

Of Metaphors and Darwinism: Deconstructing Genetic Programming's Chimera

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Abstract— This paper discusses several metaphors from Darwinism that have influenced the development of genetic programming (GP) theory. It specifically examines the historical lineage of these metaphors in evolutionary computation and their corresponding concepts in evolutionary biology and Darwinism. It identifies problems that can arise from using these metaphors in the development of GP theory.

1. Introduction

Darwinism has strongly influenced the development of theory in genetic programming (GP), as well as the entire field of evolutionary computation (EC). In many ways, the ultimate *arbitre* of development and conflict resolution in evolutionary computation has been based on what Darwinism has to say. That might be acceptable if Darwinism represented a monolithic research tradition. However, as we demonstrate in this paper, Darwinism is anything but a monolith.

In this paper, we indict metaphors of Darwinism as sources of difficulty in GP theory. Close inspection of these metaphors reveals borrowed concepts from different, even antagonistic research traditions in evolutionary biology. Our investigation has focused on the historical and philosophical traditions in evolutionary computation and Darwinism, with the aim of understanding of what GP theory has borrowed from Darwinism. We maintain that difficulties in GP theory have occurred in part because of uncritical borrowing. We do not go so far as to say these metaphors are wrong. Instead, the purpose of this paper is twofold. First, this paper seeks to make the reader aware that casual borrowing of concepts can lead to problems in the synthesis of GP theory. Second, this paper seeks to make the reader aware that in borrowing concepts from Darwinism, we may have also unwittingly borrowed some of that tradition's baggage as well.

We note that metaphors are not intrinsically falsifiable, at least not in a way that a well-crafted scientific hypothesis should be (Popper 1958). By nature, a metaphor implicitly draws loose comparisons between distinctive objects or concepts. Metaphors caricature and represent non-literal descriptions that can stimulate thought. A well-chosen metaphor provokes discussion and yields additional insight—a well-chosen metaphor displays richness. One does not spend time falsifying caricatures (metaphors) because of their literal fidelity to the phenomena under investigation. That effort is better spent on falsifying hypotheses based on those metaphors. One, however, can promote or discount metaphors on the basis of their worth (in our case, their contributions towards theory).

We especially note that a metaphor's worth extends far beyond its explanatory power. As Depew and Weber stated, metaphors are not rhetorically innocent (as in the case of metaphors in evolutionary biology).

...just because metaphors play roles in explanations that one is not entitled simply to say, "Oh, that's just my way of putting it." Even when they perform little or no explanatory work, moreover, metaphors carry a good deal of metaphysical and epistemological freight. Indeed, whenever there is a deficit between theoretical reach and empirical support, the difference is usually made up by invoking ontology to do the missing work. Similarly, epistemological and methodological ideals are sometimes used to intimate on highly general grounds that the theory in question must be true. In such cases, Lewontin and Levins argue, *we are entitled at least to suspect that ideology may be involved* (Levins and Lewontin 1985) [italics ours]. (Depew and Weber 1995, p. 374)

The use of metaphors gains added potency in evolutionary computation because of two additional factors. First, metaphors play a significant, if not decisive, role in the synthesis of the field and the creation of the theory, algorithms, and phenomena subsumed by this field—e.g., (Fogel 1995; Bäck 1996). Second, certain research agendas in evolutionary computation posit that not only does Darwinism have a say about the way that evolutionary computation proceeds, but that evolutionary computation has a say about the reality of living things—e.g., (Holland 1961; Holland 1975; Holland 1992; Frank 1996).

This paper consists of three contentions and conclusions, each of which is highlighted in the sections that follow.

2. Metaphors and GP Theory

Contention 1: *Theoretical arguments in GP have been strongly influenced by several key metaphors of Darwinism and evolutionary biology.*

One can think about a metaphor in science as a synthesis of disparate concepts that are "thrown together," like throwing bits of clay together to form a sculpture. The "throwing together" can be done systematically or accomplished with great (artistic) license—either can work to produce a rich and useful metaphor. In any case, one needs to keep in mind that metaphors are not strictly logical, isomorphic entities that allow one to chart unambiguous mappings from one domain to the next. We note that the metaphors discussed in this section have been "thrown together" from several different directions.

In particular, a common route for metaphors to occur in GP has been through the genetic algorithm (GA) research tradition, which in turn has taken its metaphors from Darwinism

and evolutionary biology. However, other routes can lead from other research traditions in evolutionary computation. Significant metaphors from Darwinism and evolutionary biology tend to resonate simultaneously in several research traditions in evolutionary computation. We also note that GP metaphors can have multiple origins or originate directly from work in the biological sciences.

In this section, we concentrate on several key metaphors that can ultimately be traced to Darwinism and evolutionary biology. In each case, we start with the metaphor as used in the GP research tradition. Where possible, we indicate the usage and context of these metaphors in other research traditions in evolutionary computation (especially in the GA research tradition). We then indicate where in the Darwinist literature the concepts occurred.¹

Introns. The term *introns* refer to portions of code within a GP individual that do not directly contribute to the fitness of that individual. Koza (1992, p. 7) first noted the analogy between introns in DNA (deoxyribonucleic acid) and functionally inert code in GP individuals. Angeline (1994) reinforced that analogy by saying that those unused code portions *are* introns in GP. Tackett (1994) noted that GP individuals grew unchecked because of “hitchhiking” sections of code, which seemed not to contribute to an individual’s fitness. This unchecked growth in GP individuals during the course of a run is now described by the term *bloat*. Strong evidence supports the contention that bloat consists mostly of introns (McPhee and Miller 1995; Nordin and Banzhaf 1995; Nordin, Francone et al. 1996; Soule, Foster et al. 1996; Soule and Foster 1997). Banzhaf et al. (1998, p. 182) has said that, “the evidence is strong that evolution selects for the existence of GP introns.”

