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Clonal Amplification of Behavior: A Simple Interpretation of the Effect of Reinforcement

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An abstract of
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Abstract

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The theory of neuronal group selection (Edelman, 1987) is an account of neural development and dynamics that has been used as the theoretical basis for autonomous agents that are capable of an impressively wide range of adaptive behaviors (e.g., Edelman, 2007; Krichmar & Edelman, 2002; 2005; Krichmar, Nitz, Gally, & Edelman, 2005; Krichmar, Seth, Nitz, Fleischer, & Edelman, 2005; Seth & Edelman, 2007). Edelman's theory draws parallels between natural selection and the adaptive dynamics of neuronal groups in response to environmental consequences. Critics have focused on the theory's use of clonal amplification as the reproduction method, which they see as insufficiently adaptive (Crick, 1989; Fernando, Karishma, & Syathmary, 2008; Fernando, Goldstein, & Syathmary, 2010; Fernando, Szathmary, & Husbands, 2012). When comparing Edelman's theory to the evolutionary theory of behavior dynamics (McDowell, 2004), McDowell argued that the theories differ in their reproduction methods and that a simulation that more purely models the clonal amplification dynamic may assess its viability (2010). This dissertation reports the results of the proposed simulations, which indicate that an implementation of the theory of neuronal group selection using clonal amplification can produce patterns of behavior that are quantitatively and qualitatively like humans and animals in operantly reinforcing environments. However, the range of viable parameters is smaller than for the evolutionary theory of behavior dynamics. There are also differences in the patterns of behavior predicted by the two theories that would need to be assessed with human or animal experiments to determine which is the better account.

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TABLE OF CONTENTS

Chapter 1: General Introduction 1

1.1. The Matching Law 2

1.2. The Evolutionary Theory of Behavior Dynamics (ETBD) 4

1.3. Theory of Neuronal Group Selection (TNGS) 6

1.4. Practical Importance of Adaptive Models of Behavior 9

1.5. Objective of this Dissertation 11

Chapter 2: General Methods 13

2.1. ETBD Creatures 13

2.1.1. Representation of potential behaviors within the ETBD 14

2.1.2. Step 3A: Beneficial selection 17

2.1.3. Step 4: Reproduction 19

2.1.4. Step 5: Variation 20

2.2. Translating the TNGS to the ETBD: Three Algorithmic Variations 20

2.2.1. Algorithmic variant of step 4: Cloning reproduction 23

2.2.2. Algorithmic variation of step 5: Phenotypic variation 24

2.2.3. Algorithmic variant of step 3A: Roulette-continuous selection 26

2.3. Virtual Environments 29

2.4. Apparatus 32

Chapter 3: ETBD and TNGS Behavior on Concurrent RI RI Schedules 33

3.1. Matching to Rates of Reinforcement on Single Schedules 33

3.2. Methods 39
3.2.1. Participants 39
3.2.2. Procedures 40
3.2.3. Analyses 41
3.2.3.1. Data pooling and averaging 42
3.2.3.2. Weighted ensemble fitting 42
3.2.3.3. Analytic approach to ensemble fits 46
3.2.3.4. Changeover profiles 48
3.3. Results 49
3.3.1. Best quantitative law of effect model 49
3.3.2. Best fitting model parameters 51
3.3.2.1. Exponent (*a*) values 51
3.3.2.2. Asymptote (*k*) values 52
3.3.2.3. Rate of the quantitative law of effect's ascent 53
3.3.3. Quadratic description of changeover profiles 55
3.3.4. Post-hoc analysis of changeover profiles 56
3.4. Discussion 62
3.4.1. Conformance to the matching law and the quantitative law of effect 62
3.4.2. Parameter values 64
3.4.3. Changeovers 65
3.4.4. Conclusion 68

Chapter 4: Matching to Rates and Magnitudes of Reinforcement 69
4.1. Methods 71

4.1.1. Participants 71

4.1.2. Procedures 72

4.1.3. Analyses 72

4.1.3.1. Data pooling and averaging 73

4.1.3.2. Bivariate matching law equation 73

4.2. Results 73

4.3. Discussion 75

4.3.1. Conclusion 78

Chapter 5: General Discussion 79

REFERENCES 84

EQUATION SUMMARY 96

FIGURES AND TABLES 99

APPENDICES 135

Appendix A: Experiment 1 Fitting Measures of the Exponential-Bitwise-Bitflip Creature Type 136

Appendix B: Experiment 1 Fitting Measures of the Exponential-Clone-Bitflip Creature Type 152

Appendix C: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Uniform Creature Type 168

Appendix D: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Linear Creature Type 184

Appendix E: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Exponential Creature Type 200

Appendix F: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Gaussian Creature Type 216

Appendix G: Experiment 1 Fitting Measures of the Linear-Bitwise-Bitflip Creature Type .. 232

Appendix H: Experiment 1 Fitting Measures of the Linear-Clone-Bitflip Creature Type 248

Appendix I: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Uniform Creature Type 264

Appendix J: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Linear Creature Type 280

Appendix K: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Exponential Creature Type 296

Appendix L: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Gaussian Creature Type 312

Appendix M: Experiment 2 Bivariate Matching Fitting Measures 328

LIST OF FIGURES

Figure 2-1. Flowchart of how the ETBD creates new generations of behaviors 100

Figure 2-2. Continuous probability density function forms with means of 40 101

Figure 2-3. The bitwise method of reproduction 102

Figure 2-4. The bitflip-by-individual variation method 103

Figure 2-5. Plots of the probability density functions of phenotypic variation methods 104

Figure 2-6. A simplified example of roulette-wheel selection 105

Figure 3-1. Scatterplot of scheduled reinforcement rates 108

Figure 3-2. Effects of the parameters *k*, *c*, and *a* on the predicted rate of behavior 109

Figure 3-3. Summary of model preferences by the BIC, AIC, and extra sums of squares difference tests 111

Figure 3-4. Exponent (*a*) parameter values of model 3 fits to simulated creature behavior....... 112

Figure 3-5. *k* parameter values of model 3 fits to the behavior of simulated creatures that used an exponential selection function 113

Figure 3-6. *k* parameter values of model 3 fits to the behavior of simulated creatures that used a linear selection function 114

Figure 3-7. *c* parameter values of model 3 fits to the behavior of simulated creatures that used an exponential selection function 115

Figure 3-8. *c* parameter values of model 3 fits to the behavior of simulated creatures that used a linear selection function 116

Figure 3-9. Predicted rates of behavior for exponential-bitwise-bitflip and exponential-clone-pheno-Gaussian creature types at 10% and 20% mutation 117

Figure 3-10. Predicted rate of behavior at 15 reinforcers per 500 time steps of simulated creatures that used an exponential selection function 118

Figure 3-11. Predicted rate of behavior at 15 reinforcers per 500 time steps of simulated creatures that used a linear selection function.. 119

Figure 3-12. Quadratic fit to changeovers per 500 time steps of exponential-bitwise-bitflip creature type behavior at 10% mutation 120

Figure 3-13. Changeovers per 500 time steps (ts) as a function of total and proportional reinforcement of the exponential-bitwise-bitflip creature type at 10% mutation........... 121

Figure 3-14. Quadratic-exponential fit to changeovers per 500 time steps (ts) of the exponential-bitwise-bitflip creature type at 10% mutation... 122

Figure 3-15. Quadratic-exponential fit to changeovers per 500 time steps (ts) of the exponential-bitwise-bitflip creature type at 10% mutation on a typical 11 schedule experiment...... 123

Figure 3-16. Exponential fit to changeovers per 500 time steps of the exponential-bitwise-bitflip creature type at 10% mutation 124

Figure 3-17. Averaged maximum changeovers (C_{Max}) predicted by the quadratic-exponential fits to simulated creature behavior.. 125

Figure 3-18. The concavity ($C_{\Delta\%}$) of the best fitting quadratic-exponential to the changeover behavior of simulated creatures that used an exponential selection function................ 126

Figure 3-19. The concavity ($C_{\Delta\%}$) of the best fitting quadratic-exponential to the changeover behavior of simulated creatures that used a linear selection function 127

Figure 4-1. Bivariate matching fit exponents of exponential-bitwise-bitflip simulated creature behavior... 129

Figure 4-2. Bivariate matching fit exponents of exponential-clone-bitflip simulated creature behavior 129
Figure 4-3. Bivariate matching fit exponents of exponential-clone-pheno-uniform simulated creature behavior 130
Figure 4-4. Bivariate matching fit exponents of exponential-clone-pheno-linear simulated creature behavior 130
Figure 4-5. Bivariate matching fit exponents of exponential-clone-pheno-exponential simulated creature behavior 131
Figure 4-6. Bivariate matching fit exponents of exponential-clone-pheno-Gaussian simulated creature behavior 131
Figure 4-7. Bivariate matching fit exponents of linear-bitwise-bitflip simulated creature behavior 132
Figure 4-8. Bivariate matching fit exponents of linear-clone-bitflip simulated creature behavior 132
Figure 4-9. Bivariate matching fit exponents of linear-clone-pheno-uniform simulated creature behavior 133
Figure 4-10. Bivariate matching fit exponents of linear-clone-pheno-linear simulated creature behavior 133
Figure 4-11. Bivariate matching fit exponents of linear-clone-pheno-exponential simulated creature behavior 134
Figure 4-12. Bivariate matching fit exponents of linear-clone-pheno-Gaussian simulated creature behavior 134

LIST OF TABLES

Table 3-1. The Twelve Simulated Creature Types 106

Table 3-2. Scheduled random-interval means of the two reinforcing target classes 107

Table 3-2. Model parameter restrictions 110

Table 4-1. Scheduled random-interval rate means and reinforcer magnitudes of the two reinforcing components 128

Chapter 1: General Introduction

We all choose to allocate our time and effort to the things we find important. Our choices are sometimes the result of deep consideration of our life goals, but more often they are of the moment and lacking that deeper insight. The accumulation of these relatively minor choices can have important mental, physiological, and social effects on our wellbeing and that of our society. A natural question arises from this need to understand ourselves and protect ourselves from the consequences of our thoughtless actions, which is how and why we choose our actions?

The unique relevance of psychology to understanding our choices was well described by Skinner in *Beyond Freedom and Dignity* (1971) when he wrote

> "The application of the physical and biological sciences alone will not solve our problems because the solutions lie in another field. Better contraceptives will control population only if people use them. New weapons may offset new defenses and vice versa, but a nuclear holocaust can be prevented only if the conditions under which nations make war can be changed. New methods of agriculture and medicine will not help if they are not practiced, and housing is a matter not only of buildings and cities but of how people live. Overcrowding can be corrected only by inducing people not to crowd, and the environment will continue to deteriorate until polluting practices are abandoned. In short, we need to make vast changes in human behavior, and we cannot make them with the help of nothing more than physics or biology…" (pg.4) "What we need is a technology of behavior." (pg. 5)

While Skinner mostly emphasized the societal consequences of not understanding human psychology, the consequences of our actions can be just as personally debilitating and devastating.

An approach to investigating why people make the choices that they do is to focus on situations where participants are provided with the opportunity to act. The participant can act in any way that they choose to, but the researcher only rewards certain behaviors. If the groups of behaviors that the researcher decides to reward are mutually exclusive, then this situation provides the crux of choice behavior. For each action the participant suffers an opportunity cost; whatever action a participant engages in, it excludes other – potentially beneficial – actions that they could engage in. By carefully controlling and manipulating this situation, it is possible to deduce what motivates the participant by observing the choices that they make as their situation changes.

1.1. The Matching Law

Surprisingly, if our behavior is somewhat unpredictably rewarded in this free-choice paradigm it is well described by an equation – the matching law. The original version of the matching law states that we allocate our behavior in proportion to the number of reinforcers we receive for doing that action (Herrnstein, 1961). This was later revised by Baum (1974) to account for participant preferences for certain consequences and a tendency for them to engage with the less rewarded side more frequently than Herrnstein's equation predicted. Baum's equation – the modern matching law – is expressed as

$$\frac{B_1}{B_2} = b\left(\frac{R_1}{R_2}\right)^a, \qquad \text{(1-1)}[1]$$

which states that behavior is allocated as a function of the rewards for those behaviors. In this equation, B is the measured rate of behavior, R is the experimentally-manipulated obtained rate of reinforcement, the subscripts indicate the experimenter-defined groups of behaviors that are measured, and b and a are free parameters.

[1] For the reader's benefit, copies of all equations that are frequently discussed are listed on page 94.

The parameter *b* is interpreted as the participant's bias towards one reinforcing consequence over the other, and this parameter captures most asymmetric qualities of the experiment that led the participant to prefer one behavior over another (Baum, 1974, 1979; McDowell, 1989; Wearden & Burgess, 1982). For example, a *b* greater than 1 could indicate a participant's greater preference for money over candy if those were the respective consequences of B_1 and B_2. A *b* greater than 1 could also indicate that the work required to earn the money was less difficult than for the candy. This parameter simply captures individual preference and cannot indicate the cause for that bias.

The parameter *a* in Equation 1-1 is sometimes referred to as sensitivity because it indicates how powerfully the rate of behavior is controlled by the rate of reinforcement, and, hence, the participant's sensitivity to changes in that variable. An exponent of 1 indicates that the ratio of behavior perfectly matched the ratio of reinforcement – excepting bias. In this case, if the participant received twice as many reinforcers for engaging in behavior B_1, then they also engaged in behavior B_1 twice as frequently. If the exponent is less than 1, which is most often observed, it indicates that there is a tendency for the participant to perform the less frequently reinforced behavior more often than the ratio of reinforcement would suggest. The parameter *a* averages around 0.8 for many experiments (Baum 1974, 1979; McDowell, 1989, 2013b; Myers & Myers, 1977; Wearden & Burgess, 1982). One interpretation for why the exponent is less than 1, which is sometimes called undermatching, is that participants adaptively engage in exploratory behavior to detect new reward opportunities (McDowell & Caron, 2007; Wearden 1983). Herrnstein's matching law (1961) is equivalent to the modern matching law (Equation 1-1) when the parameters *a* and *b* are both equal to 1.

The original and modern versions of the matching law stated that behavior is a function of the rates of reinforcement for then two choices, but this was later expanded upon. Two important ways that it was extended were to situations where the participant chooses between any number actions (Herrnstein, 1970) and to multiple differences in the consequences of behaviors (Baum, 1974; Baum & Rachlin, 1969; Rachlin, 1971; Tversky, 1969). This dissertation will be simulating the behavior of models in these two situations, and the details of how the modern matching law was extended to these situations will be provided with the relevant experiments.

1.2. The Evolutionary Theory of Behavior Dynamics (ETBD)

While the matching law accurately describes the long-term behavior of participants in free-choice environments (for review see Davison & McCarthy, 1988; McDowell, 2013a), it does not explain the dynamics of behavior. The evolutionary theory of behavior dynamics (ETBD) is a theory of adaptive behavior that overcomes this limitation of the matching law and should be considered the better understanding of choice behavior due to it explaining a wider range of phenomena than the matching law (Hempel & Oppenheim, 1948; McDowell, 2013b). The ETBD states that the behavior of humans and animals is generated through a dynamic process that is analogous to evolution (Berardi, Carretero-González, Klepeis, Machiani, Jahangiri, Bellettiere, & Hovell, 2018; Kulubekova & McDowell, 2008; 2013; McDowell, 2004; McDowell & Calvin, 2015; McDowell & Caron, 2007; McDowell, Caron, Kulubekova, & Berg, 2008; McDowell & Klapes, 2018; McDowell & Popa, 2010; McDowell, Popa, & Calvin, 2012; Popa & McDowell, 2016). The idea that behavior adapts to environmental contingencies in a way that is analogous to evolution is not novel; many researchers hypothesized this prior to the

ETBD's development (e.g., Campbell, 1960; Catania, 1978, 1987; Donahoe, 1999; Donahoe, Burgos, & Palmer, 1993; Edelman, 1987; Fuster, 1997; Gilbert, 1970, 1972; Glenn & Field, 1994; Glenn & Madden, 1995; Hayek, 1952a, 1952b; Henriques, 2003; Hughes, 2011; Pringle, 1951; Russell, 1962; Skinner, 1974, 1981, 1984; Staddon, 1975; Staddon & Simmelhag, 1971; Thorndike, 1898; Wasserman, 2012; Wasserman & Blumberg, 2010). What is unique about the ETBD is that it is the first testable model[2] that can be compared to human and animal behavior. To date, the ETBD has successfully demonstrated behavior dynamics that qualitatively and quantitatively match human and animal behavior across a wide range of situations (for review see McDowell, 2013b). There are, however, multiple ways that the theory's concept could be interpreted and only a few of these have been examined in depth. Some of these interpretations have relevance to theory development and practical applications.

Evolution is often strictly thought of as the process by which organisms adapt over time, but evolution can also be viewed more abstractly as the process of selection, variation, and reproduction. This general, three-step process is a simple problem-solving method that can find surprisingly complex solutions to problems. From this perspective, biological evolution is simply an example of how good solutions to problems – fit organisms – are found by repeating the three-step process of selection, variation, and reproduction. This abstraction of evolution as a problem-solving method is the foundation for an entire class of problem-solving methods, which are known as genetic algorithms (Holland, 1975).

Models based on the ETBD are unique subtypes of genetic algorithms, which have been used to explain the dynamics of human and animal behavior. In these models, an organism's behavior can be conceptualized as an attempt to solve the problem of their environment;

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[2] In this dissertation, "theory" strictly refers to an explanation that is built from logic and evidence, and "model" refers to how a theory is translated into a process or algorithm that produces testable hypotheses.

behavior, in this sense, is a solution to the current environment's characteristics. The wide range of behaviors that humans and animals can engage in are represented in the ETBD as a population of potential behaviors. This population of behaviors adapts to the organism's environment by – to use evolutionary terminology – selecting behaviors that previously resulted in beneficial consequences, making them become more likely via reproduction, and then adding random variation to some of these behaviors. There are many ways that selection, reproduction, and variation can be interpreted in the context of the ETBD, and this dissertation will examine a subgroup of these that have theoretical importance. The specific model dynamic that will be explored is when existing behaviors that resulted in beneficial consequences are directly amplified in frequency in a method analogous to asexual reproduction or cloning.

