein over the edge of a cliff, purifying selection can exterminate the

mutant. In the long run, it pays to keep a safe distance from cliffs. Consequently, purifying selection can lead AA sequences away from the narrow patches of the network and unto the safety of wide plateaus (Bornberg-Bauer & Chan, 1999). In this way, neutral molecular evolution provides an elegant explanation for the observed robustness in biological systems (van Nimwegen, Crutchfield, & Huynen, 1999).

This explanation is not merely conceptual. The suggestion that robustness can evolve by traversing neutral networks has been supported by simulations (Bastolla, Porto, Roman, & Vendruscolo, 2003). Moreover, in an *in vitro* experiment involving large numbers of (nearly) neutral mutations in the TEM-1 β-lactamase resistance gene in bacteria, it was found that the wild-type sequence of the TEM-1 protein is surrounded by a large neutral network, and that purifying selection kept the neutrally drifting sequences in the vicinity of more robust ancestral sequence (Bershtein, Goldin, & Tawfik, 2008).

5.5.2 Exploration of the neutral network may facilitate selective evolution

Each plateau consists of many different genotypes (nucleic acid or amino acid sequences) that produce more or less the same phenotype (a protein folded into a specific conformation). At most locations in the network all possible mutations are either neutral or deleterious. But some parts of the network are likely to be adjacent to another, higher plateau. This implies that drifting through neutral networks can bring evolving proteins in the zone of attraction of another phenotype, that has a higher fitness. The result would be periods of phenotypic stasis (but neutral genotypic drift), interrupted by sudden phenotypic shifts (van Nimwegen, 2006).

Interestingly, compelling evidence has emerged that this is the pattern followed by influenza A (subtype H3N2) as it evolves to counter human immune responses. The human immune system targets the viral surface protein hemagglutinin (HA), so the virus is under selective pressure to alter the conformation (and therefore antigenic properties) of this protein. Not surprisingly, consecutive flu outbreaks are associated with different shapes of HA. Using data from outbreaks from 1968 to 2003, Smith et al. (2004) identified 11 'clusters' of HA variants that succeeded each other in time. Each cluster is a collection of HA variants with different amino acid sequences but similar antigenic properties. Distinct protein conformations mark the differences between clusters.

Using these data, Koelle et al. (2006) suggested that each cluster represents an exploration of a neutral network. They proposed that HA randomly wanders over the neutral network, leading to a diverse population of HA variants that may differ genotypically but are similar in shape, antigenic properties, and fitness. After several years many humans have developed immunity against this HA shape, effectively lowering the elevation of the entire neutral network. But by then, one of the 'drifters' has stumbled upon another, higher plateau. At this point, after years of neutral evolution, an innovative mutation occurs, resulting in a transition to a differently shaped but still functional protein, which is not susceptible to the human immune response. The newly adapted virus is likely to be very successful, leading to a new outbreak, and to an exploration of the new neutral network.

The authors back their interpretation by computer simulations, and also cite as support the empirical fact that the genetic distances within clusters (resulting from neutral drift) are in many cases larger than the distances between clusters (which would have to be crossed by adaptive steps). Furthermore, the hypothesis neatly explains the observed 'boom and bust' pattern in viral genetic diversity, as well as the peculiar observation in viral evolution that "although genetic change is gradual, antigenic change is punctuated" (ibid., p. 1898).

In this elegant model, neutral and selective evolution work together. The selective mutation to a higher plateau is certainly the most interesting step, but it would not have been possible but for the neutral walk that preceded it.

5.6 The current status of neutral evolution

During the neutralist-selectionist controversy, selectionists defended the orthodox neo-Darwinian view that selection governs the speed and direction of evolution. By contrast, neutralists held that most molecular change is neutral, and that mutations dictate the rate of molecular evolution. While some of those involved in the debate in the 70s still resolutely support either selectionism (Ayala, personal communication, January 28, 2016) or neutralism (Nei, 2013), the controversy seems to have abated during the 80s. For most present-day evolutionary biologists it is no longer a live issue. Why is this?

The answer to this question is not that the debate has been settled in favor of either party. Strict selectionism (panselectionism) is untenable in light of the excess of synonymous mutations in protein evolution. Likewise, 'pan-neutralism' failed to account for Ayala's observations of polymorphisms in South-American *Drosophila* populations. The neutral theory had to be immunized to refutation by choosing very specific parameters for migration rates, local extinction rates, and past population sizes – clearly a degenerative shift.

The answer, I believe, lies in the fact that *most progress has been achieved* by recognizing the importance of both selective and neutral changes at the molecular level. This is clearly seen in the use of d_N/d_S ratios to identify sites where positive selection has occurred. Here, neutrality is essentially used as a null hypothesis, deviations from which are regarded as evidence for adaptive changes (Dietrich, 2011). Similarly, the 'neutral networks' hypothesis has been successful in explaining the patterns of influenza A evolution by combining neutral and selective evolution. The successful application of theories to solve problems that were undreamed of when the they were first articulated is a clear sign of progress. This progress must be accredited to the overarching program that incorporates both mechanisms.