Introns seem to have both detrimental and beneficial effects. On one hand, introns that are too large seem to cause *stagnation* (Banzhaf, Nordin et al. 1998, p. 182). On the other hand, introns seem to protect useful code within a GP individual against crossover (Nordin and Banzhaf 1995; Angeline 1996; Nordin, Francone et al. 1996). A taxonomy of introns appears in (Banzhaf, Nordin et al. 1998).

The term *intron* first appeared in the GA literature, i.e., (Levenick 1991). Levenick argued that introns can serve a beneficial purpose: to protect GA “genes” against crossover. (See also (Wu and Lindsay 1995).) We note that Angeline (1994) based his use of the term *intron* on Levenick’s paper.

On the biological side, the concept of *intron* represents a fairly new development in the history of Darwinism. The bridge paper between introns in Darwinism and introns in evolutionary computation is (Gould 1989), which Levenick (1991) cited. The discovery of introns (noncoding, base-pair sequences) and exons (base-pair sequences that code for parts

of proteins) lay the foundation for McClintock’s Nobel prize-winning work in transposons (“jumping genes”) (Keller 1983).

Building Blocks. At face-value, the term *building blocks* refers to a conceptually basic definition: simple components out of which more complex things can be made (as in the children’s toy (Goldberg 1989, p. 41)). However, the term *building blocks* represents a controversial issue in GP theory, in part because building blocks have been tied to the GA Building Block Hypothesis (Goldberg 1989).

Koza (1992) suggested that GP uses building blocks in a fashion similar to GA. Early anecdotal information seemed to bear this out, as a few researchers reported seeing repeated code in their results that have been highly suggestive of building blocks—e.g., (Tackett 1994). However, several meanings of the term *building blocks* have been subsequently offered, if only to attempt a rigorous definition. For example, a building block in a GP individual has been defined to be a subtree of an individual (Koza 1992); blocks of code (Altenberg 1994); a rooted subtree (Rosca 1997); and program semantics (Haynes 1997). Several works have addressed the issue of GP schemata, a theoretical formalism of building blocks that often presupposes a particular structural form (i.e., a subtree)—e.g., (O’Reilly and Oppacher 1995; Whigham 1995; Poli and Langdon 1997a; Poli and Langdon 1997b; Rosca 1997; Langdon and Poli 1998; Poli, Langdon et al. 1998). None of the theories about schemata have been able to predict reliably how desirable schemata propagate during the course of a run (Banzhaf, Nordin et al. 1998).

Relatively recent works have contended that building blocks (usually referring to schema) do not exist. A simplified argument proceeds as follows: GP uses crossover to preserve building blocks; GP attains a certain performance measure; an alternative operator that should not be able to preserve building blocks is substituted in lieu of crossover; GP with the alternative operator meets (or exceeds) the performance measure of GP with crossover. Consequently, the statement “GP is a building block engine” is suspect. Works along these lines include (Lang 1995; Angeline 1997a; Angeline 1997b; Chellapilla 1997; Chellapilla 1998). Works that demonstrate the equivalent or superior efficacy of alternative operators have been used or considered for use in this argument—e.g., (Harries and Smith 1997; Luke and Spector 1997; Luke and Spector 1998).

In evolutionary computation, the term *building blocks* gained widespread usage in the GA research tradition—e.g., see (Goldberg 1989; Holland 1992). The term *building blocks* has played a significant part of the narrative that explains the Schema Theorem and has appeared in a number of books and papers on genetic algorithms—e.g., (Goldberg 1989; Holland 1992; Mitchell 1996; Eshelman 1997). We note that *schema* preceded the use of *building blocks* by a number of years, even though *schema* represents a mathematical formalism of the more general and intuitive *building blocks*. The term *building blocks* was absent in Holland’s early work, which includes the first edition of *Adaptation in Natural and Artificial Systems* (Holland 1975). Widespread use of *building blocks* occurred after Goldberg described the GA Building Block hypothesis (Goldberg 1989), which can be stated as follows:

Short, low-order, and highly fit schemata [building blocks] are sampled, recombined, and resampled to form strings of potentially higher fitness. (Goldberg 1989, p. 41)

¹ In this paper, as in (Depew and Weber 1995), we consider the history of Darwinian evolutionary *theory*. The history of evolutionary theory is not identical to the history of evolutionary *biology*. The latter encompasses other evolutionary theories that are not traditionally associated with Darwinism, e.g., (Margulis 1970). We examine research traditions that have been key to the evolution of Darwinism, which does not always include research traditions that have been key to the development of evolutionary biology. For example, we only indirectly consider paleontology.

On the biological side, the concept of building blocks seems only indirectly linked with analogous concepts in evolutionary biology. Historically, the term *building blocks* is not prevalent in the primary Darwinist literature—i.e., (Darwin 1859; Fisher 1930; Dobzhansky 1937; Huxley 1942; Mayr 1942). For the most part, the term is absent in the literature. We note that Huxley did mention building blocks, but Huxley's use of the term does not coincide with usage of *building blocks* in evolutionary computation (“The building-blocks of evolution, in the shape of mutations, are, to be sure, discrete quanta of change (Huxley 1942, p. 27).”)