1.3. Theory of Neuronal Group Selection (TNGS)

Cloning in ETBD models is important to explore because of its use by other researchers (Barerdi et al., 2018) and its relation to the theory of neuronal group selection (TNGS; summarized in McDowell, 2010). In his book *Neural Darwinism: The Theory of Neuronal Group Selection* (1987), Edelman explained his selectionist theory of brain development and the brain's continuous adaptation to the environment. This theory has dynamics that are similar to the ETBD's and it specifies a plausible biological mechanism (McDowell, 2010). Edelman's wide-ranging theory covers everything from early brain development via synaptogenesis and pruning to synaptic adaptation of neuronal groups. Even greater phenomena like the mind and consciousness are explored by the theory. The synaptic adaptation of neuronal groups as an account of behavior is the element of the TNGS that matches the phenomena that the ETBD covers, and it also has dynamics that are like evolution. Neuronal group adaptation allows organisms to adjust their behavior to their environment. Its dynamics are analogous to evolution in that the neuronal groups' connectivity adapts to match the organism's environment; neuronal groups that lead to beneficial behaviors are selectively reinforced and gain more influence over future behavior.

The viability of the TNGS has been confirmed by it predicting physical characteristics of the nervous system and forming the basis for proof-of-concept artificial intelligences (McDowell, 2010). An example of how the theory predicted future discoveries of neural functioning is how Edelman (1987) deduced the necessity of bidirectional connections between neuronal groups – reentry – despite lacking evidence for it at that time. This hypothesis was later supported, and in a recent review Edelman and Gally (2013) were able to conclude that there is now some anatomical evidence that there is reentry. The proof-of-concept artificial intelligences that are based on the TNGS have been shown to be capable of numerous complicated tasks that were not strictly built into the intelligence's capacity. For example, these proof-of-concept intelligences have been implemented as autonomous robots that could remember and find hidden platforms in Morris water mazes and other robots that could search the environment for appetitive blocks while avoiding subtly different aversive blocks. (Edelman, 2007; Krichmar & Edelman, 2002; 2005; Krichmar, Nitz, Gally, & Edelman, 2005; Krichmar, Seth, Nitz, Fleischer, & Edelman, 2005; Seth & Edelman, 2007). It is important to distinguish this type of development from commercial artificial intelligences, which are often atheoretically constructed with layered heuristics and neural networks to produce satisfying answers. Developing machines and simulations from theory that are not designed to specifically perform these tasks but that nevertheless can do so, like TNGS- and ETBD-based models, are more evidentially impressive than atheoretically constructing a machine to perform only a specific task.

A major contention about the TNGS's theoretical viability is whether the dynamics it proposes are truly analogous to evolution. Edelman paints clear and pervasive parallels between his model and the evolutionary process (1987), but this has been contested by others (Crick, 1989; Fernando, Karishma, & Syathmary, 2008; Fernando, Goldstein, & Syathmary, 2010; Fernando, Szathmary, & Husbands, 2012). Crick's response (1989) was particularly critical of the notion that there is a parallel (e.g., "I have not found it possible to make a worthwhile analogy between the theory of natural selection and what happens in the developing brain and indeed Edelman has not presented one", page 246). Similarly, Fernando and his colleges have been critical of the TNGS but have primarily emphasized the perceived inadequacy of the TNGS's method of reproduction to adapt to the environment (Fernando, Karishma, & Syathmary, 2008; Fernando, Goldstein, & Syathmary, 2010; Fernando, Szathmary, & Husbands, 2012). Central to these critiques is that the direct amplification in strength of existing neuronal groups following positive outcomes, which is an aspect of the theory, is like an asexual reproduction dynamic because it increases the likelihood of an existing neural pattern of behavior but prevents novel neuronal group connections that could create new behaviors. This is believed to be too simple of a neural dynamic because it cannot account for the complex behaviors that humans learn and engage. Whether the TNGS is inadequate because of this cloning-like dynamic has been contested by Edelman (1992, pp. 94-97), and McDowell suggested that a modified version of the ETBD that quantitatively assessed this dynamic in choice environments would be able to assess the TNGS's viability (2010).

1.4. Practical Importance of Adaptive Models of Behavior

Over the last 40 years, the long-term behavior of organisms when their behaviors are unpredictably reinforced has been found to be well described by equations, such as the matching law and quantitative law of effect (summarized in McDowell, 2013a). These equations are important because they accurately describe how behavior relates to its consequences over a long period of time, which is sometimes referred to as molar behavior. A significant limit to their explanatory utility, however, is that they are incapable of describing the moment-to-moment processes that lead to these outcomes, which is sometimes called molecular behavior, and this limits their predictive utility. The ETBD fills this gap in our understanding by correctly modeling the molecular dynamics of behavior (Kulubekova & McDowell, 2008, 2013), while also explaining how the molar behavior is a direct result of that molecular behavior (McDowell, 2004; McDowell & Caron, 2007; McDowell, Caron, Kulubekova, & Berg, 2008; McDowell & Popa, 2010; McDowell, Popa, & Calvin, 2012).

By explaining the molecular behavior dynamics, the ETBD should be more applicable to clinical issues due to its greater predictive utility. At the least, the ETBD should be applicable to the same clinical phenomena to which the equations of molar behavior have been applied. The matching law (Equation 1-1) and quantitative law of effect (Herrnstein, 1970; Equation 3-1) have been found to be relevant to aggressive, antisocial, and delinquent behavior (Dishion, Andrews, & Crosby, 1995; McDowell & Caron, 2010a; 2010b; Snyder, Horsch & Childs, 1997; Snyder, Schrepferman, & St. Peter, 1997; Snyder, West, Stockemer, Gibbons, & Amquist-Parks, 1996; Snyder & Patterson, 1995), ADHD (Kollins, Lane, & Shapiro, 1997; Murray & Kollins, 2000; Taylor, Lincoln, & Foster, 2010), bipolar disorder (Szabadi, Bradshaw, & Ruddle, 1981), chronic pain syndrome (Fernandez & McDowell, 1995), developmental disabilities (Oliver, Hall, &

Nixon, 1999), and self-injurious behavior (McDowell, 1981, 1982; Symons, Hoch, Dahl, & McComas, 2003). Because the ETBD accounts for the matching law and quantitative law of effect, the ETBD is, thus, also relevant to these issues and could provide greater insight into them. Furthermore, because the ETBD accounts for more phenomena than the matching law and quantitative law of effect, it is likely that it will become relevant to other areas of clinical research.

An example of how learning more about the dynamics of behavior may inform novel clinical approaches to disorders is provided by Popa and McDowell (2016). They argued that the ETBD may inform the treatment of attention-deficit and hyperactivity disorder by identifying patterns of behavior that could indicate different subtypes of ADHD-like behavior. As an example of equifinality, they found that ADHD-like patterns of behavior could be caused in multiple ways (Popa & McDowell, 2016). This work suggests that ADHD-like behavior can be caused by either poorly-structured environments or innate characteristics of the individual, and that there are some slight behavioral differences between these two causes. More specifically, environments that reinforce behaviors infrequently, provide reinforcers of poor quality, or permit rapid switching between tasks could lead to the simulated typical individual's rapidly switching between tasks in a way that could be misinterpreted as ADHD. Alternatively, atypical simulated individuals, who had abnormally large amounts of behavioral variability, had similar patterns of ADHD-like behavior even in typical environments. These different causes of ADHD-like behavior could be classified as different subtypes of ADHD and could be targeted with interventions that are specific to their dynamic causes. For example, stimulants may be more clinically useful for individuals who express more atypical patterns of behavior in typical environments, and interventions that focus on training parents and teachers to restructure a child's environment may be better for children who express a typical-individual-but-poor-environment pattern of behavior. This research still needs to be evaluated in a clinical sample of individuals with ADHD, but it highlights how the ETBD can inform clinical research.

1.5. Objective of this Dissertation

The objective of this dissertation is to evaluate the quantitative viability of the TNGS's proposed dynamics. Specifically, the amplification of existing behaviors by replicating them in a manner akin to asexual reproduction (i.e., cloning) was evaluated because it is the most contentious aspect of the TNGS (Crick, 1989; Fernando et al., 2008; 2010; 2012). To evaluate the quantitative viability of this dynamic the TNGS was reinterpreted to more explicitly focus on the proposed evolution-like dynamics rather than constructing a brain-based device, as has been previously done (e.g., Edelman, 2007; Krichmar & Edelman, 2002; 2005; Krichmar, Nitz, Gally, & Edelman, 2005; Krichmar, Seth, Nitz, Fleischer, & Edelman, 2005; Seth & Edelman, 2007). One of the weaknesses of complicated constructions like brain-based devices is that they add numerous parameters that need to be tailored to the application, which can obscure the dynamics.

Two experiments were conducted to assess the TNGS's quantitative viability. These experiments were chosen based on their importance and previous assessment of the ETBD. The first experiment (Chapter 3) assessed the TNGS's quantitative viability as an account for human and animal behavior in environments that are unpredictably reinforcing and was a replication of McDowell and Popa (2010). The second experiment (Chapter 4) assessed the TNGS's quantitative viability as an account for pigeon behavior when reinforcers are delivered unpredictably and of different magnitudes, which was a replication of McDowell et al., 2012). For the TNGS to be considered a viable account of human and animal behavior it must behave like them. The criteria for experiments one and two are based on our best understanding of how humans and animals behave in those situations.

Chapter 2: General Methods

To assess the viability of the TNGS as an account of human and animal behavior it is necessary to translate it into a model. Previous simulation work with the ETBD will serve as the foundation for this approach, because it permits the cloning reproduction dynamic to be brought into sharp focus. Translating the TNGS into a model that is like the ETBD's requires a thorough understanding of the ETBD and a detailed examination of the TNGS. By thoroughly examining the TNGS, it is possible to identify what dynamics it suggests, and to translate that into a set of possible models that can be evaluated.

2.1. ETBD Creatures

It is necessary to build models based on the ETBD to assess the theory and its application. These models will be referred to as ETBD creatures because they are artificial constructs that are based on the theory and that interact with their environments. Within simulations, ETBD creatures fill the same role that human and animal participants do in live experiments and are expected to behave like them. Any contradiction between the ETBD creature behavior and human or animal behavior indicates that the ETBD creature is a poor model. It is necessary to create ETBD creatures and simulate entire sequences of events, because each ETBD creature is a complex system with the outcome at each step in the chain of events being probabilistic rather than purely deterministic.

The ETBD describes a rather abstract process and avoids discussing the underlying neurological mechanisms of behavior (McDowell, 2010). From an Aristotelian perspective of explaining behavior (Killeen, 2001), the ETBD explains behavior based on its final causes (i.e., the purpose of behavior) rather than its material causes (i.e., neurological mechanisms). The absence of a material explanation is why the ETBD is translated into models that have little similarity to neurology. A benefit of this is that the ETBD creatures are dramatically simpler than equivalent neural models, like TNGS-based models, because they are simply trying to model the dynamics rather than the exact mechanisms.

2.1.1. Representation of potential behaviors within the ETBD. Potential behaviors are represented within the algorithm as whole numbers, typically between 0 and 1023, and – simultaneously – the binary representation of those numbers. The whole number representation of a behavior is called its phenotype because it represents how the behavior is expressed in the environment (McDowell, 2003). The binary representation of a potential behavior is referred to as its genotype because it is never observed, but it is what the algorithm's selection, reproduction, and variation dynamics act upon (McDowell, 2003). This makes the binary representation similar to genes in biological evolution in that they are the primary unit of change but are not directly expressed.

Prior to an experiment, the researcher identifies a group of functionally-equivalent behaviors – the target class. Within ETBD-based simulations, target classes are specified as a range of phenotype values that represent a set of behaviors having the same effect. For example, pressing the 'A' key on your keyboard could be an experimenter-defined target class of behaviors, and might be represented in the simulation as the phenotype range of 1 to 10. A participant in a real situation could functionally press the 'A' key with their fingers, with a pencil in their hand, or by asking someone else to press it. These behaviors have the same effect – an 'A' is typed – and are, thus, functionally equivalent. In the ETBD these behaviors would each have different but similar phenotype values because they have the same effect.

There is a clear relationship between the phenotype and the genotype, which is that the integer value is simply transformed into its binary representation, but there are also some nuances to this relationship. For example, the 10-digit binary – genotype – of the phenotype 127 is 0001111111 and the genotype of 128 is 0010000000. This example highlights an important nuance of the genotype-phenotype relationship; while phenotypes 127 and 128 are adjacent whole numbers, their genotypes are very dissimilar. To transform 00**01111111** (phenotype 127) into 00**10000000** (phenotype 128) it is necessary to flip the eight bolded bits from 0 to 1 or 1 to 0. The number of bits required to transform one binary number into another is called the Hamming distance between two numbers (Hamming, 1950).

Popa and McDowell (2010) showed that the Hamming distances between potential behaviors is a critical aspect of the ETBD's functioning. They showed that the Hamming distance functions as a changeover delay, which is an important component of the environment. A changeover delay is typically implemented in experiments with more than one source of reinforcement to reduce switching between the target classes that are reinforced, and thus make them mutually exclusive. After switching from one target class to the other, the changeover delay imposes a waiting period that must elapse before the organism can gain reinforcement. This delay occurs after every switch, which means that if an animal continuously switches from one alternative to another then it would never receive reinforcement. In the absence of a changeover delay, animals frequently switch between the measured response alternatives (Herrnstein, 1961). The changeover delay may seem artificial at first, but it instead improves the experiment's external validity. For example, the changeover delay has been found to be equivalent to the amount of time or effort that it takes to physically travel between locations where the animal can gain reinforcement (Baum, 1982), which is clearly related to concepts like foraging behavior.

Since the Hamming distance between behaviors functions as a changeover delay it partially represents a physical property of the environment.

To summarize, each potential behavior consists of two pieces of information. The phenotype provides information about the function of behavior in an environment, and the genotype provides information about the ease of switching between groups of behaviors that are reinforced. While these are both important, it can be challenging when designing environments for ETBD creatures to interact with. The main difficulty is that, when determining which behaviors to reinforce, the experimenter must consider the time it takes to switch between an alternative – in binary – and how functionally similar behaviors are – as integers. While this is manageable, it is not intuitive.

The overall process by which the population of potential behaviors adapts to the environment is shown in Figure 2-1. Each cycle of the algorithm – going through steps 1 through 5 – creates a new "generation" of behavior. The first two steps are very simple, but steps 3 through 5 are more complicated. For step 1, one potential behavior is plucked at random from the current generation of one hundred potential behaviors and the ETBD creature engages in that behavior. Step 2 is the ETBD creature receiving environmental feedback on that behavior. This feedback determines whether the algorithm moves to Step 3A – beneficial selection – or 3B – random selection. If the expressed behavior did not result in a beneficial outcome (Step 3B), then all potential behaviors in the population have equal influence on the next generation. If that behavior resulted in a beneficial outcome (Step 3A), then the fitness of all potential behaviors in the population are inferred from how similar they are to the expressed behavior. Those that are more like the expressed behavior have a greater influence on the composition of the next generation via reproduction (Step 4).

2.1.2. Step 3A: Beneficial selection. The implementation of selection in the ETBD is very different from biological evolution. With biological evolution, selection typically occurs at the individual level; every organism in the population interacts with its environment, which determines whether it survives and reproduces. The organisms that survive and reproduce are fitter than those that don't. Selection within the ETBD does not and cannot work this way. With every generation, only one behavior in the population engages with the environment, and the algorithm therefore needs to extrapolate the likely outcomes of other behaviors based on the consequences of only the behavior it just engaged in.

Algorithmically, the likely outcomes of potential behaviors are extrapolated via continuous probability density functions. This method of selection – continuous selection – is the only method of beneficial selection that has been used in published articles (Kulubekova & McDowell, 2008; McDowell, 2004; McDowell & Caron, 2007; McDowell et al., 2008; McDowell & Popa, 2010; McDowell, Popa, & Calvin, 2012; Popa & McDowell, 2010). The purpose of continuous selection is to select potential behaviors from the population that are like the behavior that immediately preceded a beneficial consequence. There are three variations of the continuous selection method that have been used to select potential behaviors, namely, uniform, linear, and exponential selection. For all three variations, the fitness value of each potential behavior is the phenotypic distance (i.e., absolute difference in its integer representation) from the last rewarded behavior that the ETBD creature engaged in. Behaviors are probabilistically selected from the population of potential behaviors based on the functions shown in Figure 2-2. The shapes of these three probability density functions are different, but they all prefer behaviors that are phenotypically close to the behavior that preceded a beneficial consequence. The exact equations that are used to create these functions are given in McDowell (2004).

The shapes of all three functions are defined by a single parameter, the selection function's mean. In Figure 2-2, all three functions have the same mean of 40. The mean value of a function indicates its effectiveness at increasing the probability that the target behavior will be engaged in. Continuous selection function means are inversely related to the effectiveness of the reinforcer, with smaller means indicating greater changes in the population. This is analogous to the greater quantity or quality of a reinforcer being a more potent reinforcer, which is its reinforcing magnitude. The inverse of the mean, thus, indicates the reinforcer's magnitude with smaller selection function means indicating stronger magnitudes and larger function means indicating weaker magnitudes.

Two important properties of these functions are their upper limits and how behaviors are selected from these functions. The uniform and linear functions both have upper limits along the x-axis, which can be seen in Figure 2-2. Potential behaviors that are more than twice the uniform function's mean value (e.g., 80 in Figure 2-2) cannot be selected, and potential behaviors that are more than thrice the linear function's mean value (e.g., 120 in Figure 2-2) cannot be selected. The exponential function does not have an upper limit and can thus select any potential behavior from the population of potential behaviors, although behaviors that are distant from the emitted behavior are rarely selected. The process used to select behaviors using these functions is quite simple. Random fitness values are drawn from the continuous distributions until one is found that corresponds with the fitness of a behavior in the population. The selected behaviors are then used to create the next generation of behaviors via reproduction (Step 4 in Figure 2-1).

While effective under most circumstances, continuous selection functions poorly when reinforcers have a very large magnitude. The tiny mean of the selection function causes the function to be very steep. This is a weakness in that large amounts of computer processing time are wasted because the function oversamples too close to the reinforced behavior. In some circumstances, this can result in hours of processing time being spent trying to find a single behavior in the population. This occurs when there are just a few potential behaviors that are near the reinforced behavior and, thus, are unlikely to be selected by the continuous selection function. Linear and uniform continuous selection methods are particularly sensitive to this problem because of their upper limits. With large magnitudes there is a possibility that there is an absence of two behaviors – a requirement of bitwise recombination (Section 2.1.3) – within the function's limits, which means that Step 4 in Figure 2-1 cannot occur because there are not enough behaviors that could be selected for reproduction. When this occurs, the experiment is typically restarted, but there are some other potential approaches to this problem. These weaknesses have become increasingly problematic as experimentation has been done with ever more extreme magnitudes.

2.1.3. Step 4: Reproduction. The primary method of reproduction that has been used to date is bitwise recombination. With this method the genotypes of two potential parent behaviors are mixed to create a new child behavior. First, two of the behaviors that were selected in Step 3A or 3B are translated into their genotype formats (Figure 2-3). For each of the new child's bits, a bit is randomly chosen from either of the parents. In Figure 2-3, the first, fourth, sixth, seventh, and ninth bits of the child behavior were randomly picked from the first parent and the rest came from the second parent. The resulting child behaviors have qualities that are like the parents, but the child behaviors are not identical to them.