Contemporary evolutionary biologists will readily admit that much variation at the molecular level is probably neutral or nearly-neutral. Still, the most interesting changes (from a physiological or medical perspective) are the adaptive ones. Whether neutral or selective evolution generally predominates is no longer debated, but determined on a case-by-case basis. Ultimately, both selective and neutral evolution are available explanations within the larger framework of the evolutionary research program – a fact that was already anticipated by Charles Darwin:

> Variations neither useful nor injurious would not be affected by natural selection, and would be left a fluctuating element, as perhaps we see in the species called polymorphic. (C. R. Darwin, 1859/1979, p. 131)

Conclusions

In this treatise I set out to answer two questions. First, is the methodology of scientific research programs applicable to evolutionary biology? And second, to the extent that it is applicable, how well do evolutionary biology and its subsidiaries perform in terms of progressive or degenerative problem shifts?

I answer the first question in the affirmative, but with some caveats. Throughout this study, the developments within evolutionary biology have made sense from a Lakatosian standpoint: the tenacity in upholding the program in the face of contrary evidence (as was the case at the end of the 19th century), the birth of a program amidst a sea of anomalies and its subsequent triumph over these anomalies (Mendelism), the successive development of ever-more-sophisticated models (by the neo-Darwinian mathematicians), the incidence of both progressive and degenerative problem shifts, et cetera.

One of the difficulties with the model lies in defining the hard core of the program under evaluation. Lakatos did not provide criteria for distinguishing the core, so I had to formulate my own criteria (see Section 2.1). Even when applying these criteria, the delineation of the program remains arbitrary to some degree. I have chosen to define the hard core in part based on the long history of pre-scientific evolutionary thought. Others may have chosen a different point of departure, resulting in a different formulation of the hard core.

Another disadvantage of Lakatos' model is that an adequate evaluation cannot be performed until many years after the critical shifts have taken place. This limits its usefulness for assessing contemporary ideas.

Let us now turn to the second question. Evolutionary biology is a huge field, with many subsidiary disciplines. It is no surprise, then, that over the course of one and a half century both degenerative and progressive problem shifts have occurred. This treatment has been far too brief to draw strong conclusions as to the status over the overarching evolutionary research program – important aspects of it, such as the thesis of large-scale common descent, have not received their due attention. Nevertheless, some relatively firm judgments can be drawn regarding certain subprograms.

Table 7 lists the problem shifts that have been reported in this work. Note that in each case, the 'proposed solution' (third column) is a subprogram or auxiliary hypothesis within the broader research program given in the first column. The subprogram may in turn become a research program of its own that is confronted with empirical challenges. Thus, neutralism first shows up as a proposed solution to a problem confronting evolutionary biology, and is subsequently treated as a research program itself.

The table identifies four degenerative shifts and six unambiguously progressive shifts. The areas most associated with degenerative shifts (in this limited analysis) are Lamarckian inheritance and 'pan-neutralism'. Notable areas of progress are Mendelism, the Modern Synthesis, kin selection, and the integration of neutral and selective evolution.

Table 7: An overview of problem shifts discussed in Chapters 3 – 5.

Research program	Problem(s) or challenge(s)	Proposed solution	Lakatosian evaluation	Comment	Section
Evolutionary biology	Selection too slow, adaptations lost due to 'blending'	Lamarckian inheritance	Degenerative	Required degenerative shifts (next two items)	3.1
Lamarckian inheritance	Non-heritability of mutilations	Various options	Degenerative	Conventionalist stratagems to explain anomalies	3.1
Lamarckian inheritance	Weismann barrier	Pangenesis	Degenerative	Lack of positive evidence	3.1
Evolutionary biology	Adaptations lost due to 'blending'	Saltationism	Undecided	Morphed into Mendelism	3.2
Mendelism	Sex-determination, sex-linked inheritance	Sex-chro-mosomes	Progressive	Useful distinction with autosomes, explained sex-linked disorders	3.2
Mendelism	Non-independent segregation of traits	Genetic linkage	Progressive	Led to chromo-some-mapping, crossing-over observed in 1931	3.2
Evolutionary biology	Incongruity between gradualism and Mendelism	Modern Synthesis	Progressive	Featured many subsequent progressive shifts	3.3
Selectionism	Non-selfish behavior	Group selection	Undecided	Requires improba-ble conditions, experimental evidence is shaky	4.1
Selectionism	Non-selfish behavior	Kin selection	Progressive	Helps explain sex ratios in social in-sects, fostered inte-rest in sociobiology	4.2
Selectionism	Investment choices	Game theory, ESS	Undecided	Partial confirmation in digger wasps	4.3
Sociobiology	Eusociality	Parental manipulation	Progressive	Predicted characteristics of eusocial vertebrate	4.3
Evolutionary biology	Genetic load	Neutralism	Partly progressive	Featured both progressive and degenerative shifts	5.1
Neutralism	Similar allele frequencies in different populations	Migration	Scientific	Led to new prediction, but was not corroborated	5.3
Neutralism	Not enough heterozygosity in panmictic population	Recent population expansion	Degenerative	Immune to falsification	5.3
Evolutionary biology	Incongruity between selectionism and neutralism	Recognition of both	Progressive	Led to use d_N/d_S ratios, neutral network hypothesis	5.4 5.5

Naturally, this table is not intended to fully capture the progressiveness shown by neo-Darwinism. It only shows problem shifts, but neo-Darwinism should also be credited for anticipating numerous observations and concepts. Examples include the existence of balanced polymorphisms (Section 3.3), the high levels of variability in larger species (3.3), the conditions under which group selection may work (4.1), and the development of the relatedness quotient by Sewall Wright before William Hamilton utilized it in a different context (4.2).

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