Evidence suggests that the term as used in evolutionary computation originated independently of evolutionary biology. The EC concept of building blocks, however, resonates with key tenets of Darwinism in the 1930s to mid 1940s, when Mendelian genetics merged with Darwinism. This merger represented a fundamental shift in the history of Darwinism, since prior to it, Mendelian genetics and Darwinism existed as wholly separate research traditions. As Huxley (1942, p. 47) succinctly stated, “The essence of Mendelian heredity is that it is particulate.” Before the synthesis, Darwinists contended that for natural selection to result in gradual change, what enabled that change was a continuous, blending process. During the synthesis, Huxley and others argued for a mechanism that was inherently not continuous. Instead, they argued that heredity is discrete and measured in units of genes; an idea not unlike having discrete units of schemata in GA (which Goldberg later referred to as building blocks (Goldberg 1989)). The “mechanism of particulate inheritance” was *the* focus of one of the earliest neo-Darwinists, Fisher (1930). Fisher posed the rhetorical question, “Is *all* inheritance particulate [italics ours]?” He replied, “The Mendelian theory is alone competent...” (See (Fisher 1954, pp. 17–18).)

Genotype and Phenotype. The metaphors of *genotype* and *phenotype* have been liberally used in the GP literature. The “usual” definition for genotype is that which underlies a single trait or a set of traits—i.e., a parse tree in GP. For phenotype, the “usual” definition is (GP individual) behavior. These definitions are based on those provided in (Bäck and Fogel 1997). Beyond these “usual” connotations of the term is a controversy over what exactly is meant by these terms when concerning GP. For example, the metaphor of phenotype has several meanings. Some have gone so far as to define the phenotype as equivalent to vector values, as in those used for fitness scoring (Altenberg 1994). Others have opted for a more abstract definition by equating phenotype with semantics (Haynes 1997). Some researchers simply define phenotype as observed behaviors (Banzhaf, Nordin et al. 1998, p. 185).

A significant portion of this controversy arises from the use of genotype and phenotype in relation to building blocks. The predominant view is that building blocks are genotypes (structures) and that the mathematical formalism of a building block is a schema, e.g., (Poli and Langdon 1997b). One alternative view holds that for GP, the genotype and the phenotype are one and the same (Nordin, Francone et al. 1996). Another alternative view is that building blocks in GP exist in both the genotype and the phenotype (Haynes 1997). For as much controversy as these terms have engendered, however, we note that the *earliest* GP theory did not depend upon having precise definitions of genotype and phenotype. For example,

(O'Reilly and Oppacher 1995) used neither terms. The metaphors were not directly employed in the early synthesis of GP, either (i.e., Koza used neither term in (Koza 1989; Koza 1992)).

In the broad context of the evolutionary computation field, the metaphors of *genotype* and *phenotype* are common. Nevertheless, as in GP, these metaphors were *not* essential to much of the *earliest* works in evolutionary computation. Neither term appears in the early work of the principals who are credited with the three primary research traditions in evolutionary computation: genetic algorithms (Holland 1961; Holland 1962; Holland 1967; Holland 1973), evolutionary programming (Fogel 1962; Fogel, Owens et al. 1965; Fogel 1968), and evolution strategies (Rechenberg 1964). Contemporary usage of these metaphors in GA stems from (Holland 1975). Contemporary usage of these metaphors in evolutionary strategies and evolutionary programming stems largely from (Atmar 1992),² which came at roughly the time these three research traditions began to interact (Bäck, Hammel et al. 1997, p. 4).

On the biological side, Lewontin's work has been one of the bridges from which contemporary EC usage of genotype and phenotype has stemmed (Lewontin 1974). In a later work, Lewontin has defined the genotype of an organism to be the “class of which it is [a] member based upon the postulated state of its internal hereditary factors, the genes (Lewontin 1992, p. 136).” Similarly, Lewontin has defined the phenotype of an organism to be the “class of which it is a member based upon the observable physical qualities of the organism, including its morphology, physiology, and behavior at all levels of description (Lewontin 1992, p. 136).”

One can trace these concepts further back in the history of evolutionary biology than as indicated by (Lewontin 1974). Johannsen first coined the terms in 1909 (Dunn 1965, p. 79) (i.e., see (Johannsen 1911)) to distinguish between an unchanging heritable part (genotype) and a changing appearance (phenotype). Although the terms were not invented then, the idea of genotype and phenotype is implicit in Weismann's classic work (Weismann 1893) that distinguished between germ (heritable part) and soma (body). Even before Weismann, Mendel argued for heritable factors that explained the manifest state of an organism (Mendel 1865; Lewontin 1992).

3. Tradition and Conflict in Darwinism

Contention 2: The use of several of these metaphors in evolutionary computation has been significantly, if not unconsciously influenced by differences, biases, and even personalities of antagonistic research subtraditions within the neo-Darwinist framework.

Mayr (1998) has argued that Darwin's Darwinism consisted of five separate theories: naturalism, transmutation, descent with modification, natural selection, and casual pluralism. At the conceptual core of these theories and the Darwinian research tradition is natural selection (Depew and Weber 1995, p. 2).