2.1.4. Step 5: Variation. There are many possible methods of implementing variation within the ETBD, but the most frequently used method is bitflip-by-individual (see McDowell 2004 or McDowell & Caron 2007 for exceptions). With this method there is a probability that each child behavior will have some random variation added to its binary representation, which results in changes to its phenotype. The probability that variation will change a child behavior (i.e., the mutation rate) has been systematically varied in multiple experiments (McDowell, 2004; McDowell & Caron, 2007; McDowell et al., 2008; McDowell & Popa, 2010; McDowell, Popa, & Calvin, 2012). If the behavior is randomly chosen to be mutated, then 1 of its 10 bits is flipped from 0 to 1 or 1 to 0. In Figure 2-4, the eighth bit from the left of the new child behavior was flipped from 1 to 0. This only changed the phenotype of the behavior by 4. If the leftmost bit had been flipped instead, however, then the phenotype would have changed to 870, which is a phenotypic difference of 512. This method adds significant variation to the population of potential behaviors over the course of the experiment.

2.2. Translating the TNGS to the ETBD: Three Algorithmic Variations

The TNGS conceptualizes the nervous system as being composed of primary and secondary repertoires of behavior (Edelman, 1987). The TNGS's primary repertoire specifies the evolutionarily adaptive behavioral capacities that an organism develops during synaptogenesis and pruning. These behavioral capacities are presumed to have evolved over time to be adaptively advantageous and are considered innate elements of the nervous system. Within behavioral analysis, these capacities are like the older concepts of modal action patterns and reflexes, but this theory is a mechanistic explanation for them. The primary repertoire enables behaviors like limb movement, reproductive behavior, and vocalizations, but does not adaptively determine which behaviors the organism will do. This responsibility is instead the secondary repertoire's, which controls the dynamics of behavior. The secondary repertoire does this by tapping into the behavioral capacities that the primary repertoire provides and then modifying the probabilities of engaging in the behaviors by altering synaptic connections at the neural group level. Neural groups are large clusters of interconnected nerve cells that receive stimuli from other neurons and generate output that is translated into behavior through the primary repertoire.

Both repertoires translate relatively directly into the ETBD. The ETBD's range of behavioral phenotypes and the phenotype-genotype relationship of the ETBD's behaviors are analogous to the primary repertoire in that they establish the ETBD creature's behavioral capacities and their relationship to the environment. The secondary repertoire directly translates to the ETBD's population of potential behaviors in that both specify the adaptive probabilities that certain behaviors will be engaged in at different times. The challenging part of this translation is how the TNGS's dynamics map onto the ETBD's.

Secondary repertoire dynamics are, unfortunately, unclearly presented in genetic algorithm terms within Edelman's writings (Crick, 1989, McDowell, 2010; Edelman, 1987). This lack of evolutionary dynamic clarity has permitted extensive freedom of interpretation of the theory's dynamics (Carlton & Shane, 2014; Crick, 1989; Fernando, Karishma, & Syathmary, 2008; McDowell, 2010). The selection dynamics are the most straightforward with neuronal groups that fire together becoming bound together when they are predictively useful. The design of the primary repertoire is such that neuronal groups that are proximally located tend to be highly connected and, thus, more likely to fire together (visually represented in Edelman 1987's Figure 7.5). This conceptually maps well onto the ETBD's abstraction of the selection function preferring similar phenotypes (Figure 2-2), but it does not suggest any particular selection function form. The reproduction dynamics of the TNGS have been argued to be most like cloning or asexual reproduction (Crick, 1989; Fernando, Karishma, & Syathmary, 2008; Fernando, Goldstein, & Syathmary, 2010; Fernando, Szathmary, & Husbands, 2012; McDowell, 2010). However, different authors have focused on different mechanisms for this type of reproduction. Crick and Edelman both emphasized the adaptive strengthening of neuronal group connections as a form of selectionism (Crick, 1989; Edelman, 1987), whereas Fernando emphasized the direct replication of entire neuronal groups (Fernando, Karishma, & Syathmary, 2008; Fernando, Goldstein, & Syathmary, 2010; Fernando, Szathmary, & Husbands, 2012). Fernando, Szathmary, and Husbands (2012) classified the TNGS as a "parallel search with competition" model, which describes how the neuronal groups compete with one another to control behavior but do not directly inform each other. The lack of information conveyed between neuronal groups means that replication is best described as a direct amplification of the neural patterns that led to the behavior, rather than as the ETBD's sexual-like reproduction of behaviors, because there is no combining of neuronal groups. The TNGS's variation dynamic can be found as either imperfect replication of neuronal groups (Fernando, Karishma, & Syathmary, 2008; Fernando, Goldstein, & Syathmary, 2010) or randomness in connection strengthening (Edelman, 1987; Crick, 1989). Edelman modelled this randomness as a Gaussian noise generator that influenced the state of neuronal groups (e.g., Edelman, 1984, pp. 273-274), which in turn modified the degree of connection strengthening and weakening. The Gaussian noise generator is a common element of neural networks and is not unique to the TNGS. Within the ETBD, this dynamic could jointly be considered the randomness of the selection process and the bit-flip-by-individual mutation method. The TNGS does not strongly suggest a genotypic mutation method like bit-flip-by-individual mutation, however. Rather, the organization of the primary repertoire could equally suggest a phenotype-based mutation method, which was explored in early ETBD simulations (McDowell, 2004; McDowell & Caron, 2007).

These similarities suggest three major variations to the ETBD algorithm that are of practical and theoretical interest. The most important task is to evaluate whether reproduction by cloning is a viable alternative to the sexual-like reproduction that has been explored with the ETBD. In addition to this being an important theoretical issue, it is algorithmically simpler than bitwise recombination, and is a more direct interpretation of reinforcement. The second variation is phenotypic variation because the TNGS does not strongly suggest genotypic variation – as the ETBD currently functions. Of secondary interest with this variation is that it would eliminate the genotype-phenotype distinction of how behaviors are represented, which could conceptually streamline the ETBD. The third variation is a modification of continuous selection, which is of practical interest because it does not have the large-magnitude problem that can be problematic with cloning-based ETBD models. In summary, this project seeks to evaluate novel variations of selection, reproduction, and variation that may further the theoretical development of the ETBD and the TNGS.

2.2.1. Algorithmic variant of step 4: Cloning reproduction. Cloning, or asexual reproduction, is the simplest method of reproduction and is easier to conceptualize than bitwise recombination. With this method, selected parent behaviors are simply copied to produce new child behaviors for the next generation. Behaviors that were beneficial become more likely to occur in the future, which is, essentially, Thorndike's law of effect (1898) and the definition of operant reinforcement. If cloning generates behavior like living organisms, then it would suggest that bitwise recombination (Section 2.1.3) is not a required mechanism of the ETBD.

2.2.2. Algorithmic variation of step 5: Phenotypic variation. Phenotypic variation adds novel behaviors to the population by acting on the phenotypes of the behaviors, rather than on their genotypes. Besides the relevance to the TNGS, this method – when combined with cloning reproduction – would result in there being no need for the phenotype-genotype distinction of behavioral representation. The algorithm would represent behaviors only as integers rather than the more complex representation of behaviors as simultaneously bit strings and integers. With this method, behaviors with more similar integer values are easier to switch between and have similar effects on the environment.

Discarding the genotype-phenotype distinction simplifies the design of simulated environments and their interpretation. With our previous research, it has been necessary to define target classes at very specific locations. These locations have been where the two target classes are most different in their binary representations (Popa & McDowell, 2010). For example, the two groups of behaviors that are reinforced have typically been defined as the integer ranges (i.e., phenotype ranges) of 471 to 511 and 512 to 552. While adjacent to each other phenotypically, 511 is maximally different from 512 in their binary representations; 511 is represented as 0111111111 and 512 as 1000000000, which is a Hamming distance of 10. The presence of behaviors that are very genotypically different within a target class also has significant effects on the behavior of ETBD creatures (Popa & McDowell, 2010). Removing the genotype-phenotype distinction makes the environment simpler to define and design because only phenotypes need to be considered.

Phenotypic variation is not a novel implementation of ETBD creatures. Gaussian mutation is a method of phenotypic variation that was used in the earliest research with the ETBD (McDowell, 2004; McDowell & Caron, 2007). With this method, each potential behavior has a probability that it will be changed. If changed, then a number is generated from a Gaussian distribution and added to that behavior's integer representation (i.e., phenotype). If the behavior mutates outside the permissible range of behaviors, then it is moved to the opposite end of the range. For example, if the range of behavior is from 0 to 1023 (i.e., the range permissible with 10 bits) and a child behavior is mutated outside of this range to 1025 then it would become 2 (1025 – 1023).

In addition to this method, the continuous selection functions have inspired an additional three methods of phenotypic mutation, which are displayed in Figure 2-5. While the following phenotypic mutation methods are based on the same probability density functions used in continuous selection, they have been modified to generate both positive and negative values from a single random number. These functions are:

Uniform: $$\Delta P = 4\mu(r - 0.5)$$

Linear: $$\Delta P = \begin{cases} -3\mu\left(1 - \sqrt{2r}\right), & if\ r < 0.5; \\ 3\mu\left[1 - \sqrt{2(1-r)}\right], & otherwise \end{cases}$$

Exponential: $$\Delta P = \begin{cases} \mu \log(2r), if\ r < 0.5; \\ -\mu \log[2(1-r)], otherwise \end{cases}$$

In these equations ΔP is the change in the integer representation of the behavior, μ is the mean of the absolute value of the ΔP function, and *r* is a random decimal value. Based on these distributions, a ΔP will be randomly drawn that will be added to the current integer representation of the behavior. For the experiments conducted in this dissertation, the absolute means of the uniform, linear, and exponential continuous mutation methods were set to 50, as was the standard deviation of the Gaussian continuous mutation method. The Gaussian standard deviation is twice that of previous research (McDowell, 2004; McDowell & Caron, 2007), and was so chosen on the basis of pilot data to make the mutation rate more like bitflip-by-individual mutation rates (discussed in Section 2.1.4).

2.2.3. Algorithmic variant of step 3A: Roulette-continuous selection. Roulette-continuous selection is a new method of selection for the ETBD that has some practical benefits. It is a combination of continuous selection (discussed in Section 2.1.2) and roulette-wheel selection (Goldberg, 1989). In the context of the ETBD, roulette-wheel selection would choose parent behaviors from the population based on their fitness values, with the likelihood that a behavior will be selected being equal to its fitness value divided by the sum of all fitness values within the population of potential behaviors. For example, if a behavior has a fitness value of 15 and the sum of all fitness values in the population is 100 then there is a 15% chance that that behavior will be selected for reproduction. This method of selection can be easily imagined as a roulette wheel with the relative fitness indicating what percentage of the wheel is associated with each behavior of the population. If the wheel were spun it would come to rest on the area of one behavior, with the behaviors that have greater areas being more likely to be randomly chosen.

Like most genetic algorithm methods of selection that were not designed for the ETBD, roulette-wheel selection assumes that all elements of the population have been assigned a fitness value by interacting with the environment. This is not the case with the ETBD, which must instead extrapolate the fitness of behaviors that were not emitted. Because roulette-wheel selection requires that fitter behaviors have higher values, it is necessary to develop a new definition of fitness for this method. It is simplest to incorporate the continuous selection's method of assigning fitness values into roulette wheel selection, because it creates a property of behaviors that becomes larger as they become more like the reinforced behavior. This requires measuring the area under the curve of the fitness functions (Figure 2-2), which can be calculated by integrating the functions. Rather than defining fitness as the distance from the last emitted behavior, fitness will be more directly defined as the probability that a behavior would be selected for reproduction.

By integrating the functions used to produce the curves used in Figure 2-2, it is possible to calculate the exact probability that a potential behavior would be randomly selected in a single sampling. Without going into their derivation, the definite integrals that need to be calculated for each of the continuous function methods are:

$$Uniform\colon \int_{x}^{x+1} (x/2\mu)^2,\ \ if\ x < 2\mu$$

$$Linear\colon \int_{x}^{x+1} [-(x/3\mu)^2 + (2x/3\mu)]/2\,,\ \ if\ x < 3\mu$$

$$Exponential\colon \int_{x}^{x+1} \left(1 - e^{-1/x\mu}\right).$$

In these equations x is the absolute distance of the potential behavior from the emitted behavior and μ is the mean of fitness function. The uniform and linear functions are limited because they do not extend infinitely like the exponential does. The uniform function is limited to twice its mean and the linear to thrice its mean. Any potential emitted behavior that is outside these bounds has zero probability of being selected.

This combination of roulette-wheel and continuous selection can be termed roulette-continuous selection. Figure 2-6 illustrates how this method would be used with a tiny population of three potential behaviors. The phenotypic integer distance of behaviors 1, 2, and 3 from the reinforced behavior are 5, 20, and 30. The probability of selection becomes smaller as we go from potential behaviors 1 to 2 and from 2 to 3 as is indicated by the area under of the curve for each behavior. If the shaded portions are turned into a single wheel, then it would look like the roulette-wheel that is shown in the top right of Figure 2-6. Since the area of behavior 1 is roughly equal to the combined size of behaviors 2 and 3, it takes up half of the wheel's area. Similarly, behaviors 2 and 3 have progressively smaller areas and take up less of the wheel. We would select a single behavior by spinning this wheel and a pointer would come to rest on one of those 3 behaviors.

Roulette-continuous selection has advantages over continuous selection. While it is computationally more intensive to calculate the areas under the curve for each behavior than to just measure the difference between behaviors in the population, it does not suffer from the large magnitudes (i.e., small fitness density function means) problem. If there are potential behaviors in the population that are within the limits of the function, then roulette-continuous selection will operate without issue. This is guaranteed with cloning reproduction because the behavior that was emitted and resulted in reinforcement will always be within the function's range. Another important element of this method is that it maintains the forms of continuous selection, which connects it to previous research. Despite the computational intensity of calculating areas under the curve, roulette-continuous selection is a more efficient algorithm. Drawing random numbers – as continuous selection does – is a computationally more intensive task than calculating the probability of each behavior via integrals. Roulette-continuous selection only requires that one random number be drawn for each behavior rather than the expected average of 10 (the range of phenotypes – 1024 – divided by the population size of 100) for the continuous selection function method.

2.3. Virtual Environments

The simulated environments that the ETDB creature will be interacting with must be defined prior to experimentation. This is a critical aspect of modelling because it delineates what the researcher believed was relevant to the situation being examined. The inappropriate addition or omission of a critical component to the environment can produce results that have poor external validity because the reality of the situation was not modelled. Critical assumptions about how environments were designed for the experiments of this dissertation will be identified and briefly discussed.

For both experiments only two target classes are defined. These two target classes established which emitted behaviors were reinforced. All previous studies that have examined ETBD behavior in concurrently reinforcing environments have been conducted with just two target classes (Kulubekova & McDowell, 2013; McDowell et al., 2008; McDowell & Calvin, 2015; McDowell & Klapes, 2018; McDowell & Popa, 2010, 2016; McDowell, Popa, & Calvin, 2012; Popa & McDowell, 2010). A potential limitation to this design's external validity is that matching law theory (Herrnstein, 1970) assumes that there are other reinforced behaviors that a participant engages in that are not measured by the experimenter, and this assumption also holds for concurrent schedules. While the experiments described in this dissertation followed the typical design for concurrent environments that have been conducted in the past, this design may lack external validity because there is no simulated unscheduled reinforcement which would exist in any experiment or real-world situation. Given the ratio form of Equation 1.0, however, it is assumed that the unmonitored behaviors and unmeasured reinforcers would cancel out and thus not affect the results.

For the simulations, reinforcers were provided on random-interval (RI) schedules, which are idealized Fleshler and Hoffman (1962) VI schedules (McDowell et al., 2008). On VI schedules, reinforcers become available to the participant after variable periods of time have elapsed since the last reinforcer was collected (Ferster & Skinner, 1957). RI schedules are only different in that new intervals are created as the experiment is conducted, which is a minor distinction, but it does prevent the participant from potentially identifying reinforcement patterns that could exist with poorly preconstructed VI schedules. The random intervals were drawn from an exponential distribution (Fleshler & Hoffman, 1962). Exponential distributions are useful for eliminating the confound of memory, because the probability that a reinforcer will become available does not change as time elapses (Fleshler & Hoffman, 1962; Catania & Reynolds, 1986). For example, if the RI mean is 10 seconds then there is a 50% chance that the reinforcer will become available within the next 10 seconds. If the reinforcer does not, however, become available within that first 10 seconds, then there is still a 50% chance that it will become available within the next 10 seconds, and so on. As long as no reinforcer has become available then the likelihood that it will become available within the next 10 seconds is the same regardless of how much time has elapsed.

A necessary component of concurrent VIVI schedules for them to produce behavior that follows the matching law is a changeover delay (COD). A COD prevents the participant from immediately receiving a reinforcer when they switch from one target class to the other (Findley, 1958; Herrnstein, 1961; Ferster & Skinner, 1957). Herrnstein (1961) demonstrated that the absence of a COD results in frequent switching between target classes – a changeover – and that the behavior is less well controlled by the environmental contingencies. The concept of CODs has been further explored, and it was found that CODs can be any type of punisher or cost for switching between target classes and are not limited to simply imposing a delay in obtaining reinforcers (summarized by Baum, 1982). These costs encourage participants to remain in one target class rather than switch, which makes their behavior more strongly controlled by the reinforcing contingencies.

Implementing CODs for ETBD creatures is complicated by the genotype-phenotype distinction. Popa and McDowell (2010) found that the Hamming distance between behaviors was the most analogous characteristic of ETBD simulations to a COD. The Hamming distances between target classes and within target classes controlled what the exponent in Equation 1.0 would be, which is consistent with how CODs work with humans and animals. A rough rule is that the Hamming distance between target classes minus the Hamming distance within the target classes must be greater than 3 for the matching law exponent (Equation 1-1) to be within the range of what is typical of experiments (Popa & McDowell, 2010). The two target classes for ETBD creature experiments in the concurrent RI RI schedule environment are most often located at 471 to 511 and 512 to 552 (Kulubekova & McDowell, 2013; McDowell et al., 2008; McDowell & Calvin, 2015; McDowell & Popa, 2010, 2016; McDowell, Popa, & Calvin, 2012; Popa & McDowell, 2010). This was the location of the target classes for ETBD creatures that used bitflip-by-individual mutation (Section 2.1.4) for Step 5 of the ETBD algorithm (Figure 2-1). With phenotypic mutation (Section 2.2.2), the target classes need to be separated phenotypically, because a short phenotypic distance like 471 to 511 and 512 to 552 will have excessively frequent changeovers. The target classes, thus, needed to be phenotypically separated, and the target classes of 225 to 275 and 725 to 775 were chosen for this reason. The mutation mean of the phenotypic mutation methods was set to 50 on the basis of pilot data and the expected average of 10 mutations in one direction to switch between target classes. This number of mutations is analogous to bitflip-by-individuals average number of bit flips that are needed to go from one target class to another.