As Mayr (1964, p. xxv) has noted, “it is well known that Darwin did not understand the causation of variability.” As

² While most researchers may have not read (Atmar 1992), many researchers have been introduced to his diagram that has been recapitulated from (Lewontin 1974). This diagram has appeared in recent works, including (Bäck et al. 1997; Fogel 1995).

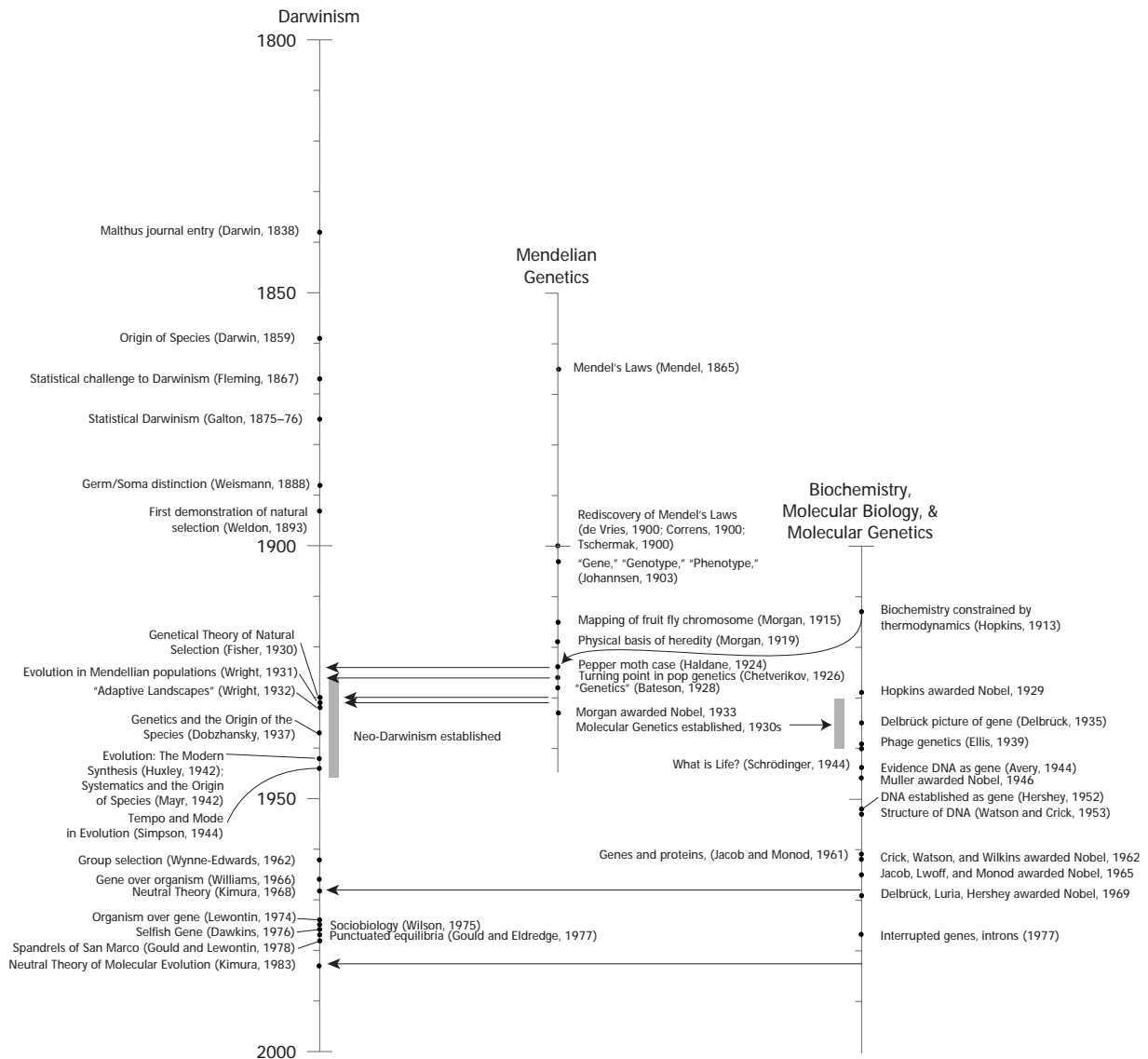


Figure 1. Darwinism and Associated Research Traditions. This figure highlights relationships between Darwinism and several selected research traditions in the period roughly spanning 1838–1983.

shown in Figure 1, some six years would pass after Darwin published *On the Origin of Species* before Mendel would publish his experiments with pea plants in an obscure journal (Mendel 1865). Another 41 years would pass before Mendel’s work would be “rediscovered” (Tschermak 1900; Correns 1901; de Vries 1901). Nearly three decades would pass before Mendelian genetics would be reconciled with Darwinism, in a merger that would be known later as neo-Darwinism (Depew and Weber 1995) or the modern synthesis (Huxley 1942). For this paper, neo-Darwinism is generally taken to mean the period in which the merger occurred (i.e., 15 - 20 years).

To understand the nature of conflict within neo-Darwinism, one needs to understand that Darwinism does not represent a monolithic research tradition. Instead, Darwinism includes of several distinct research traditions, each with their own view of the world, each with their own idea of what is important. Figure 1 diagrams both chronology and relationships among three of the major research traditions that have contributed to Darwinism. The diagram shown in Figure 1 was derived largely

from (Depew and Weber 1995), with supplements from (Morgan, Sturtevant et al. 1922; Morgan 1926; Dunn 1965; Mayr 1988; Burian 1992; Keller and Lloyd 1992; Rose and Lauder 1996). We note that the charting of relationships and influences is not an exact science, even though diagrammatic arrows and endpoints may suggest that. (For example, a person contributing to evolutionary biology might have been influenced more by a talk or a mentorship than by a paper or an award.)

These differing views have given occasion for conflict to arise among research traditions associated with Darwinism, as well as research subtraditions from within Darwinism, particularly around the neo-Darwinist period. We describe two of those conflicts: continuous change v. discrete change, phenotype v. genotype.

Continuous Change v. Discrete Change. At issue was Darwin’s adherence to gradualism and aversion to saltations. To support this, Darwin proposed a mechanism of inheritance he called *pangenesis*, where inheritance is carried by *gem-*

mules that are “inconceivably minute” (Darwin 1868; Depew and Weber 1995, p. 131ff). The result of gemmule exchange was a *blending inheritance* of traits. Darwin’s younger cousin Galton extended the notion of blending inheritance into a statistical framework—i.e., one characterizes traits by their statistical distributions (Depew and Weber 1995, p. 201ff). The science of measurement of traits—including those morphological or intangible (like intelligence)—is called biometry.

In direct contrast to blending inheritance is *particulate inheritance* (i.e., *Mendelian genetics*). Mendel was the first to articulate laws governing these particles known as “genes” (Mendel 1865). Mendel published his findings in a journal that was not widely read. Unaware of Mendel’s work, Darwin died about eight years before Mendel was “rediscovered” in c. 1900. At the outset of both Darwinism and Mendelian genetics, both remained as separate research traditions (Dunn 1965).

Not only was Mendelian genetics a wholly separate research tradition from Darwinism for nearly 60 years, but the last thirty years of that period was characterized by intense and vitriolic antagonism between Mendelian geneticists and Darwinian biometricians. Provine (1971) characterized that period as the “thirty years’ war.” The principals of that war include Mendelian geneticist W. Bateson (who coined the term “genetics” (Bateson 1928) and gave the then fledgling field stature) and Darwinian biometrician W. F. Weldon (who provided the first proof of natural selection through his statistical analysis of crab morphologies (Weldon 1893)). Bateson and Weldon were close friends until Bateson became a geneticist. Their personal antagonisms for each other were well known. On one occasion, Bateson “had it out with Weldon” in a momentous, well-documented debate (Depew and Weber 1995, p. 227).

Phenotype v. Genotype. The conflict involving continuous change v. discrete change was resolved in part by employing Johannsen’s concepts of genotype and phenotype (Johannsen 1903; Johannsen 1911). Phenotypes portray continuous traits that biometricians observed. Genotypes refer to the units of inheritance that underlie phenotypes (Depew and Weber 1995, p. 226). In effect, both continuous change and discrete change could coexist. However, instead of quelling this conflict, these terms framed the next series of conflicts, which have not yet been truly resolved. Behind these contemporary conflicts lies the question, “Which is the primary level of selection, phenotype or genotype?”

Depending on one’s answer, common terms can take on very different meanings. For example, one can consider the term *gene*. To many molecular geneticists, who would consider genotype an answer, the term takes on a very specific meaning. A gene is a cistron, “a segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as intervening sequences (introns) between individual coding segments (exons) (Lewin 1994, p. 1242).” To many evolutionary biologists, who would consider phenotype an answer, the term has been left ambivalent. In *Keywords of Evolutionary Biology*, the term *gene* means “anything a competent biologist calls a gene (Kitcher 1992, p. 131) [italics ours].”

We use this distinction of the term *gene* to caricature differences between research traditions. In actuality, the differences have not been so clear. It was not unusual for a neo-Darwinist

to also be a Mendelian geneticist, many of whom would also respond “genotype.” Having said this, we consider R. A. Fisher and E. Mayr, two of those responsible for Darwinist subtraditions within modern synthesis.

Fisher would have responded “genotype.” Fisher’s Fundamental Theorem of Natural Selection states, “The rate of increase in fitness of any organism at any time is equal to its genetic variance in fitness at that time (Fisher 1954, p. 37).” Fitness, as meant by Fisher, refers to comparative reproductive rate. Fisher treated genes as independent and linear entities, which further meant that genes have a cumulative effect. In effect, Fisher’s theorem suggested that “natural selection speeds up as usable [genetic] variation is fed to it (Depew and Weber 1995, p. 251).” Fisher has been credited to being one of the early founders of the modern synthesis and a founder of modern statistics. Fisher has also been credited for being the first to explicitly apply the Boltzmannian model to genes (Depew and Weber 1995, p. 11).