2.4. Apparatus

I wrote the software that was used to conduct the experiments, which were all conducted on a computer using the Windows 10 operating system. The computer used for experimentation had a dual core 2.3 Ghz processor with 8 GB of RAM. The ETBD and laboratory code were written in VB.Net 2015, which is a common programming language. The timing, emitted behaviors, and reinforcement counts were recorded and stored in standard databases (i.e., XML files and Microsoft Excel). Data were analyzed using standard software (i.e., Microsoft Excel & R).

Chapter 3: ETBD and TNGS Behavior on Concurrent RI RI Schedules

For new theories to be considered strong alternatives to existing ones, a new theory either must account for more phenomena or better predict phenomena than existing theories (Hempel & Oppenheim, 1948; Killeen, 2001; Platt, 1964; Popper 1959; Staddon & Bueno, 1991). The ETBD has already demonstrated that it can explain a wider range of phenomena than the matching law (Equation 1-1; for review see McDowell, 2013a), which suggests that it may be a better account of operant behavior. The first steps that were taken to assess the ETBD's viability as an account of human and animal operant behavior consisted of examining its performance on single RI and concurrent RI RI schedules (McDowell, 2004; McDowell & Caron, 2007; McDowell et al., 2008). Because the TNGS's sustained operant behavior has not been assessed, those same experiments provide an opportunity to assess its viability as a quantitative account of behavior. The clinical relevance of behavior in those circumstances is another reason why single RI and concurrent RI RI schedules are a good starting point (Section 1.4). Fortunately, a single experimental design can simultaneously assess a model's explanatory viability for both concurrent RI RI and single RI environments (McDowell & Popa, 2010).

3.1. Matching to Rates of Reinforcement on Single Schedules

Two separate equations that are based on the matching law are used to describe human and animal behavior in concurrent RI RI and single RI environments. Behavior on concurrent RI RI schedules is typically described with the modern matching law (Equation 1-1; Section 1.1) and a derivation of it is fitted to behavior on single RI schedules. The derivation entails theoretical assumptions that make it distinctly different from the matching law because it ascribes more characteristics to the participant and the environment than the matching law. The original derivation was based on the original matching law equation (Herrnstein, 1961), which is like Equation 1-1 but expresses behavior and reinforcement as proportions and omits the *a* and *b* parameters. The original matching law equation is

$$\frac{B_1}{B_1+B_2} = \frac{R_1}{R_1+R_2}, \tag{3-1}$$

where *B* is the rate of behavior, *R* is the rate of obtained reinforcement, and the subscripts indicate the target classes. This equation is strictly inferior to the modern matching law (Equation 1-1) as a description of human and animal behavior (for review see McDowell, 2013b). Both Equations 1-1 and 3-1 are limited in that they only apply to the specific circumstance of two target classes. This dramatically limits their external validity because natural environments may reinforce any number of behaviors, not just behaviors that neatly fall into two target classes.

Herrnstein addressed this limitation by making two important assumptions (1970). The first assumption is that humans and animals engage in behaviors at a constant rate, and the second is that the environment reinforces behaviors outside of the target classes at constant rates. By making these assumptions a new equation could be derived that extended the matching law to any number of target classes. This equation is called the quantitative law of effect because it was a quantitative interpretation of Thorndike's law of effect (1911). The quantitative law of effect is expressed as

$$B_i = \frac{kR_i}{R_i+r_e}, \tag{3-2}$$

where *B* is the rate of behavior, *R* is the obtained rate of reinforcement, *k* is the estimated constant total rate of behavior, r_e is the estimated rate of unmeasured reinforcement, and *i* identifies the target class. In theory, *k* represents the sum of all rates of behavior, ΣB_x, and r_e

represents the sum of all rates of reinforcement, ΣR_x, minus the rate of reinforcement from the target class, R_i (i.e., $r_e = \Sigma R_x - R_i$).

An alternative to the quantitative law of effect that makes the same assumptions but is derived from the modern matching law is

$$B_i = \frac{kR_i{}^a}{R_i{}^a + \frac{r_e^a}{b_i}} \tag{3-3}$$

(Dallery et al., 2005; McDowell, 1986, 2005; Soto et al., 2005). *B, R, k*, r_e, and *i* have the same meanings as in Equation 3-2. The parameters *a* and *b* have similar, but not identical, interpretations to Equation 1-1, which is that *a* is the sensitivity to the rate of reinforcement and b_i reflects relative preference for the identified target class over all other measured and unmeasured target classes. When fitted to data, r_e and *b* cannot be separately estimated and are, thus, combined into the parameter *c* (Dallery et al., 2005; McDowell, 2005; 2013b; McDowell & Calvin, 2015). With the substitution of *c,* Equation 3-3 becomes

$$B_i = \frac{kR_i{}^a}{R_i{}^a + c}. \tag{3-4}$$

In a recent review, Equation 3-4 was found to provide a better description of behavior on single alternative schedules than Equation 3-2 (McDowell, 2013b).

In Equations 3-2, 3-3, and 3-4, the parameters *k* and r_e represent information that the researcher can only indirectly and uncertainly assess during an experiment. For example, an important caveat to *k* representing the sum of all behaviors is that all behaviors are of the same form and effort (Herrnstein, 1970). This requires the interpretation of *k* in terms of target-class-equivalent behaviors even when the unmeasured behaviors are dramatically different. The estimated values are an amalgam of effort, cost, frequency, and other qualities that are roughly equivalent to the measured behavior. If typing was the target class, then *k* is measured in typed words per minute despite the forms of the unmeasured behaviors diverging from that (e.g., grading, cooking, or socializing). In this way *k* is like measuring the worth of everything in a grocery store in terms of apples, so its validity is difficult to assess. Similarly, the parameter r_e is the sum of reinforcement rates and has the same measurement caveat as *k* inasmuch as the value is relative to the measured reinforcers. Unsurprisingly given these caveats, researchers have heavily critiqued Equation 3-2 despite its utility (Baum, 1981; 2012; Baum & Davison, 2014; Dallery, McDowell, & Lancaster, 2000; Dallery, McDowell, & Soto, 2004; Dallery, Soto, & McDowell, 2005; Davison, 1993; McDowell, 2005; 2013b; McDowell & Dallery, 1999; McDowell & Calvin, 2015; Pear, 1975).

The primary criticism of Equation 3-2 is that Herrnstein's first assumption – that the rate of behavior, *k*, is constant – is refuted by data. Numerous studies have found that *k* varies with the size or quality of the reinforcers (Dallery et al., 2000; 2004; 2005; McDowell, 2005; 2013a; McDowell & Dallery, 1999). The impact of a reinforcer on future behavior is often called its magnitude and it can refer to either the quality (e.g., sucrose concentration) or quantity of the reinforcer. Dallery et al. (2004; 2005) and McDowell (2005) found that *k* estimates of human and rat behavior changed with the reinforcers' magnitude. McDowell (2013) revised his opinion, however, when he conducted a more powerful reanalysis of McDowell and Dallery (1999). McDowell concluded that their experiment lacked the statistical power to determine whether *k* varied with reinforcer magnitude. This lingering uncertainty about *k*'s constancy led to the development of an ETBD simulation which predicted that *k* varies with the reinforcer's magnitude (McDowell & Calvin, 2015). This seemed to be confirmed when McDowell et al. (2017) reanalyzed McDowell and Dallery (1999), again, using a new statistical approach and concluded that *k* did vary. However, the statistical technique they used was novel (McDowell, Calvin, & Klapes, 2016) and overly focused on residuals being homoscedastic. It would be better if a new experiment was conducted that were more clearly identify differences in *k* values with reinforcer magnitude using traditional statistical approaches.

To assess the viability of the TNGS it is necessary to see what patterns of behavior it predicts and assess whether that pattern is like those produced by humans and animals. The criteria of a successful simulation of human and animal behavior in concurrent RI RI and single RI environments are multifaceted. The first criterion is that the simulation must result in patterns of behavior that are better described by the modern versions of the matching law (Equation 1-1) and quantitative law of effect (3-4) than their original versions (Equations 3-1 and 3-2), which is supported by McDowell's review (2013b). Secondly, the parameters found with Equations 1-1 and 3-4 must be consistent with those found with humans and animals in single-RI and concurrent-RI RI environments. The average exponent value must be near 0.8 (Baum 1974, 1979; McDowell, 1989, 2013b; Myers & Myers, 1977; Wearden & Burgess, 1982), although a range of 0.7 to 0.9 is permissible inasmuch as the 0.8 criteria is a rough estimate that has not been thoroughly assessed via meta-analysis. Additionally, the bias parameter should reflect differences and similarities in reinforcer magnitudes. If a reinforcer is stronger for one target class than another, then the bias parameter should favor that side. If the reinforcers' magnitudes are equivalent across target classes, then the bias parameter should favor neither target class (i.e., have a value of 1). Thirdly – but to a lesser extent because it is under examined – the rate of switching between target classes should be greatest when the rate of reinforcement is equivalent for the two target classes and smallest when the rate of reinforcement strongly favors one target class over another (Alsop & Elliffe, 1988; Baum, 1974; Brownstein & Pliskoff, 1968;

Herrnstein, 1961). If a simulation meets these criteria, then it would indicate that it is in accordance with animal and human behavior in similar situations.

Another goal of this experiment was to assess whether the TNGS makes the same predictions as the ETBD (McDowell & Calvin, 2015). The purpose of this simulation was to determine which interpretation of the matching law the ETBD predicted. As proposed by McDowell (2013b), matching theory can be separated into four categories based on the form of the equation and assumptions about *k*. These are the classical response-strength, classical algebraic, modern response-strength, and modern algebraic interpretations. The first classification entails the equation's form (classical vs. modern) and refers to whether behavior is best described by the classic quantitative law of effect (Equation 3-2) or the modern quantitative law of effect (Equation 3-3). The second classification is whether the parameter *k* has the same value in all situations or if it can vary across situations. This entails whether the theory that underlies the quantitative law of effect – Herrnstein's assumptions (1970) – is supported by the data or if the equation should be viewed simply as being an algebraic description. This was assessed in the McDowell and Calvin (2015) simulations by holding the magnitude of reinforcement for one target class constant while varying the magnitude of the other target class. If Herrnstein's assumptions were correct, then the parameter *k* should always be the same regardless of the target class's magnitude.

McDowell and Calvin (2015) found that the typically used version of the ETBD predicts that behavior is best described by the modern quantitative law of effect (Equation 3-3), but that Herrnstein's assumptions were not supported by the data (i.e., the modern algebraic interpretation). The best descriptor of behavior was a version of the modern quantitative law of effect that allowed the *k* and *c* parameters to vary across magnitudes. For the new models to make the same predictions, the best descriptors of their behavior should also find that the *k* parameter values vary with reinforcer magnitude. This is not a strict criterion because it needs to be more strongly verified than in McDowell et al. (2017), but it is important to identify deviations in theory predictions because they can inform the development of critical experiments (Platt, 1964).

3.2. Methods

3.2.1. Participants. Twelve different simulated creature types were assessed and are listed in Table 3-1. These twelve creature types are various combinations of the selection, reproduction, and variation algorithm methods that were possible implementations of the TNGS and ETBD. For the sake of conciseness, the abbreviated simulated creature names that are listed in the table will be used in the text and figures. In the abbreviated format, the first word is the form of the selection function, the second is the method of reproduction, and the last is the method of variation. This considerably improves readability because describing a creature's algorithm as "linear-bitwise-bitflip" is much briefer than "continuous-linear selection, bitwise reproduction, and bitflip-by-individual variation" while conveying the same meaning.

The twelve types of simulated creatures can be organized by their relationship to the TNGS and ETBD. The first two simulated creatures that are listed in Table 3-1 under the ETBD-based heading (linear-bitwise-bitflip and exponential-bitwise-bitflip) are comparison models and are replications of the same ETBD algorithms that have been used in previous research. These were included to identify problems with the simulation and differences between the TNGS and – as previously implemented – the ETBD. The two versions of the TNGS that are genotype based (Table 3-1; linear-clone-bitflip and exponential-clone-bitflip) maintain the distinction between the behavioral genotype and phenotype, whereas the remaining eight that are phenotype based only represent behaviors as phenotypes. Please note that, the dissertation proposal only suggested using the exponential selection function but – for reasons that will become apparent in the second experiment – the creature types that used linear selection functions had to be added. This was unanticipated and doubled the size of this experiment. While the linear and exponential replications are presented together, the true order of events was that the simulations with the six creature types that used the exponential selection function were conducted first and then later the simulations with the six creature types that used the linear selection function were conducted.

The mutation rate for all creature types was systematically manipulated from 5% to 20% in steps of 2.5%. This gave seven rates of mutation, which were 5%, 7.5%, 10%, 12.5%, 15%, 17.5%, and 20%. At each combination of creature type and mutation rate ten creatures were simulated, and each creature worked on 208 concurrent RI RI schedules for 20,500 time steps per schedule. This resulted in 298,480,000 simulated behaviors (7 mutation rates • 10 creatures • 208 schedules • 20,500 time steps) for each creature type, so great confidence can be placed in the observed patterns of behavior being representative of that creature type's predictions. Since there were twelve different types of simulated creatures, this experiment represents a total of 3,581,760,000 simulated behaviors that were produced by 840 simulated creatures.

3.2.2. Procedures. This experiment's procedures generally followed McDowell and Popa (2010) but deviated in some minor respects. All simulated creatures worked on 52 concurrent RI RI schedules (Table 3-2) at four different reinforcer magnitude pairs, which gives a total of 208 schedules of reinforcement. At each reinforcer magnitude pair, the 52 schedules were presented to the simulated creature in a random order. This wide range of concurrent RI RI schedules is necessary for simultaneously fitting the modern quantitative law of effect (Equation 3-4) and modern matching law (Equation 1-1), because the two equations have different fitting requirements. The modern matching law requires a wide range of reinforcement ratios, whereas the modern quantitative law of effect requires a wide range of obtained reinforcement rates.

The 52 schedules of this experiment deviated from McDowell and Popa's 54 schedules (2010) to better sample the lean range of concurrent RI RI reinforcement rates (i.e., RIs between 20 and 80 time steps). The random-interval means ranged from 2.5 to 80 time steps, which is slightly wider than McDowell and Popa's 1 to 70 (2010). The range of scheduled RI ratios was slightly more restricted in this experiment with its largest ratio being 1:4, whereas it was 1:5 in McDowell and Popa (2010). The 52 schedules were constructed by creating 4x4 grids of reinforcement ratios at RIs 2.5, 5, 10, and 20 time steps. Each grid was created by multiplying those interval rates by the ratios 1:1, $1{:}1.\overline{3}$, 1:2, 1:4, $1.\overline{3}$, 1, $1.\overline{3}$: $1.\overline{3}$, $1.\overline{3}{:}2$, $1.\overline{3}{:}4$, 2:1, 2: $1.\overline{3}$, 2:2, 2:4, 4:1, $4{:}1.\overline{3}$, 4:2, and 4:4 (visualized in Figure 3-1). This method provides an even sampling of the rate of reinforcement domain, which McDowell and Popa's (2010) experiment lacked. McDowell and Popa sampled the richest rates of reinforcement (i.e., RIs 1 through 10) with many ratios, whereas they only sampled the lean schedules (i.e., RIs 20 to 80) at a 1:1 ratio.

At each mutation rate, the simulated creatures were assessed at 4 pairs of reinforcer magnitudes. The reinforcer magnitude pairs were fitness density function mean pairs of 20 & 20, 40 & 40, 60 & 60, and 80 & 80. Recall that fitness density functions means are inversely related to their reinforcing magnitudes; for example, a fitness density function mean of 20 represents a greater reinforcer magnitude than a mean of 80.

3.2.3. Analyses.

3.2.3.1. Data pooling and averaging. Simulated behavior during the first 500 time steps of each schedule was excluded from analyses to assess each simulated creature type's steady-state behavior rather than behavior during transition. Observed reinforcement and behavior frequencies during the remaining 20,000 time steps were divided by 500 time steps to create rates of reinforcement and behavior. These rates were then averaged across simulated creatures of the same type as a precaution against individual creatures becoming stuck in unrepresentative local minima. In summary, each data point represents 200,000 behaviors from 10 simulated creatures.

3.2.3.2. Weighted ensemble fitting. To estimate parameter values for the matching law and quantitative law of effect it is necessary to simultaneously fit both equations while using the same parameter values (McDowell, 2005). In total, it was necessary to simultaneously fit three equations: the modern quantitative law of effect to the first target class, the modern quantitative law of effect to the second target class, and the modern matching law to the ratio of the two target classes. The theoretical formulations of the modern matching law (Equation 1-1) and quantitative law of effect (Equation 3-3) are inadequate for fitting data because b cannot be estimated for the quantitative law of effect and r_e cannot be estimated for the modern matching law. The parameter c from Equation 3-4, captures both elements, however, and thus can be used to create an important equality that bridges the two (McDowell, 2005). The c parameter for each target class represents the extraneous rate of reinforcement to the power of a divided by the bias towards that side. Since c_1 represents r_e^a/b_1 and c_2 represents r_e^a/b_2, the ratio of those c estimates represents bias in the modern matching law equation because r_e^a cancels out (i.e., $c_2/c_1 = b$).

Based on this, the modern matching law and quantitative law of effect equations were modified to forms that are better suited for data analysis (McDowell, 2005; McDowell & Calvin, 2015; McDowell & Popa, 2010). To highlight the relationship between these equations and their theoretical counterparts they are designated by their base equation with a prime added to it. The modern matching law is typically log transformed to make it a linear equation, which gives

$$\log\left(\frac{B_1}{B_2}\right) = a \cdot \log\left(\frac{R_1}{R_2}\right) + \log\left(\frac{c_2}{c_1}\right). \tag{1-1′}$$

The modern quantitative law of effect must be simultaneously fitted to both target classes by using the equations

$$B_1 = k\left(\frac{c_1}{R_1^a} + \frac{c_1 R_2^a}{c_2 R_1^a} + 1\right)^{-1} \tag{3-4a′}$$

and

$$B_2 = k\left(\frac{c_2}{R_2^a} + \frac{c_2 R_1^a}{c_1 R_2^a} + 1\right)^{-1} \tag{3-4b′}$$

(McDowell, 2005; McDowell & Calvin, 2015; McDowell & Popa, 2010). The parameters in these three equations are the same as those in the modern matching law (Equation 1-1) and quantitative law of effect (Equation 3-4).