Mayr has responded “phenotype.” Mayr’s chief contribution to the modern synthesis has been “to shift attention from genotypic aspects of evolution to phenotypes as they appear in biogeographic space (Depew and Weber 1995, p. 310).” Mayr has long argued that between genotype and phenotype, the “causal accent [is placed] on the phenotypic level (Mayr 1988, pp. 97ff; Depew and Weber 1995, p. 315).” In a sense, Mayr argues that an organism has to survive long enough in its environment before it can reproduce successfully. Mayr does *not* argue that genotypes are inconsequential. Depew and Weber summarize this view as

For Mayr, genetics is a black box whose mechanisms are less important than what naturalists can observe about populations. He simply infers that it must happen and implies that geneticists, by restricting their views about natural history to known genetic mechanisms, may put unwise constraints on progress in evolutionary theory, which, on the whole, will more profitably be led by naturalists than by geneticists, *particularly overt theoretical ones*. (Depew and Weber 1995, p. 313) [italics ours]

Provine (1986, pp. 477ff) has contended that Mayr’s view on genetics has accounted for Mayr’s pronounced hostility towards Fisher. That Mayr has held Fisher in contempt has been well documented. His use of the term “bean bag genetics” (Mayr 1959; Mayr 1965; Mayr 1983) is a pejorative one that has been aimed directly at Fisher. The extent of Mayr’s contempt for Fisher is revealed in Mayr’s account of the modern synthesis. In the following passage, Mayr talks about the critics of the modern synthesis and argues the following:

The thinking of the reductionists was strongly influenced by R. A. Fisher, and this school has therefore sometimes been designated as Fisherian Darwinism.... [Critics like Gould and Lewontin] very much confuse matters when they designate the reductionist school as neo-Darwinism or imply that it includes people like Huxley, Dobzhansky, Wright, Rensch, or myself, all of whom distinctly rejected the reductionist conclusions of the Fisherian school. (Mayr 1988, p. 535)

By arguing this, Mayr declared that critics of the modern synthesis have been misguided because their ire has been misdirected at the “true” neo-Darwinists. Instead, Mayr argued, their ire should be reserved for Fisher and his ilk, i.e., the “false” neo-Darwinists. To accomplish this revision, Mayr redefined the modern synthesis as that which modified Darwinism in

which “population thinking [was] emphasized; [increasing] interest in the evolution of diversity, allopatric speciation, [and] variable evolutionary rates (Mayr 1988, p. 536).” Mayr dealt with the merger of Mendelian genetics and Darwinism by “eliminating” the merger altogether. In Mayr’s synopsis, Mendelian genetics was but a stage in the Darwinian research tradition; he framed Fisher as the maverick reductionist who led Darwinism astray.

Recapitulation in EC. The conflicts of continuous change v. discrete change and phenotype v. genotype in evolutionary biology have their parallels in EC. In EC, debates have included real number (continuous) v. bitstring (discrete) representations; the irrelevancy of building blocks (blending) v. the efficacy of them (particulate); and genotype v. phenotype. As it turns out, these parallels are more than coincidental.³

Evolutionary programming’s principal L. Fogel was primarily interested in artificial intelligence (AI). At the outset of EP, L. Fogel and his colleagues Owens and Walsh took on the task of making the paradigm of evolution acceptable to others in the field of artificial intelligence. Their energies went into promoting and defending just the idea of natural selection as an acceptable paradigm, as opposed to exploring the ramifications of their work in terms of biology. Their list of citations on evolutionary biology in (Fogel, Owens et al. 1966) included work by notable neo-Darwinists—i.e., (Huxley 1953; Haldane 1954; Dobzhansky 1955).

In contrast to Fogel et al., GA’s principal, Holland, side-stepped the issue of addressing whether genetic algorithms are a form of artificial intelligence. Instead, Holland took an interest in all things adaptive, which also meant that he was interested in contributing in fields like theoretical biology. His bibliography for his monograph listed a different set of neo-Darwinists than Fogel: (Fisher 1930; Fisher 1954; Mayr 1965), as well as a number of his students’ doctoral theses (several of which concerned theoretical biology).

Evolutionary strategies principals, Rechenberg and Schwefel, also took to different interests. Their interests lay in doing better engineering, whereupon evolutionary biology provided the inspiration to do so. They borrowed only as much biology as was needed for engineering optimization problems, and that which they needed to borrow were general ideas about evolution—e.g., see (Rechenberg 1964). If the resulting algorithm did not strictly adhere to an evolutionary biological concept, that was acceptable so long as one could demonstrate the efficacy of their engineering methods. Consequently, the evolutionary biology literature was the least emphasized of the three research traditions.

Strikingly, no overlap in citations in Darwinism occurred between Fogel and Holland, even though the latter was familiar with the former’s work. (Holland (1975) cites (Fogel,

Owens et al. 1966).) The differences between the two principals are even more striking when examining their work prior to their respective monographs. Fogel (e.g., (Fogel 1962; Fogel, Owens et al. 1965)) seldom cites any of the Darwinist literature. In contrast, Holland (e.g., (Holland 1961; Holland 1962; Holland 1962; Holland 1967; Holland 1973)) consistently cited only one —(Fisher 1958), a later edition of (Fisher 1930).

As it turned out, Fisher proved to be a great source of inspiration for Holland. In a sense, what Holland did for the field of evolution computation was to formalize Fisher’s Fundamental Theory of Natural Selection as a mathematical proposition. That proposition is known in EC as the Schema Theorem.

L. Fogel’s work and interests of mainstreaming evolutionary computation in fields like artificial intelligence has continued through his son, D. Fogel. That Mayr has strongly influenced D. Fogel’s writings is something of an understatement. For example, in D. Fogel’s chapter on “Natural Evolution” in his monograph (Fogel 1995), Mayr is cited more than 30 times, which is about three times greater than the next most cited work in that chapter. Notably, D. Fogel uses Mayr’s work as a touchstone to which all other works in evolutionary biology should compare. The citations of (Mayr 1982; Mayr 1988) appear consistently in other works of D. Fogel.