The effect of the free parameters on the shape of Equations 3-4a′ and 3-4b′ are shown in Figure 3-2[3]. The unbroken black line serves as a reference for the effects of changing *k*, *c*, and *a*. The dashed line shows the effect of reducing *k*, which is that it lowers the function's asymptote.

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[3] For the sake of clarity, Figure 3-2 shows the predicted rate of responding for one target class when there is no reinforcement from the other target class, which means that Equations 3-4a′ and 3-4b′ can be simplified to Equation 3-4. The true shape of Equations 3-4a′ and 3-4b′ is three dimensional with the axes being the rate of reinforcement from the 1st target class, the rate of reinforcement from the 2nd target class, and the rate of behavior. The effects of the free parameters that are described by this paragraph are not significantly affected by the rate of reinforcement in the 2nd target class.

The dotted line shows the effect of increasing *c*, which is that it takes longer to reach the asymptote. It is important to note that *c* is the rate of reinforcement that predicts a rate of responding that is half of *k* (Bradshaw, Szabadi, & Bevan, 1976). For example, in Figure 3-2, when the rate of reinforcement is 50 along the dotted line, then the predicted rate of behavior is 250. The dot-dash line shows the effect of undermatching (i.e., *a* less than 1). The effect of an *a* value less than one is like increasing *c* in that reduces the rate of ascent to the asymptote. However, it has less of an effect at low rates of reinforcement and a greater one at high rates of reinforcement.

The simultaneous fitting of Equations 1-1′, 3-4a′, and 3-4b′ complicates the analysis in a way that precludes ordinary least squares (OLS) fitting (McDowell, 2005). OLS is a poor fitting method in this case because it cannot account for B_1, B_2, and B_1/B_2 sample variance differences, which can bias fits. The variances of behavior in the target classes strongly differs from the variance of the behavioral ratio by orders of magnitude. Even the sample variances of B_1 and B_2 may be slightly unequal in spite of the experiment's symmetrical design.

A solution to this problem is ensemble least-error fitting (McDowell, 2005). This approach is like OLS in that the sum of squares is minimized, but it also takes into account the different sample variances. Ensemble least-error fitting minimizes

$$\sum_{i=1}^{k} \frac{RSS_i}{SS_i},$$

where *k* is the number of data subsets being fitted, *RSS* is the residual sum of squares for a data subset, and *SS* is the total sum of squares for a data subset (McDowell, 2005). The residual sum of squares divided by the total sum of squares is closely related to the percentage of variance accounted for, so it can also be thought of as maximizing the overall percentages of variance accounted for. This approach has been successfully used to analyze quantitative law of effect fits to rat behavior under multiple deprivation conditions (McDowell, 2005; McDowell, Calvin, Hackett, & Klapes, 2017), to analyze the simultaneous fit of the quantitative law of effect to simulated creature behavior on concurrent RI RI schedules (McDowell & Calvin, 2013; McDowell & Calvin, 2015), and to analyze the simultaneous fit of the quantitative law of effect and matching law to simulated creature behavior (McDowell & Popa, 2010).

A potential problem with ensemble least-error fitting is suggested by McDowell and Popa (2010). They simultaneously fitted Equations 1-1′, 3-4a′ and 3-4b′. Figure 3 of that paper shows differences in the percentages of variance accounted for by the matching law and quantitative law of effect fits, with the quantitative law of effect fits having larger percentages of variance accounted for. This difference may be due to the quantitative law of effect equation implicitly having twice as much weight on the overall percentage of variance accounted for because it constitutes two of the three fitted equations. However, this difference disappears when a larger sampling area of reinforcement rates (i.e., 54 data points rather than 11) is used, which suggests that this would not be a problem for this experiment.

To prevent any possible impact of the greater implicit weighting towards the quantitative law of effect, a weighting parameter was added to the ensemble least-error fitting method. Attaching a weighting value is a simple way to account for the implicit imbalance of equation forms. With the weighting adjustment, the ensemble least-error fitting takes the form of

$$\sum_{i=1}^{k} w_i \frac{RSS_i}{SS_i},$$

in which *RSS, SS,* and *k* have the same meaning as ensemble least-error fitting and *w* represents the weighting for a fit. By weighting the matching law fit twice as much as the two quantitative law of effect fits, it should prevent overfitting to the quantitative law of effect. In this experiment, Equation 1-1′ was weighted at 0.5 and Equations 3-4a′ and 3-4b′ were each weighted at 0.25.

3.2.3.3. Analytic approach to ensemble fits. A nested model analysis approach was taken to determine how the behavior of the simulated creatures could be best described. The nested-models approach is used to refine an equation with many parameters to the lowest justifiable number of parameters (Loehlin, 2004). To do this, the experimenter evaluates various parametric assumptions that simplify the equation and then evaluates whether each of those assumptions can explain the data just as well as the more general account. A simile for this approach is that the equations are like Russian nesting dolls (i.e., Matryoshka dolls) and that the data is like a ball that can fit into some but not all dolls. More specific equations with fewer parameters are like smaller dolls that fit within the largest doll, which represents the most general equation. The analyst’s goal is fit the ball – data – within the smallest doll they can – an equation that describes the data without sacrificing any explanatory power. An equation that describes the data as well as the most general equation is the most parsimonious account.

For this approach, the most general fit serves as a baseline that accounts for the largest percentage of variance but may have the least explanatory utility due to possibly unnecessary parameters. This baseline fit is then compared to simplified versions of that equation that are made by making certain assumptions about the parameters. For example, the classic quantitative law of effect (Equation 3-2) is nested within the modern quantitative law of effect (Equation 3-4), because they produce the same predictions when a equals 1 and there is no bias ($c_1 = c_2$). The classic quantitative law of effect is a more restricted version of the modern quantitative law of effect and is, thus, nested within it.

This logic can be applied to compare multiple versions of the quantitative law of effect that make different assumptions about the parameters. To deduce the best version of the quantitative law of effect, eight models that made different assumptions were fitted to simulated creature behavior and then compared (Table 3-2). These different models are roughly ordered by the level of restriction. Model 1 is the least restrictive and Model 8 is the most restrictive because it makes the most assumptions about the parameters. These comparisons models can support one of four major interpretations (McDowell, 2013b), which are the classic algebraic (models 6 and 7 in Table 3-3), classic response strength (model 8), modern algebraic (models 1 through 4), and modern response strength (model 5).

There are many ways to compare models within a nested-models analysis (Loehlin, 2004). To prevent overreliance on any given comparison method, the extra sum of squares difference test (Motulsky & Christopolous, 2004), Akaike Information Criterion (AIC; Akaike, 1974), and Bayes Information Criterion (BIC; Schwarz, 1978) were used. The extra sum of squares difference test was chosen over the frequently used root mean square error of approximation (RMSEA), because the weighted least-error ensemble fitting method is closest to OLS. RMSEA is based on a χ^2 difference test and is thus nonparametric.

The extra sum of squares difference test is a generalization of a typical F-test used in ANOVA (Motulsky & Christopolous, 2004, pg. 142). The F-test is

$$F = \frac{(SS_{large} - SS_{small})/(DF_{large} - DF_{small})}{(SS_{large}/DF_{large})},$$

where *SS* is the sum of squares, *DF* is the degrees of freedom, *large* refers to the more general equation, and *small* refers to the more specific equation (Motulsky & Christopolous, 2004). This is a null-hypothesis test which has the alternative hypothesis that the more restrictive equation explains less of the variance. If there is a significant difference, then the simpler model does not account for the data as well as the more general model and, thus, should be rejected. A failure to reject suggests that the simpler model is a better description via Occam's razor. By comparing ever simpler models, the simplest explanation that still describes the data can be found.

A second and distinct approach to model evaluation from extra-sum-of-squares difference testing is to compare information criteria (Motulsky & Christopolous, 2004). Two commonly used and important information-criteria-based measures are the AIC and BIC. When comparing models, the model with the smallest information criterion is considered the best model among those fitted. The AIC is an estimator of the information provided by a model (Akaike, 1974; Hurvich & Tsai, 1991), and is given by the equation

$$AIC = N\left[ln\left(\frac{RSS}{N}\right) + 2k\right],$$

where N is the sample size, RSS is the residual sum of squares, and k is the number of parameters (Motulsky & Christopolous, 2004). BIC is similar, but is based on Bayesian prediction (Schwarz, 1978) and is given by the equation

$$BIC = N\left[ln\left(\frac{RSS}{N}\right)\right] + k \cdot ln(N).$$

These three methods of assessing the fit of the eight models (Table 3-3) were used to determine which quantitative law of effect model best described the simulated creature behavior.

3.2.3.4. Changeover profiles. An under examined aspect of human and animal behavior on concurrent RI RI schedules is how frequently participants switch their behavior between target classes. When a participant switches from one target class to the other it is called a changeover. Changeovers indirectly describe the participant's sustained persistence at tasks, with fewer changeovers suggesting longer durations of sustained behavior within a target class. A clinically relevant example of a changeover is when a client with attention deficit hyperactivity disorder stops doing their homework to go watch television.

On concurrent RI RI schedules, changeovers are most frequently observed when reinforcers are obtained equally from the two target classes, and least frequently when reinforcers are obtained from just one target class (Alsop & Elliffe, 1988; Baum, 1974; Brownstein & Pliskoff, 1968; Herrnstein, 1961). Mathematically, changeovers follow a quadratic pattern (for example see Figure 4 of Alsop & Elliffe, 1988). This quadratic pattern can be described by the equation $C = aP^2 + bP + c$, where C is the number of changeovers, P is the proportion of obtained reinforcers for behavior in the first target class, and a, b, and c are fitted parameters (McDowell et al., 2008). The proportion of reinforcement, P, is defined as $R_1 / (R_1 + R_2)$, and its range of possible values is 0 to 1. Two important elements of this quadratic are the maximum rate of changeovers and the range of changeover rates (McDowell et al., 2008). The quadratic equation's parameter values can be used to calculate the maximum rate of changeovers, C_{Max}, with the equation $c - b^2/4a$, and the range of changeovers, C_{Δ}, with $-b^2/4a$ (McDowell et al., 2008). In previous simulations, this has been an effective method of describing the changeover behavior of linear-bitwise-bitflip creatures (McDowell et al., 2008; 2012).

3.3. Results

3.3.1. Best quantitative law of effect model. Overall, the twelve ETBD algorithms were best described by the third quantitative law of effect model, which set c_1 equal to c_2 (i.e., no bias towards either target class) and enforced a constant a across reinforcement magnitudes (Figure 3-

3). Preference count is simply the number of times (across all 84 creature types and mutation rate combinations) that the criterion measure or difference test determined that model was better than the other models. For the information criterion measures (i.e., AIC and BIC), the preferred models were those with the smallest criterion value at each combination of creature type and mutation rate. For the extra sum of squares difference test measure, the preferred model was the most restricted model that was not significantly different from model 1. All classic quantitative law of effect models (models 6 through 8) were dramatically worse than model 3. The BIC provided the clearest support for model 3, whereas the AIC's and extra sum of squares tests equally supported models 1 through 3 (Figure 3-3).

The selection function form affected the fitting measure's model preferences. The BIC, AIC, and extra sum of squares tests all preferred model 3 when the simulated creatures used an exponential selection function (black bars of Figures 3-3), whereas the results were more mixed when they used a linear selection function (white bars of Figures 3-3). In all cases, the modern algebraic interpretation was supported.

The AIC and extra sum of squares tests were oversensitive to slight random differences in simulated creature behavior, which is in line with recent simulations that included models that permitted overfitting of the AIC (Huang, 2017; Lin, Huang, & Weng, 2017). This oversensitivity was suggested by how frequently model 1 was preferred over model 2. No asymmetries in reinforcer magnitudes were designed into the simulation, which means that c_1 should always equal c_2. The failure of the AIC and extra sum of squares difference tests to properly eliminate model 1, which permits c_1 to not equal c_2, suggests that those comparison methods poorly discriminated between the quantitative law of effect models. This was further supported by the lack of consistency of model preference across mutation rates, which can be observed in

Appendices A through L. Given the AIC and extra sum of squares difference test's poor ability to discriminate between models, the BIC is the best tool for deciding with model is best.

Simulated creature behavior was very well described by model 3. Across the twelve types of simulated creatures and their seven mutation rate combinations, the lowest percentage of variance accounted for by the modern quantitative law of effect (Equations 3-4a′ and 3-4b′) was 91% (Table 3 of Appendices A through L). The modern quantitative law of effect's (Equations 3-4a′ and 3-4b′) median percentage of variance accounted for ranged between 98% and 100% across the twelve types of simulated creatures. Similarly, simulated creature behavior was well described by the modern matching law equation (Equation 1-1′). The median percentage of variance accounted for by the modern matching law equation ranged between 99% and 100% (Table 3 of Appendices A through L).

3.3.2. Best fitting model parameters. Since model 3 was the best overall descriptor of simulated creature behavior, the parameter values of its fits were used as the basis of comparison across all simulated creature types. With model 3, the fitted exponent (a) was constant across magnitudes, there was a single c parameter at each magnitude, and the asymptote of the quantitative law of effect, k, could vary across magnitudes. Model 3 does not permit bias towards either target class because c_1 equals c_2. Model 3 used 9 parameters to fit simulated behavior at each mutation rate.

3.3.2.1. Exponent (a) values. The exponent (a) estimates of all twelve simulated creature types were between 0.7 and 0.9 – the range typically observed by humans and animals – across all seven mutation rates (Figure 3-4). The form of the selection function that the simulated creature used affected the exponent; simulated creatures that used an exponential selection function (top panel of Figure 3-4) had exponents that were roughly 0.05 higher than those that used the linear selection function (bottom panel of Figure 3-4). The method of variation also affected exponent values, with the simulated creatures that used bitflip-by-individual variation (squares and circles in Figures 3-4) having greater exponent values than the phenotypic variation methods.

3.3.2.2. Asymptote (k) values. The asymptotes of the modern quantitative law of effect (*k*) followed interesting patterns across the four magnitude pairs of reinforcement, two methods of selection, and seven mutation rates (Figures 3-5 and 3-6). A unique characteristic of the linear and exponential bitwise-bitflip ETBD creatures was that the *k* parameter estimates were relatively stable across mutation rates at each reinforcer magnitude pair (squares in Figures 3-5 and 3-6). Reinforcer magnitude did, however, have a large effect on the *k* parameter estimates; *k* estimates systematically decreased as the reinforcer became weaker (i.e., as the selection function's mean increased from 20 to 80). The linear-bitwise-bitflip ETBD creatures showed larger changes in the *k* parameter estimates than the exponential-bitwise-bitflip ETBD creatures.

The bitwise-bitflip ETBD creatures' *k* parameter stability across mutation rates strongly differs from the TNGS-based creature types. The TNGS-based simulated creatures had decreasing *k* parameter values as the rate of mutation increased. The bitflip-by-individual variation method in conjunction with cloning ameliorated this (circles in Figures 3-5 and 3-6), but strong downward trajectories were still observed with the linear-clone-bitflip creatures at the reinforcer magnitude pairs of 60 & 60 and 80 & 80 (circles in the bottom two panels of Figure 3-6). While all phenotypic variation methods showed substantial decreases in the asymptote (*k*) as the mutation rate increased, they were also strongly affected by the form of the selection function. The change in *k* values was similar across the four phenotypic variation methods when combined with the linear selection function (triangles, diamonds, and asterisks in Figure 3-5), but they greatly differed when combined with the exponential selection function (triangles, diamonds, and asterisks in Figure 3-6).

3.3.2.3. Rate of the quantitative law of effect's ascent. The *c* parameter estimates of the modern quantitative law of effect, which is a measure of its rate of ascent (Section 3.2.3.2; Figure 3-2), showed distinctly different patterns across the bitflip and phenotypic methods of variation (Figures 3-7 and 3-8). The bitwise-bitflip and clone-bitflip simulated creatures' behavior (squares and circles in Figure 3-7 and 3-8) showed increases in *c* as the rate of mutation increased regardless of the magnitude of the reinforcer pairs, which indicates a lower rate of ascent as the mutation rate increases. The phenotypic methods of variation (triangles, diamonds, and asterisks in Figures 3-7 and Figures 3-8) only showed this increase at the stronger magnitude pairs (i.e., 20 & 20 and 40 & 40) and were, otherwise, stable or decreasing with the mutation rates. Overall, this suggests that the rate of ascent does not change as the mutation rate increases for the simulated creatures that used phenotypic variation.

However, comparisons of *c* are most meaningful when two equations have the same *k* parameter value because *c*'s meaning is dependent upon *k* (Bradshaw et al., 1976). While the simulated creatures that used phenotypic variation had stable *c* values as the rate of mutation increased, those creatures also had decreasing *k* values. This combination of *k* and *c* parameter value changes could result in a pattern of behavior that is like an increase in *c* if a limited range of reinforcement rates is observed (Figure 3-9). Figure 3-9 shows quantitative law of effect fits

(Equation 3-4) to the behavior of exponential-bitwise-bitflip and exponential-clone-pheno-Gaussian creatures, which had opposite changes in *k* and *c* as the mutation rate increased, at the mutation rates of 10% and 20%. The exponential-bitwise-bitflip creatures had relatively stable *k* values (417 at 10% and 380 at 20) but increasing *c* values as the rate of mutation increased (21 at 10% and 38 at 20%), whereas the exponential-clone-pheno-Gaussian creatures had decreasing *k* values (444 at 10% and 348 at 20%) but stable *c* values as the rate of mutation increased (19 at 10% and 22 at 20%). Despite these differences, the fits to these creature types' behavior at 20% mutation are relatively similar within the bounds of the observed rates of obtained reinforcement (the greatest obtained rate of reinforcement was nearly 150 reinforcers per 500 time steps). Thus, examining *c* and *k* separately may be misleading. Another approach would be to compare the predicted rates of behavior at a specific rate of reinforcement. Looking at the predicted rate of behavior at a specific rate of reinforcementpermits a direct comparison of the Equation 3-4's rate of ascent to the asymptote *k* across the simulated creatures. A rate of reinforcement of 15 reinforcers per 500 time steps was selected, because it was greater than the lowest *c* values and could highlight differences in the rates of ascent.

The predicted rate of behavior at 15 reinforcers per 500 time steps showed surprisingly consistent patterns of behavior regardless of the simulated creature type. All simulated creatures showed lower rates of predicted behavior as the mutation rate increased (Figures 3-10 and 3-11), which indicates slower rates of ascent. The clone-bitflip simulated creatures (circles in Figures 3-10 and 3-11) showed the fastest rates of ascent at mutation rates 5% through 12.5% but their behavior tended to fall below clone-pheno-Gaussian at mutation rates 15% through 20% (asterisks in Figures 3-10 and 3-11). The ETBD-based bitwise-bitflip simulated creatures (squares in Figures 3-10 and 3-11) were most affected by the mutation rate; their rate of ascent was the second fastest at mutation rate 5% and the lowest at mutation rate 20%.

3.3.3. Quadratic description of changeover profiles. The initial examination of the simulated creature changeovers quickly revealed that a quadratic (Section 3.2.3.4) was an inadequate descriptor of changeover behavior. As can be seen in Figure 3-12, while the changeovers were roughly quadratic, there was significantly greater variation around the quadratic than previous research with animals (Alsop & Elliffe, 1988; Baum, 1974a; Brownstein & Pliskoff, 1968; Herrnstein, 1961) and the ETBD (McDowell et al., 2008; 2012) suggested. Those experiments consistently showed that there were more changeovers when the obtained rate of reinforcement was equal across the target classes and that – except for Herrnstein (1961) which did not plot changeovers as a function of relative reinforcement – there was a quadratic profile to the changeovers. The quadratic pattern was consistent and showed little variation around the quadratic, unlike Figure 3-12.

The quadratic equation's poor descriptive utility was highlighted by the relatively small percentages of variance it accounted for. The median percentage of variance accounted for by the exponential-bitwise-bitflip simulated creatures was only 12% (Appendix A.20). The changeovers of all five simulated creatures that had exponential selection functions and reproduced by cloning were also poorly described by the quadratic. The median percentages of variance accounted for were 28% for the exponential-clone-bitflip (Appendix B.20), 4% for the exponential-clone-pheno-uniform (Appendix C.20), 2% for the exponential-clone-pheno-linear (Appendix D.20), 6% for the exponential-clone-pheno-exponential (Appendix E.20), and 2% for the exponential-clone-pheno-Gaussian (Appendix F.20) simulated creature types. The changeover behaviors of the simulated creatures that used linear selection functions were also poorly described by the quadratic (Appendices G-L.20).

3.3.4. Post-hoc analysis of changeover profiles. The observed changeover patterns (as exemplified in Figure 3-12) differed markedly from McDowell et al.'s Figure 2 (2008). McDowell et al.'s Figure 2 showed a good fit of the quadratic with small, homoscedastic residuals. Figure 3-12, in comparison, showed the exact opposite with poor fit and heteroscedastic residuals. While the percentages of variance accounted for by the quadratic equation were not listed in McDowell et al. (2008), the differences between their Figure 2 and this experiment's Figure 3-12 suggested that that there was a major procedural difference.

The major procedural difference between this experiment and McDowell et al. (2008) was that McDowell et al. held the total scheduled rate of reinforcement constant while this experiment did not. When plotted as a 3-dimensional figure with the obtained total rate of reinforcement (i.e., R_1+R_2) added as a new axis (Figure 3-13), it is apparent that the total rate of reinforcement has a systematic effect on the changeover rate. There was an inverse relationship between changeovers and the total rate of obtained reinforcement. Note that the total rate of reinforcement axis in Figure 3-13 was reversed to enhance visual clarity.

Given the sharp rise in the number of changeovers as the total rate of reinforcement approached zero, I fitted various two-variable exponential functions (i.e., surfaces). An exponential function seemed like a natural choice because it stays relatively flat before rapidly accelerating. The exponential equation that accounted for the largest percentages of variance incorporated McDowell et al.'s (2008) quadratic but multiplied it by an exponential. This equation, a quadratic-exponential, was

$$C = (aP^2 + bP + c) \cdot 10^{-d \cdot T}, \tag{3-5}$$

where C is the number of changeovers, P is the proportion of obtained rate of reinforcement for the first target class [i.e., $R_1 / (R_1 + R_2)$], T is the total rate of obtained reinforcers (i.e., $R_1 + R_2$), and *a, b, c,* and *d* are fitted parameters.

Figure 3-14 is representative of how well this equation fits the changeover profiles of the simulated creatures. The quadratic-exponential accounted for large percentages of variance; the median percentage of variance accounted for was greater than 96% for all twelve simulated creature types (Appendices A-L.21). While generally a good descriptor, the quadratic-exponential changeover function tends to account for less changeover behavior as the mutation rate increases. Another weakness is that there are trends in the residuals, which suggests that the quadratic-exponential function is an imperfect description of changeover behavior. This trend can be observed in Figure 3-14 by the pattern of white and black dots against the total-rate-of-reinforcement axis. There is a small but systematic range at low rates of reinforcement where the actual values are above the predicted values (black dots), whereas the rest of the actual values (white dots) tend to fall below what is predicted. Overall, this pattern suggests a quadratic trend in the residuals with the quadratic peaking (black dots) at the low rate of reinforcement.

The quadratic-exponential can explain why McDowell et al. (2008) observed a quadratic despite that equation's poor fit to changeover behavior in this experiment. As part of this post-hoc analysis, McDowell et al. (2008) was replicated with an exponential-bitwise-bitflip simulated creature at 10% mutation, and its changeover behavior was plotted against the quadratic-exponential function that was fitted to that creature type (Figure 3-15). If changeovers were solely examined as a function of the proportion of reinforcement, then it would look like a quadratic, as McDowell et al. (2008) observed. The quadratic-exponential function suggests a different interpretation, however. The quadratic component of the quadratic-exponential is concave upwards in Figure 3-15 (i.e., the lowest changeover rate was at $P = 0.5$), which is the opposite direction of the quadratic proposed by McDowell et al. (2008). The slight differences in the total obtained rates of reinforcement are what causes the concave-downwards quadratic pattern (i.e., the highest changeover rate was at $P = 0.5$). The quadratic-exponential suggests that the simulated creature's changeover behavior increases because it obtains fewer reinforcers at $P = 0.5$. The quadratic pattern was observed simply because the data points rest upon the quadratic-exponential's surface in a way that appears quadratic when changeovers are narrowly viewed as a function of the proportion of reinforcement.

One of the benefits of McDowell et al.'s quadratic (2008) is its ability to characterize changeover behavior in terms of two useful quantities, namely, the maximum rate of changeovers and the range of changeovers. To maintain these conceptualizations, the equations for the two quantities, C_{Δ} and C_{Max}, (Section 3.2.3.4) had to be reevaluated for the quadratic-exponential because some of the implicit assumptions no longer held. Given the quadratic-exponential's form, the maximum rate of changeovers is predicted to occur when the total rate of obtained reinforcement is zero. It is important to note, however, that neither the quadratic nor the quadratic-exponential apply when the total rate of reinforcement is zero. This is because P becomes zero divided zero, which is undefined, and thus outside of the function's domain. Because the predicted rate of changeovers could not be evaluated when the rate of reinforcement is zero, limits were used to find the changeover function's value as it approached a total reinforcement rate of zero. There are multiple ways that the total rate of obtained reinforcers can approach zero, but the two most important cases to consider are when R_1 is 0 and R_2 is approaching 0 (case 1) and when R_1 equals R_2 and both are approaching 0 (case 2). For case 1, C_{Max} can be expressed and solved as

$$\lim_{R_2 \to 0^+} 10^{-d(0+R_2)} \cdot \left[a\left(\frac{0}{0+R_2}\right)^2 + b\left(\frac{0}{0+R_2}\right) + c\right]$$

$$= 10^{-d0} \cdot [a0^2 + b0 + c]$$

$$= 1 \cdot [0 + 0 + c]$$

$$= c$$

For case 2, C_{Max} can be expressed and solved as

$$\lim_{R \to 0^+} 10^{-d(R+R)} \cdot \left[a\left(\frac{R}{R+R}\right)^2 + b\left(\frac{R}{R+R}\right) + c\right]$$

$$= 10^{-d0} \cdot \left[a\left(\frac{1}{2}\right)^2 + b\left(\frac{1}{2}\right) + c\right]$$

$$= 1 \cdot \left[\frac{a}{4} + \frac{b}{2} + c\right]$$

$$= \frac{a}{4} + \frac{b}{2} + c.$$

Because the quadratic portion of the quadratic-exponential can be concave upwards (when the smallest value is at $P = 0.5$) or downwards (when the largest value is at $P = 0.5$), it is necessary to define C_{Max} as the greater of cases 1 and 2. Thus, C_{Max} is the greater of c and ($a/4 + b/2 + c$). This contrasts with McDowell et al.'s (2008) C_{Max}, which implicitly assumed that the quadratic was always concave downwards.

McDowell et al.'s C_Δ (2008) also had to be reinterpreted for the quadratic-exponential. The first difficulty was that C_Δ could be evaluated for both the proportion of obtained reinforcement, P, and total rate of obtained reinforcement, T, axes. The difference in the changeover rate along the obtained total reinforcement axis is trivially equivalent to C_{Max}, because the upper limit (+∞) of the exponential is zero and the lower limit is C_{Max} (Figure 3-16). Thus, it is unnecessary to use as a descriptor since C_{Max} already captures that information. Examining the function on the proportional axis when the total rate of reinforcement is held constant, however, is useful, and is also closest to McDowell et al.'s (2008) C_{Δ}. This leads to the second difficulty, which is that the difference between the minimum and maximum changeover rates changes with the total rate of reinforcement. The multiplication of the exponential and the quadratic results in the difference between the highest and lowest changeover rates exponentially increasing as the obtained reinforcer rate decreases. For example, at the zero limit of Equation 3-5 C_{Δ} would be the difference between the two C_{Max} cases, but C_{Δ} would also approach zero as Equation 3-5 approaches positive infinity. Since the absolute changeover differences on both axes are inadequate descriptors, another measure of curvature was examined.

An equation that preserves the utility of C_{Δ} while making it have the same value across the entire total-reinforcement axis is $C_{\Delta\%} = [(a + 2b) / 4c] \cdot 100\%$. This equation is simply the percentage difference between the two C_{Max} cases divided by the parameter c. The value of $C_{\Delta\%}$ is only indicative of the predicted range of changeovers when none are delivered, so it is best to consider $C_{\Delta\%}$ as the concavity of the quadratic-exponential (Equation 3-5) along the proportion of reinforcement axis instead. Positive $C_{\Delta\%}$ values indicate that the function is concave downwards – like a hill – and negative $C_{\Delta\%}$ values indicate that the function is concave upwards – like a valley. At all total rates of reinforcement $C_{\Delta\%}$ has the same value, unlike C_{Δ}. $C_{\Delta\%}$ values close to 0% indicate that the quadratic is flat, a $C_{\Delta\%}$ value of 100% indicates that the changeover rate at the center of the quadratic is twice that at P of 0 or 1, and a $C_{\Delta\%}$ value of -100% indicates that the changeover rate at the center of the quadratic is 0. This is an attractive descriptor of changeover behavior on the proportion of reinforcement axis because it describes this behavior regardless of the total rate of reinforcement.

The new C_{Max} and $C_{\Delta\%}$ descriptors of changeover behaviors provide insights into the behavior of the simulated creatures. The maximum rate of changeovers predicted for the 4 different magnitude conditions were averaged together, because they are all estimates of changeovers in the absence of reinforcement and thus reinforcer magnitude should have no effect. For all simulated creature types, the maximum rate of changeovers (C_{Max}) increases as the mutation rate increases, but there were large differences in each creature types' maximum rate of changeovers (Figures 3-17). Cloning-bitflip simulated creatures (circles) produced the highest maximum rates of changeovers, which were roughly twice that of the typically used bitwise-bitflip ETBD creatures (squares) across all mutation rates. The four phenotypic mutation methods (triangles, diamonds, and asterisks) showed dramatically lower maximum changeover rates with their highest rates of changeovers at 20% mutation being relatively close to bitwise-bitflip ETBD creatures' rate of changeovers at 5% mutation. The selection function method had no effect on maximum changeover rates, which was expected since the selection function form should have no effect in the absence or reinforcement.

The concavity of the simulated creatures' changeover behaviors ($C_{\Delta\%}$) were surprisingly consistent across selection function forms, mutation rates, and reinforcer magnitudes (Figures 3-18 and 3-19). Regardless of the selection function form, the curvatures were similar (compare Figures 3-18 and 3-19), although at the lower mutation rates there were some slight discrepancies. For example, at a 5% mutation rate the changeover profiles of the linear-clone-pheno-Gaussian simulated creatures (bottom panel of 3-19) are more concave upwards (i.e., the lowest changeover rate was at P = 0.5) than the exponential-clone-pheno-Gaussian simulated creatures (bottom panel of 3-18). The magnitude of the reinforcers had inconsistent and seemingly random effects on the concavity. The simulated creatures' changeover concavities were relatively consistent across the mutation rates except for the clone-bitflip simulated creatures, which showed a linear increase in concavity as the mutation rate increased. The linear increase in concavity of the exponential-clone-bitflip creature represents a qualitative difference in form across the mutation rates. At the lowest mutation rates the quadratic is flat or valley-like and at the highest mutation rates its hill-like; low mutation rates have the greatest rates of changeovers occurring when more reinforcers are obtained from one of the target classes and highest mutation rates have the greatest changeover rates when reinforcers are equally distributed across the two target classes. The concavities of the other creature types were consistently concave upwards (i.e., the lowest changeover rate was at $P = 0.5$) across mutation rates and reinforcer magnitudes.

3.4. Discussion

All twelve simulated creature types met the criteria for a successful simulation of human and animal behavior in concurrent RI RI and single RI environments. This supports the TNGS as an alternative to the ETBD and the matching law. While all creature types were viable, there were unique differences between the TNGS and ETBD simulated creature types. Some of these differences may help identify potential experiments that could elucidate whether the TNGS or ETBD is the better explanation for human and animal behavior.

3.4.1. Conformance to the matching law and the quantitative law of effect. The third model of the quantitative law of effect, which assumed a constant a and no bias ($c_1 = c_2$), was the best overall descriptor of ETBD and TNGS based simulated creature behavior. This model is best described as an algebraic interpretation of the modern quantitative law of effect and matching law (Equations 3-4 and 1-1, respectively). It is important to note that this model rules out the theoretical justifications for the quantitative law of effect and supports a strictly descriptive interpretation of k and c (McDowell, 2005). For example, k should be interpreted as the maximum rate of behavior within the target class given a reinforcer's magnitude. In this way, k is more related to the value of a reinforcer than it is an innate characteristic of the participant. Similarly, c is simply how many reinforcers need to be obtained before the predicted rate of behavior is half of k. The meaning of parameters a and b are unchanged with this new interpretation.

McDowell and Calvin (2015) also found that the algebraic version of the matching law was the best account, which indicates that this is a robust finding. This experiment was unable to assess a different equation that was proposed by McDowell and Calvin (2015), which permitted differences in k for each target class based on the magnitude of the reinforcers. This experiment was incapable of this assessment because no asymmetries in reinforcer magnitudes were scheduled. Figures 3-5 and 3-6, however, suggest that the McDowell and Calvin's (2015) varying k equation would be a good account since the k estimates change with reinforcer magnitude. This is especially the case with the cloning TNGS models because their k estimates also change with mutation rate. To conclusively assess whether the TNGS makes the same predictions as the ETBD it would be necessary to perform a simulation that created asymmetries of reinforcer magnitude like McDowell and Calvin (2015).

3.4.2. Parameter values. The exponent values of all ETBD creatures across the seven mutation rates met the 0.7 to 0.9 criterion, but there were notable differences between the twelve types of simulated creatures (Figure 3-4). The simulated creatures that used exponential selection function forms had exponents that were roughly 0.05 higher than those that used linear selection function forms. The exponent values of the eight simulated creature types that used cloning reproduction and phenotypic variation tended to be below the commonly estimated 0.8 exponent average for humans and animals (Baum 1974, 1979; McDowell, 1989, 2013b; Myers & Myers, 1977; Wearden & Burgess, 1982). This suggests that those creature types are less likely to be truly representative of human and animal behavior than the bitflip-bitwise and cloning-bitwise simulated creature types. Basing this conclusion on the 0.8 criterion is, however, inconclusive; a meta-analysis of human or animal performance on concurrent RI RI schedules should be conducted to determine what *a* value is representative of human and animal behavior.

The *k* parameter estimates showed a qualitative difference between the bitwise-bitflip ETBD creatures and the TNGS-based cloning creatures. The *k* values of the bitwise-bitflip simulated creatures tend to be similar regardless of the mutation rate, whereas the TNGS-based simulated creatures mostly showed a decrease in *k* values as the mutation rate increased (Figures 3-5 and 3-6). If high mutation rates are analogous to the cause of ADHD-like behavior, as Popa and McDowell (2016) suggested, then it may be possible to eliminate either the TNGS or ETBD in a critical experiment by comparing *k* parameter estimates of individuals with and without ADHD. If the average *k* value for those with ADHD is lower than for those without, then it would suggest that the TNGS is a better than the ETBD. If there is not a difference between the two groups, then it would suggest that the ETBD is a better account. An important caveat, however, is that reinforcer magnitude must be controlled across the groups because it affects *k* estimates. This would be a difficult – if not impossible – task because there may be group differences in the perceived reinforcing value of identical reinforcers. It may be possible to control for this by pairing participants diagnosed with ADHD and non-ADHD beforehand based on their relative reinforcer preferences and then comparing the groups with a matched-pairs dependent t-test. This would be suggestive but inconclusive, however, because it is possible that the same relative preferences would fail to properly account for a true difference in perceived value.

3.4.3. Changeovers. The post-hoc analysis revealed that McDowell et al.'s quadratic function (2008), despite describing changeovers when the total rate of scheduled reinforcement was constant across reinforcement schedules, is unable to generalize to experiments that vary the total rate of scheduled reinforcement. The changeover behavior of these simulated creatures is better understood by the quadratic-exponential function. That function's exponential decrease in changeover behavior as the rate of obtained reinforcers increases suggests a different purpose for changeovers than the proportional account. The proportional account suggests that participants more frequently switch between alternatives when the source of the next reinforcer is uncertain, whereas the total reinforcement account argues that participants are simply more likely to switch between target classes in the absence of reinforcement.