Given that Fisher and Mayr have become woven into the research traditions of EC, it is not surprising that antagonisms between Fisher and Mayr may have also followed.

4. GP’s Chimera

Contention 3: The maintenance of current metaphors in genetic programming theory has resulted in a chimera of Darwinism.

A chimera is a mythological monster, which possesses the head of a lion, the body of a goat, and the tail of a serpent. In current usage, a chimera refers to monsters that have been assembled from disparate parts. By borrowing Darwinism to explain phenomena in GP, the research community may have inadvertently created such a monster. We explain the genesis of four parts of GP’s chimera by recapitulating the previous sections.

Chimera Part i. In Section 2, we noted that GP is a derivative of genetic algorithms—the metaphors of natural selection and genetic crossover in GA have carried over to GP. However, instead of bit strings, Koza used parse trees. Therein lies a first part of the chimera.

In Section 3, we noted how the research tradition of genetic algorithms has been influenced by R. A. Fisher. We noted how Holland’s Schema Theorem is a mathematical formalism of Fisher’s Fundamental Theorem of Natural Selection. We have also noted that Holland was able to demonstrate the consequences of his theorem with a genetic algorithm.

When Fisher (1930) formulated his Fundamental Theorem of Natural Selection, he assumed *linear* arrays of genes. Holland’s bitstrings represent a computational instance of Fisher’s gene arrays—linearly separable. On the other hand, parse trees are inherently nonlinear representations.

Chimera Part ii. In Section 2, we noted the metaphorical use of introns in GP. Therein lies a second part of the chimera.

³ As of this paper, we have found the history of contemporary EC research traditions to be ambiguous, particularly concerning their origins. For example, it is clear that Friedburg (1958) introduced concepts that are analogous to Holland’s GA (Holland 1975). It is harder to demonstrate that Friedburg is in the direct lineage of contemporary GA research, especially if Holland and his students, without knowledge of Friedburg’s work, ended up reinventing some of Friedburg’s concepts.

In the formulation of GP, the computational representation of parse trees were implicitly mapped to organismal chromosomes. We say this because Koza adopted Holland's metaphors. It was Holland who made that mapping explicit (Holland 1975). Neither Holland nor Koza made any claim that either bitstrings or parse trees were DNA.

Subsequent researchers in GP, however, have claimed that introns do exist in parse trees. While that, in and of itself, does not mean that parse trees *are* DNA, the logical inference is that introns are made up of DNA, so therefore parse trees are DNA. That, in and of itself, is harmless. After all, genes are made up of DNA and DNA is the "active ingredient" in chromosomes. It is not unusual for researchers to treat parse trees and DNA as interchangeable in metaphor.

Of concern, however, has been the casual insinuation that the underlying science of molecular genetics easily fits into the underlying science in Darwinism. It implies that the physics of molecular biology has been reconciled with the mathematics that have been developed under Darwinism. As implied by Figure 1, that has only rarely been the case.

Nevertheless, EC practitioners treat the two research traditions as one. A consequence of this is a surreal biological treatment of genetic programming, whereby researchers attempt to fit 1990s discoveries in molecular biology into a 1930s neo-Darwinist mathematical framework. While the possibility of such a synthesis does exist, researchers do need to exercise care because the assumptions that exist behind the mathematics of the neo-Darwinists may not necessarily hold up to the phenomenology noted in molecular genetics.

Chimera Part *iii*. In Section 2, we noted the metaphor of building blocks. Therein lies the third part of the chimera. The metaphor of building blocks is an apt description of Fisher's linear array of genes. Fisher's linear array is a lot like the children's toy of building blocks. In the children's toy, each block is generally available at all times—if a block is on a table, it can be used. The creation of structures with the children's toy is basically an additive process—a seven-block high tower can be created by stacking seven blocks.

We and others have shown in other work (Daida, Bertram et al. 1999) that building blocks, at least for GP, represent a non-linear process. There is strong evidence that building blocks start out from the root node, e.g., (Rosca 1997). What happens after that, however, apparently is a situation in which both context and content matter. Subtrees that can be used as components that build toward a solution can be functionally expressed or sequestered and hidden in unexpressed portions of a subtree. In a sense, building blocks in GP apparently have an ephemeral, transitory nature because the projection of such subtrees into the space of worthwhile information would result in blocks that alternately appear and disappear. Such a notion of building blocks is non-Fisherian.

Chimera Part *iv*. In Section 2, we noted that the GA (and GP) research tradition has presumed that representations, like bitstring and parse trees, map to genotypes. Likewise, individual "traits," like real numbers or program behaviors, have been mapped to phenotypes. The reasons for this mapping, at least for GP, is in part, because it is historical, and in part because the change in representation did not seem to warrant profound changes in metaphorical usage. Therein lies a fourth part of the chimera.

It is not clear that for GP, the current frame of, say, genotype as parse trees and phenotype as program behavior is the best frame to use. For example, the dynamics associated with code that is not functionally expressed can suggest that parse trees are *both* phenotype and genotype. Banzhaf, Nordin et al. (1998) have proposed as much. Likewise, the dynamics associated with "neutral mutations" and other emergent processes can suggest that parse trees are *all* phenotype—the only genotype is represented by the function and terminal sets. This radical framing follows because both neutralism and structuralism have been used to describe changes in phenotype (the latter more so than the former). In any case, the dynamics associated with GP suggest a rethinking of this framing.