The qualitative differences in creature type changeover rates are helpful to understanding their behavioral dynamics. For instance, the higher maximum number of changeovers (C_{Max}) exhibited by the cloning-bitflip simulated creatures seems contradictory to it also having the highest maximum rate of behavior in the target classes – k (Figures 3-5, 3-6, and 3-17). Higher rates of changeovers typically indicate that behavior is more variable and exploratory, but the higher rates of behavior in the target class contradicts that by suggesting that behavior is more reinforcer directed. The population of potential behaviors does not seem to drift from one target class to the other as it does with bitwise-bitflip creatures. Rather, it is possible that the population of potential behaviors may be distributed across both target classes as two distinct sub populations. This is possible with clonal amplification because, unlike bitwise reproduction, cloning does not mix elements of the population to create new behaviors. To highlight this difference, if there were only two potential behaviors in the population then cloning reproduction could result in a new population of behaviors that is roughly half of the first behavior and half of the second behavior. In the same situation, bitwise reproduction would instead result in a new, variable population that contains all possible genotypic combinations of the two potential behaviors. To assess whether this is occurring, an analysis of the population of potential behaviors would have to be conducted, which would require a new simulation because that data was not recorded in this experiment. By examining the population of potential behaviors from this new simulation, it would be possible to observe how the population's density within the target classes change in reaction to environmental consequences. Simultaneously high population densities within both target classes would suggest that there are two distinct subpopulations.

The lower changeover rates of the phenotypic variation methods (Figures 3-17) indicates that those simulated creatures have prolonged bouts of behavior within the target classes relative to the bitwise-bitflip ETBD creatures. Of the phenotypic variation methods, only phenotypic Gaussian variation has been used in previous research (McDowell, 2004; McDowell & Caron, 2007). In McDowell (2004) and McDowell and Caron (2007), the standard deviation of the Gaussian was set to 25 – only half of this experiment's phenotypic standard deviation. Since the simulated creatures that used the Gaussian variation method were extremely perseverative in this experiment it suggests that the results of McDowell (2004) and McDowell and Caron (2007) should be viewed with some caution and not overgeneralized. Those experiments should be replicated with the typically used creature type – linear-bitwise-bitflip – to ensure that it also exhibits undermatching on a single alternative. This experiment suggests that this is the case, but there are important procedural differences that could influence results such as the absence of a second target class.

Another insight from the C_{Max} parameter is that the underlying populations of potential behaviors are not randomly distributed across the entire phenotype range in the absence of reinforcement. This must be the case because C_{Max} increases with the mutation rate and varies by creature type. In a population of potential behaviors that is evenly distributed across the entire phenotype range, which would be the case if the population was truly random, the probability of a behavior in the target class being emitted at each time step would be the size of the target class divided by the size of the phenotype range, which is 3.9% for a 40 phenotype-wide target class. Given that probability, it should be expected that there would be 19.6 behaviors emitted in each target class over the course of 500 time steps simply due to chance. If we also assume that the probability of the next measured behavior being in the other target class is 50% then we can calculate the expected rate of changeovers from a truly random population. This can be calculated by multiplying the probability of a changeover by the number of behaviors emitted within the target classes, which would be 19.6 changeovers per 500 time steps if the target classes are 40 phenotypes wide. Similarly, the simulated creatures that used the 50-phenotype wide target classes (those that used phenotypic variation) have an expected changeover rate of 24.4 per 500 time steps. Since most of the simulated creature types never reach the expected changeover rates, it suggests that the underlying populations of potential behaviors are distributed in many small clumps that drift across the phenotype range.

The cloning-bitflip simulated creatures are odd in that the C_{Max} estimates exceed the expected rate of changeovers at the higher mutation rates (Figures 3-17). Notably, these are also the only simulated creature types that have positive $C_{\Delta\%}$ values. Positive $C_{\Delta\%}$ values indicate that the quadratic-exponential's greatest changeover rate is when the rate of reinforcement is evenly distributed between the two target classes. It may be that the C_{Max} estimates are only greater than the expected rate, because the quadratic-exponential is inappropriately quadratic when there are no reinforcers. This intuitively seems likely – how could the distribution of reinforcement across the target classes have an effect when there are no reinforcers being delivered? Different versions of the quadratic-exponential that become flatter on the proportion dimension as it approaches zero reinforcers should be explored, and those functions should be assessed against human and animal behavior rather than against a simulation, because there are some implicit assumptions built into the simulation that may not be externally valid.

3.4.4. Conclusion. This experiment indicated that TNGS-based simulated creatures are viable models of human and animal behavior. The different behavioral dynamics of the TNGS-based simulated creatures suggest potentially fruitful directions for future research. Given the TNGS viability, it warrants further examination. The next major quantitative assessment of the ETBD was an investigation of whether it could simultaneously match its behavior to the scheduled reinforcer magnitudes and reinforcement rates (McDowell et a., 2012). Experiment 2 replicates McDowell et al. (2012) to assess whether the TNGS-based creatures can do this.

Chapter 4: Matching to Rates and Magnitudes of Reinforcement

A conceptual interpretation of the matching law is that humans and animals match their behavior to the value of that behavior's consequences (Baum, 1974; Baum & Rachlin, 1969; Killeen, 1972; Rachlin, 1971). The consequent's value can be construed as a combination of its qualities (Baum, 1974; Baum & Rachlin, 1969). The three primary qualities of the consequent that influence its value are the rate of reinforcement, the reinforcer magnitude, and the immediacy of reinforcer delivery. An expression for how these variables may be related I s

$$\frac{B_1}{B_2} = \frac{R_1}{R_2} \cdot \frac{M_1}{M_2} \cdot \frac{I_1}{I_2} \cdot \frac{X_1}{X_2} = \frac{v_1}{v_2}, \tag{4-1}$$

where *B* is the rate of behavior, *R* is the obtained rate of reinforcement, *M* is the magnitude of the reinforcer, *I* is the immediacy of reinforcer delivery, *X* is any other quality of reinforcement that affects behavior, *v* is the value of the consequent, and the subscripts indicate the target classes (Rachlin, 1971)[4].

A commonly investigated combination of those qualities is reinforcer magnitude and rate (Aparicio, Baum, Hughes, & Pitts, 2016; Davison & Hogsden, 1984; Dunn, 1982; Elliffe, Davison, & Landon, 2008; Keller & Gollub, 1977; McLean & Blampied, 2001; Schneider, 1973; Todorov, 1973; Todorov, Hanna, & Bittencourt de Sa, 1984). When Equation 4-1 is simplified to just those qualities and combined with the modern matching law (Equation 1-1), it gives the bivariate matching law (Schneider, 1973; Todorov et al., 1984) which is

$$\frac{B_1}{B_2} = b\left(\frac{R_1}{R_2}\right)^{a_R}\left(\frac{M_1}{M_2}\right)^{a_M}. \tag{4-2}$$

[4] This is presented slightly differently from its original version to highlight the equation's development into the bivariate matching equation (4-2). In the original equation the rate of behavior is expressed as the amount of time spent engaging in target class behavior. Similarly, I substituted the reinforcing magnitude – a combination of quality and quantity – for the quantity of reinforcers.

B, R, M, and the subscripts have the same meanings as in Equation 4-1. The free parameters are b, a_R, and a_M and have similar meanings as they do in the modern matching law (Equation 1-1). The exponents a_R and a_M indicate the participant's sensitivities to the rate of reinforcement and reinforcer magnitudes, respectively. This equation describes animal behavior very well (for review see Cording, McLean, & Grace, 2011), but has not been fitted to human behavior.

Cording, McLean, and Grace (2011) meta-analyzed the available data of pigeon behavior on reinforcement schedules that systematically varied both the rate and magnitude of reinforcement. This meta-analysis allowed them to find estimates of a_R and a_M that best represented pigeon behavior. This was a particularly valuable meta-analysis because the sample sizes of the six individual studies that comprised it were very small; even when combined the sample of the meta-analysis was only 25 pigeons. Cording et al. (2011) found that the average sensitivity to the rate of reinforcement – a_R – was 0.74 across all six studies, but that there were unsurprisingly large differences between the studies. The lowest study's a_R mean value was 0.47 (reanalysis of Keller & Gollub, 1977; N of 3) and the highest was 1.01 (reanalysis of Elliffe et al., 2008; N of 5). The average sensitivity to the magnitude of reinforcement – a_M – was 0.60 across the six studies and showed similar amounts of variation. The smallest average a_M value was 0.26 (reanalysis of Todorov et al., 1984; N of 2) and the largest was 0.87 (McLean & Blampied, 2001; N of 8). While the parameter estimates of the individual studies are not compelling due to their small sample sizes, the meta-analysis provides a better estimate of what a simulation of behavior should strive to observe.

The ETBD's behavior in experiments that simultaneously vary the rate and magnitude of reinforcement has already been assessed (McDowell et al., 2012). The behavior of the linear-bitwise-bitflip ETBD simulated creatures was most like those found in Cording et al.'s (2011) meta-analysis for the mutation rate range of 7.5% through 14%. Within that mutation range, the fits to the simulated behavior lacked residual trends, which Cording et al. (2011) had also found. While less emphasized, the ETBD's behavior was very well described by Equation 4-2, which accounted for 99% of the variance on average.

The exact criteria for a successful simulation of behavior in this type of experiment were not clearly defined by McDowell et al. (2012). Their analysis emphasized residual trends and bivariate matching law (Equation 4-2) parameter values, but did not delineate a range of viable parameter values *a priori*. For this experiment, a range of plus or minus 0.1 from the parameter estimates found by Cording et al. (2011) was used as the viability criterion for the simulated creatures. This gives parameter criteria of 0.65 to 0.85 for a_R values and 0.5 to 0.7 for a_M values, which must be met simultaneously. The plus or minus 0.1 range was chosen because it was consistent with Experiment 1 and because it also considered the uncertainty of the parameter values that were found in Cording et al.'s (2011) meta-analysis. The third criterion of this experiment was that Equation 4-2 accounted for a large percentage of variance, as was found by Cording et al. (2011). No residual trend criterion was used for this simulation, because Cording et al. (2011) only found no residual trend when they removed a study from the meta-analysis – Elliffe et al. (2008) – and because they could only assess for a quadratic trend.

4.1. Methods

4.1.1. Participants. The same twelve creature types that were used in Experiment 1 (Table 3-1) were simulated, but over a wider range of mutation rates. Mutation rates of 0.5%, 1%, 2.5%, 5%,7.5%, 10%, 12.5%, 15%, 17.5%, 20%, 25%, 30%, 35%, 40%, 45%, and 50% were simulated for the TNGS-based creatures. A smaller mutation rate range of 5%, 7.5%, 10%, 12.5%, 15%, 17.5%, 20%, 25%, 30%, 35%, 40%, 45%, and 50% was used for the bitwise-bitflip ETBD creatures because they were unable to complete the simulations at the lower mutation rates of 0.5%, 1%, and 2.5%. At each mutation rate, 10 creatures were simulated, and each simulated creature's behavior was observed as it engaged with 25 concurrent RI RI schedules for 20,500 time steps. This resulted in 8,200,000 behaviors (16 mutation rates • 10 creatures • 25 conditions • 20,500 generations of behavior) being observed for the simulated creature types that used cloning reproduction, and 6,662,500 behaviors (13 mutation rates • 10 creatures • 25 conditions • 20,500 generations of behavior) for those that used bitwise reproduction. In total, this experiment represents 83,325,000 simulated behaviors and 1,860 simulated creatures

4.1.2. Procedures. Concurrent RI RI schedules were simulated that used the same target classes as Experiment 1, but different reinforcement rates and magnitudes. The schedule design was identical to phase 3 of McDowell, Popa, and Calvin (2012). Twenty-five schedules were constructed to systematically sample the reinforcement and reinforcer magnitude dimensions (Table 4-1). These 25 schedules are all possible combinations of five pairs of reinforcer magnitudes – 15 & 90, 34 & 71, 52 & 52, 71 & 34, and 90 & 15 – and five pairs of reinforcement rates – RI 15 RI 180, RI 56 RI 139, RI 98 RI 98, RI 139 RI 56, and RI 180 RI 15. Since the reinforcer magnitudes are in terms of the mean values assigned to the simulated creatures' selection fitness density function (Section 2.1.2), the values are inversely related to their effects; a small fitness density function mean represents a stronger reinforcer than a large fitness density function mean.

4.1.3. Analyses

4.1.3.1. Data pooling and averaging. Simulated behavior during the first 500 time steps of each schedule were excluded from analyses to assess each simulated creature type's steady-state behavior rather than behavior during transition. Observed reinforcement and behavior frequencies during the remaining 20,000 time steps were divided by 500 time steps to create rates of reinforcement and behavior. These rates were then averaged across simulated creatures of the same type as a precaution against individual creatures becoming stuck in unrepresentative local minima. In summary, each data point represents 200,000 behaviors from 10 simulated creatures.

4.1.3.2. Bivariate matching law equation. The log transformed version of the bivariate matching law was fitted to the 25 averaged data points at each mutation rate. The fitted equation was

$$\log\left(\frac{B_1}{B_2}\right) = a_R \cdot \log\left(\frac{R_1}{R_2}\right) + a_M \cdot \log\left(\frac{F_2}{F_1}\right) + \log(b). \tag{4-2′}$$

In this equation, B is the observed rate of behavior, R is the obtained rate of reinforcement, F is the scheduled fitness density function mean, the numerical subscripts indicate the target class, and a_R, a_M, and b are free parameters. The fitness density function means were substituted for reinforcer magnitudes because that is the equivalent measure of reinforcer magnitude for this type of algorithm. The fitness density function mean ratio is also inverted – relative to the magnitude expression in Equation 4-2 – because the scheduled fitness density function means are inversely related to reinforcer strength. For example, a fitness density function mean of 15 is stronger than 180. This equation was fitted using OLS.

4.2. Results

The behaviors of the twelve creature types were well described by the bivariate matching law (Equation 4-2′). The median percentages of variance accounted for by the bivariate matching law were above 98% for all creature types (Appendix M). The smallest percentage of variance accounted for was 94%, which was when the equation was fitted to the linear-cloning-pheno-Gaussian creature type's behavior at the 0.5% mutation rate. Although the behavior of the creature types was well described by the bivariate matching law, the fitted parameter values did not meet the simulation's criteria for a viable account.

The simulated creature types that used an exponential selection function generally had sensitivity to magnitude exponent values that were below criteria. Only the exponential-bitwise-bitflip ETBD creatures met the criteria – albeit marginally. In the mutation rate rage of 5% to 12.5%, the sensitivity to rate was at the upper limit of its criterion – 0.85 – while the sensitivity to magnitude was at the lower limit of its criterion – 0.5 (Figure 4-1). All TNGS-based simulated creatures that used exponential selection had sensitivities to magnitude that were below its lower bound criterion of 0.5 (Figures 4-2, 4-3, 4-4, 4-5, and 4-6). The sensitivities to the rate of reinforcement found in this study corroborated those found in Experiment 1. In summary, the only viable simulated creature type that used exponential selection was the exponential-bitwise-bitflip ETBD creature type within the mutation rate range of 5% to 12.5% and it barely met the criteria within that range.

The simulated creatures that used linear selection functions tended to be more viable. The linear-bitwise-bitflip ETBD creature type's behavior met viability criteria for the mutation rate range of 5% to 20% (Figure 4-7). The parameter values of its behavior at 15% mutation were almost an exact match to those estimated by Cording et al. (2011). The linear-cloning-bitflip TNGS creature type's behavior met criteria in the mutation rate range of 2.5% to 15% (Figure 4-

8). In some ways the parameter values of these simulated creatures better approximate Cording et al. (2011) than linear-bitwise-bitflip ETBD creatures because the estimated parameter values are closer to those found in the meta-analysis across a wider range of mutation rates. However, the lack of a_R and a_M variability may be a double-edged sword; if a new meta-analysis found that the a_M value should be greater than Cording et al. (2011) suggested then there is very little leeway for it to match that meta-analysis because a_M seems to be capped at 0.60 for the linear-cloning-bitflip TNGS creature type. Cloning reproduction with phenotypic variation only produced patterns of behavior that matched Cording et al. (2011) at very specific mutation rates, which suggests that they are unlikely to be viable models of behavior. Linear-cloning-pheno-linear TNGS creatures met criteria at the mutation rates of 1% and 2.5% (Figure 4-10), which is very limited. The flatter phenotypic variation forms – uniform and Gaussian – were even more restrictive and only met criteria at the mutation rate of 2.5% (Figures 4-9 and 4-12). The steepest variation function – exponential – did not meet criteria at any mutation rate (Figure 4-11).

4.3. Discussion

These results indicate that both the ETBD and TNGS are viable accounts for behavior on concurrent schedules when the rate and magnitude of reinforcement are varied, but that the TNGS is more limited. If the viable creature types are listed in order of viability, then the order would be linear-bitwise-bitflip, linear-clone-bitflip, and exponential-bitwise-bitflip. Given the criteria, linear-bitwise-bitflip ETBD creatures and linear-clone-bitflip TNGS creatures seem equally likely to represent human and animal behavior because they meet the criteria for a wide range of mutation rates, but linear-bitwise-bitflip has a slight edge because it can meet a wider range of possible a_M values. The exponential-bitwise-bitflip ETBD creature type meets the criteria but is unlikely to represent animal behavior because there is a larger difference between the a_R and a_M values than Cording et al.'s meta-analysis suggests (2011). A few of the simulated creatures that used linear selection and phenotypic variation had very small regions of viability, but these are so restricted that they are unlikely to be representative of human and animal behavior. Overall, the TNGS is less likely to represent human and animal behavior than the ETBD. Only one of the ten TNGS-based models met the criteria for a successful simulation of behavior, whereas all of the ETBD-based models did. This suggests that the ETBD is a more robust account of behavior than the TNGS

This simulation identified two major algorithmic requirements for simulated behavior to match human and animal behavior in concurrent RI RI schedules that vary the rate and magnitude of reinforcement. The first of these requirements is that behaviors must be represented as a series of bits and cannot be only represented by phenotypes. This was evidenced by all creature types that used phenotypic variation methods being unable to compellingly simulate pigeon behavior because the a_M parameter estimates were too low. This is a robust finding; four different phenotypic variation alternatives were examined and they all had the same flaw. So why is phenotypic variation such a poor account? By combining cloning reproduction and phenotypic variation behaviors are solely expressed as phenotypes. This changes the nature of the process the algorithm uses to find a behavioral solution to the environment in a way that makes it more like a hill-climbing algorithm than a genetic algorithm. Hill-climbing algorithms systematically vary each of the parameters on a single dimension until they find a maximum. Genetic algorithms – like the ETBD – instead vary the parameters multidimensionally. It does this because each bit of the genotype can be thought of as a separate dimension to solving the problem of the environment. This means that the genotype can be thought of as representing the problem space as a hypercube with the number of sides equaling the number of bits (Whitley, 1994). By searching the environmental problem space multidimensionally, the simulated creature types that represent behaviors with genotypes may be far more adaptive than anything that relies on a purely phenotypic approach.