5. Conclusions

This paper has described three contentions:

1. *Theoretical arguments in GP have been strongly influenced by several key metaphors of Darwinism and evolutionary biology.* This contention argued for the pervasiveness and depth in which four metaphors (i.e., introns, building blocks, genotype and phenotype) have worked their way into GP theory and the rest of evolutionary computation. We further described how these metaphors were linked to evolutionary biology.
2. *The use of several of these metaphors in evolutionary computation have been significantly, if not unconsciously influenced by differences, biases, and even personalities of antagonistic research subtraditions within the neo-Darwinist framework.* This contention's argument consisted of three parts. First, we established that there were different research traditions associated with Darwinism. Second, we demonstrated antagonism within neo-Darwinism. We argued this by showing how different research traditions have influenced subtraditions within neo-Darwinism and have become personified by those associated with the modern synthesis. Third, we showed how these conflicts may have transferred over to evolutionary computation. We focused largely on the Mayr v. Fisher conflict, because these two neo-Darwinists have strongly influenced the content and direction of evolutionary computation. We suggested that it is likely that the differences and antagonisms in evolutionary computation has been influenced by antagonisms like those represented by Mayr and Fisher.
3. *The maintenance of current metaphors in GP theory has resulted in a chimera of Darwinism.* We have argued that maintaining these four metaphors in GP theory has resulted in a fourfold chimera of Darwinism. We have shown how this chimera is at odds with itself over its neo-Darwinist's origins. We have also shown how this chimera is at odds with empirical findings, observations, and analyses of GP dynamics.

We acknowledge that even a metaphorical chimera may have enormous value in inspiring a researcher to discovery. That is not the problem. Rather, what is at stake are other, problematic uses of metaphors. We describe these other uses by posing four questions that researcher should ask themselves when using or examining metaphors in GP.

1. *Are metaphors clarifying or muddling a description?* A researcher can find great value by thinking in terms of metaphors, even a chimerical ones. How one thinks, however, does not always represent the best means to communicate. Researchers should take particular care in communicating their work using metaphors—an overuse of metaphors tends to obscure.
2. *Are metaphors being used in place of theory?* Theories can be constructed in such a way that they are falsifiable; metaphors inherently cannot be. In the case of GP, there currently exists a significant shortfall in falsifiable theory that can describe phenomena. In a worse case scenario, a researcher “proves” (or “disproves”) a metaphor and not a theory. In another scenario, a researcher constructs a falsifiable theory, but uses a metaphor to cover gaps in this theory (e.g., relying on metaphors rather than posing an explicit statement of assumptions). While all metaphors can be problematic when used incorrectly, a metaphorical chimera can compound those problems because it can contend to be “all things to all theories.”
3. *Are reverse claims being made about that which has been borrowed (i.e., Darwinism)?* A metaphor has at least two domains: that of borrower (e.g., EC) and borrowee (i.e., Darwinism). A reasonable use of a metaphor has been to assist describing a difficult concept in the borrower’s domain. One should tread very carefully, however, in extending claims made in the borrower’s domain back to the borrowee’s. A metaphorical chimera in EC becomes literal in the borrowee’s domain of Darwinism. In a worse case scenario, a metaphorical chimera can represent gibberish to a biologist. Strong claims made about biology while using a metaphorical chimera can result in a substantial loss in credibility. A researcher needs to communicate clearly when biological terms have nonstandard definitions (or perhaps even discard the use of the biological terms in favor of plain language). A researcher should avoid a metaphorical chimera whenever possible.
4. *To what degree is ideology being evoked?* Metaphors form part of the mythos associated with each contemporary research tradition in EC. As we have mentioned before, metaphors are not always rhetorically innocent, but can also evoke strong emotional (and unintended) reactions. Failure to address ideology behind metaphor usage can have significant political ramifications. We have attempted to show that GP (as well as the rest of EC) is ripe for this type of interaction, if only because the field has been influenced by Darwinists at odds with each other.

Metaphors from Darwinism has significantly enriched the development of thought in evolutionary computation. Researchers owe a substantial debt to neo-Darwinists like R. A. Fisher and E. Mayr, whose works have helped to inspire. It is our hope that this paper assists in the reader in understanding the historical context of these metaphors. It is our further hope that one would see that there are appropriate seasons in which metaphors take their place in the sun. To do so otherwise diminishes both evolutionary computation and Darwinism.

One could argue that the milieu of thought in evolutionary computation made inevitable the genesis of GP’s chimera. Perhaps so. Even chimera have their day in the sun. One should ask, though, is theory a place where chimera should thrive?

Acknowledgments

We thank G. Fogel and K. Chellapilla for their kind invitation and constructive critique of this paper. This work has been largely possible because of two recent publications: *Evolutionary Computation: The Fossil Record* (Fogel 1998) and *Darwinism Evolving* (Depew and Weber 1995). The former allowed us to have access to rare, primary source material; the latter gave us an excellent narrative of the evolution of Darwinism. We thank L. Fogel and D. Fogel for access to additional primary source material. This paper has been enriched because of personal conversations with J. Holland, D. Goldberg, and D. Fogel. We thank J. Koza and R. Riolo for commenting on a white paper of this publication. The first author thanks F. Bookstein, whose conversations have inspired this line of inquiry, as well as S. Daida and I. Kristo, for their insight and assistance.

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