The second algorithmic requirement is that the form of the selection function be linear. The linear selection function form is preferable to the exponential, because it results in greater sensitivities to magnitude and lower sensitivities to the rate reinforcement (for example compare Figures 4-1 and Figure 4-7). This combination of effects makes the simulated creature's behavior better approximate pigeon behavior on concurrent RI RI schedules that vary the reinforcer rates and magnitudes. Since there is a difference between exponential and linear selection functions, it may be informative to investigate the performance of the third type of selection function form, which is uniform (Figure 2-2). If the selection function's slope has a systematic effect, then it may be that a uniform selection function form could raise the sensitivity to magnitude even higher than the linear selection function.

A major limitation of this experiment is that the basis for the criteria are not as strongly supported as they were for Experiment 1. The criteria of this study may be flawed because they are based solely on pigeon behavior, which is the only animal that Equation 4-2 has been evaluated with. This poses a significant risk to this experiment's conclusions; if there are species specific differences to magnitude sensitivities or to certain types of reinforcers, then the a_M criterion range that was used in this experiment is not warranted. The behavior of a wider range of species on schedules that simultaneously vary rate and magnitude of reinforcement needs to be explored.

4.3.1. Conclusion. This simulation provided limited support for the TNGS as a viable account of behavior in environments in which the rate and magnitude of reinforcement are simultaneously varied. The phenotypic variation versions of the TNGS were all rejected as accounts of behavior, because the estimated sensitivity to magnitude exponents – a_M – were too low. ETBD-based simulated creatures were more robustly able to produce patterns of behavior that were like animals in environments in which the rate and magnitude of reinforcement are simultaneously varied. The number of possible algorithms was also significantly reduced by this study because it identified the necessity of the linear selection function form. Given the successes of the linear-cloning-bitflip TNGS simulation, the behavioral dynamics of that model should be further explored.

Chapter 5: General Discussion

A version of the TNGS was found to be a viable account for human and animal behavior inasmuch as the simulations were valid. The only version of the TNGS that met criteria in both Experiments 1 and 2 used a linear-clone-bitflip algorithm. The other nine versions of the TNGS failed to meet criteria in Experiment 2. While there is a version of the TNGS that met criteria, the overall failure of the TNGS-based simulated creatures suggests that it is not as robust an explanation as the ETBD. Since a version of the TNGS is viable, however, it suggests that the critiques of its dynamics (Crick, 1989; Fernando, Karishma, & Syathmary, 2008; Fernando, Goldstein, & Syathmary, 2010; Fernando, Szathmary, & Husbands, 2012) may have been premature.

While Experiments 1 and 2 provided support for the linear-clone-bitflip algorithm, more studies need to be conducted that focus on its behavioral dynamics. Experiments 1 and 2 examined long-term steady state behavior, which is important, but short-term patterns of behavior like response bouts and how behavior changes immediately following reinforcement also need to be investigated. Kulubekova and McDowell (2008; 2013) investigated these dynamics with the ETBD in a pair of studies. They found that the behavior predicted by the ETBD is like humans and animals. It would be informative to replicate these two studies with the TNGS-based linear-cloning-bitflip simulated creature type to determine if it is also a viable account.

A novel finding of Experiment 1 was the quadratic-exponential function that describes changeover behavior. This equation was preferable to McDowell et al.'s proportion of reinforcement equation (2008), because that equation fails to adequately describe changeover behavior when the total rate of reinforcement varies. To the extent that the simulation is externally valid, the exponentially decreasing rate of changeovers as the total rate of reinforcement increases suggests that human and animal changeover behavior could be controlled by the overall reinforcement rate of the environment more than the uncertainty of the next reinforcer.

It seems unlikely, however, that the quadratic-exponential that was found in Experiment 1's simulation can be generalized to other circumstances, because the experiment's design lacks external validity. It seems more likely that the quadratic-exponential function is simply an artifact of the simulation's design rather than a true prediction of the theory. One reason why it seems unlikely is that the expected C_{Max} estimates depend on the size of the target classes, which is an arbitrary element of the simulation. As was discussed in Experiment 1, the expected changeover rates of a truly random population of behaviors are 20 for genotypic mutation methods and 25 for phenotypic mutation methods per 500 time steps. This probability is much higher than what is typically observed with humans or animals in the absence of scheduled reinforcement. Making the simulated target classes smaller relative to the phenotype range could correct for this, but there are other issues that limit the simulation's external validity.

Experiment 1's design does not account for unmeasured behaviors being reinforced. By only defining two reinforcing target classes within the simulation, the experimental design implicitly suggests that these are the *only* reinforcing events during a concurrent RI RI experiment, which is not true of the real world. In the absence of reinforcers provided by the experimenter, humans and animals will seek out other sources of reinforcement. Even in the highly controlled situation of a Skinner box, an animal can sleep, scratch an itch, explore the box, or engage in any other behavior that is intrinsically reinforcing. Appropriately simulating these alternative behaviors and their consequences would reduce the observed maximum changeover rates when the rate of reinforcement is low because the simulated creatures would allocate their behavior towards those alternatives instead. This would improve the simulations' external validity but would likely invalidate the quadratic-exponential account of changeover behavior.

A novel approach to assess the TNGS to the ETBD would be to determine parameter values that describe a participant's behavior and then see if it can predict that same participant's behavior in the future. Li, Elliffe, and Hautus (2018) recently developed a method for determining parameter values for the ETBD that correspond to a participant's behavior. If the parameter values that are found from this approach can predict future behavior, then the theories' predictions could be strongly compared. After finding optimal parameters for both theories, a participant's behavior could be predicted in a novel environment and then later compared with the participant's actual behavior when they engage with that environment. The theory that better predicts future behavior would be the stronger theory.

The ability to determine parameter values for individuals and predict their future behavior also has numerous potential clinical applications. If future behavior can be predicted from these algorithms, then the effects of behaviorally-focused therapies could be assessed prior to implementing them with a client. After developing a case conceptualization of the problem, the therapist could have the client work on a concurrent schedule that would be used to determine parameter values that describe their behavior. The therapist could then use the ETBD algorithm to predict how that client's behavior may change in response to treatments. By selecting the simulated therapeutic approach that predicted the desired changes to the client's behavior it may be possible to tailor the treatment to the patient and, thus, achieve better treatment outcomes.

Another opportunity for this type of simulation work to be applied to clinical treatment is just-in-time adaptive interventions (Berardi et al., 2018). Just-in-time adaptive interventions are computer programs that are designed to recognize detrimental changes in patient behavior and correct them before they become a larger problem (Nahum-Shani, Hekler, & Spruijt-Metz, 2015; Spruijt-Metz & Nilsen, 2014; Spruijt-Metz et al., 2015). These programs work with computers, laptops, or mobile phones and have the client frequently report on their behavior. A strong emphasis is placed on the dynamics of behavior, which the ETBD is particularly well suited to because – unlike the matching law – it is a dynamic model of behavior. Some preliminary work with the ETBD has already been conducted to see how well it could suit this function (Berardi et al., 2018), but the implementation of the theory in that study was novel. Berardi et al. (2018) implemented the ETBD by using an odd version of cloning reproduction, which makes that simulation more akin to the TNGS. However, they did not directly replicate behaviors as this study did, but rather used a complicated Gaussian-kernelling method to create population distributions that were then used to generate the next generation of potential behaviors. The authors never explained why they decided to implement the ETBD this way and there were numerous other oddities in its design, but this preliminary work suggests that there are potential clinical applications to this type of intervention.

In summary, limited support was found for the TNGS but it was not as robustly supported as the ETBD. All versions of the TNGS were viable accounts of behavior on concurrent RI RI and single RI schedules, but only one version of the TNGS was a viable account of matching to simultaneously varying rates of reinforcement and reinforcer magnitude. The dynamics of the only viable version of the TNGS need to be further assessed by replicating Kulubekova and McDowell (2008; 2013). Future studies should also emphasize the clinical utility of these simulations. By pursuing these projects, the TNGS may become better supported as an account of human and animal behavior.

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EQUATION SUMMARY

EQUATION SUMMARY

Matching Law and Theory

Theoretical Equations

Equation 3-1: The classic matching law (pg. 34) $$\frac{B_1}{B_1+B_2} = \frac{R_1}{R_1+R_2}$$

Equation 1-1: The modern matching law (pg. 2) $$\frac{B_1}{B_2} = b\left(\frac{R_1}{R_2}\right)^a$$

Equation 3-2: The classic quantitative law of effect (pg. 34) $$B_i = \frac{kR_i}{R_i+r_e}$$

Equation 3-3: The modern quantitative law of effect (pg. 35) $$B_i = \frac{kR_i{}^a}{R_i{}^a+\frac{r_e^a}{b_i}}$$

Equation 3-4: The modern quantitative law of effect w/ *c* (pg. 35) $$B_i = \frac{kR_i{}^a}{R_i{}^a+c}$$

Fitted Equations

Equation 1-1′: Log-transformed modern matching law (pg. 43)

$$\log\left(\frac{B_1}{B_2}\right) = a \cdot \log\left(\frac{R_1}{R_2}\right) + \log\left(\frac{c_2}{c_1}\right)$$

Equation 3-4a′: Modern quantitative law of effect to the first target class (pg. 43)

$$B_1 = k\left(\frac{c_1}{R_1^a} + \frac{c_1R_2^a}{c_2R_1^a} + 1\right)^{-1}$$

Equation 3-4b′: Modern quantitative law of effect to the second target class (pg. 43)

$$B_2 = k\left(\frac{c_2}{R_2^a} + \frac{c_2R_1^a}{c_1R_2^a} + 1\right)^{-1}$$

B = Observed rate of behavior

R = Rate of obtained reinforcement

a = Sensitivity to reinforcement

b = Bias

b_i = Bias towards the target class

k = Maximum rate of behavior

r_e = Extraneous Reinforcement

c = Composite parameter

subscripts = Target class specifiers

Note: Variables identified by uppercase are manipulated or observable, whereas variables identified by lowercase are estimated free parameters.

Concurrent RI RI Changeover Profiles

Unlabeled Equation: Quadratic changeovers (pg. 49)

$$C = (aP^2 + bP + c)$$

Equation 3-5: Quadratic-exponential changeovers (pg. 57)

$$C = (aP^2 + bP + c) \cdot 10^{-d \cdot T}$$

P = Proportion of reinforcement [i.e., $R_1/(R_1+R_2)$]

T = Total rate of reinforcement (i.e., R_1+R_2)

a, b, c, & d = Free parameters

Bivariate Matching Law

Theoretical Equations

Equation 4-1: Multivariate matching law (pg. 69) $$\frac{B_1}{B_2} = \frac{R_1}{R_2} \cdot \frac{M_1}{M_2} \cdot \frac{I_1}{I_2} \cdot \frac{X_1}{X_2} = \frac{v_1}{v_2}$$

Equation 4-2: Bivariate matching law (pg. 69) $$\frac{B_1}{B_2} = b\left(\frac{R_1}{R_2}\right)^{a_R}\left(\frac{M_1}{M_2}\right)^{a_M}$$

Fitted Equation

Equation 4-2′: Log-transformed bivariate matching law (pg. 73)

$$\log\left(\frac{B_1}{B_2}\right) = a_R \cdot \log\left(\frac{R_1}{R_2}\right) + a_M \cdot \log\left(\frac{F_2}{F_1}\right) + \log(b)$$

B = Observed rate of behavior

R = Rate of obtained reinforcement

M = Reinforcer magnitude

I = Immediacy of reinforcement

X = Any other quality of reinforcement

F = Mean of the fitness density function

v = Value of the reinforcer

a_R = Sensitivity to the rate of reinforcement

a_M = Sensitivity to the reinforcer magnitude

b = Bias

subscripts = Target class specifiers

FIGURES AND TABLES

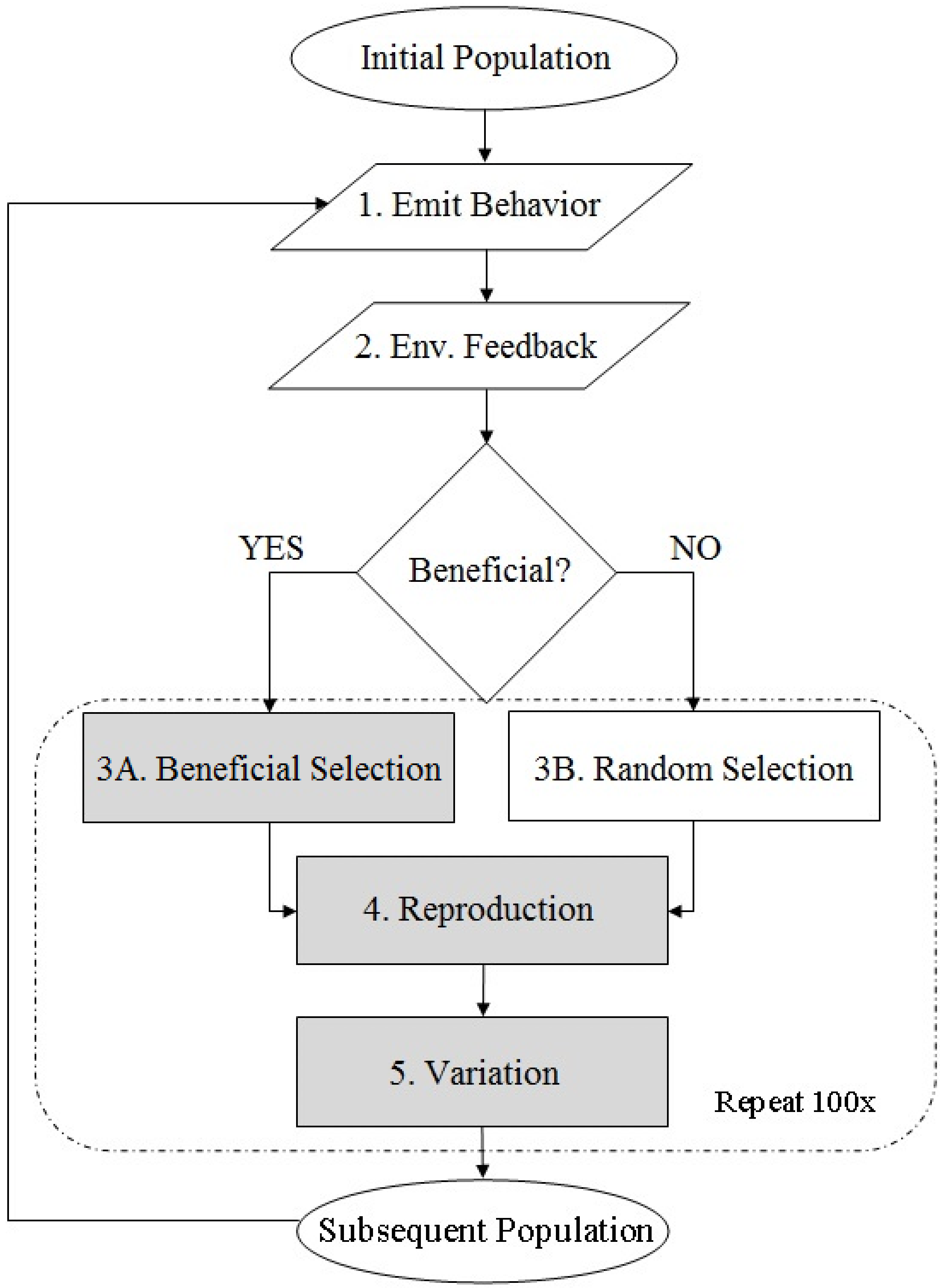


Figure 2-1. Flowchart of how the ETBD creates new generations of behaviors

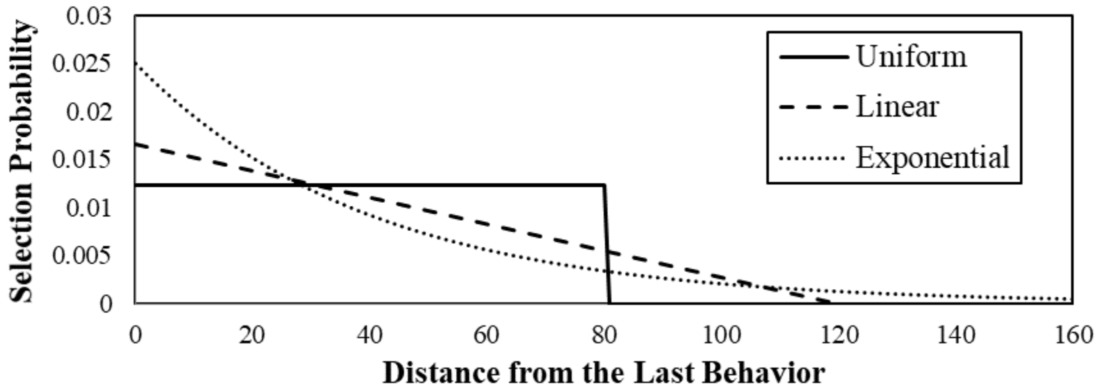
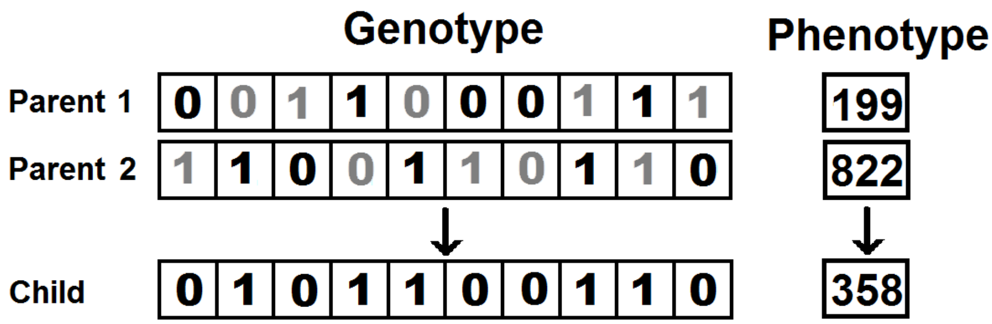


Figure 2-2. Continuous probability density function forms with means of 40



Note: The bolded 0s and 1s were randomly selected from the two parents to create the new child behavior.

Figure 2-3. The bitwise method of reproduction

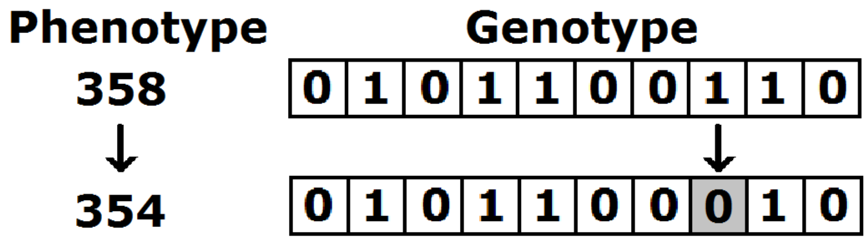


Figure 2-4. The bitflip-by-individual variation method

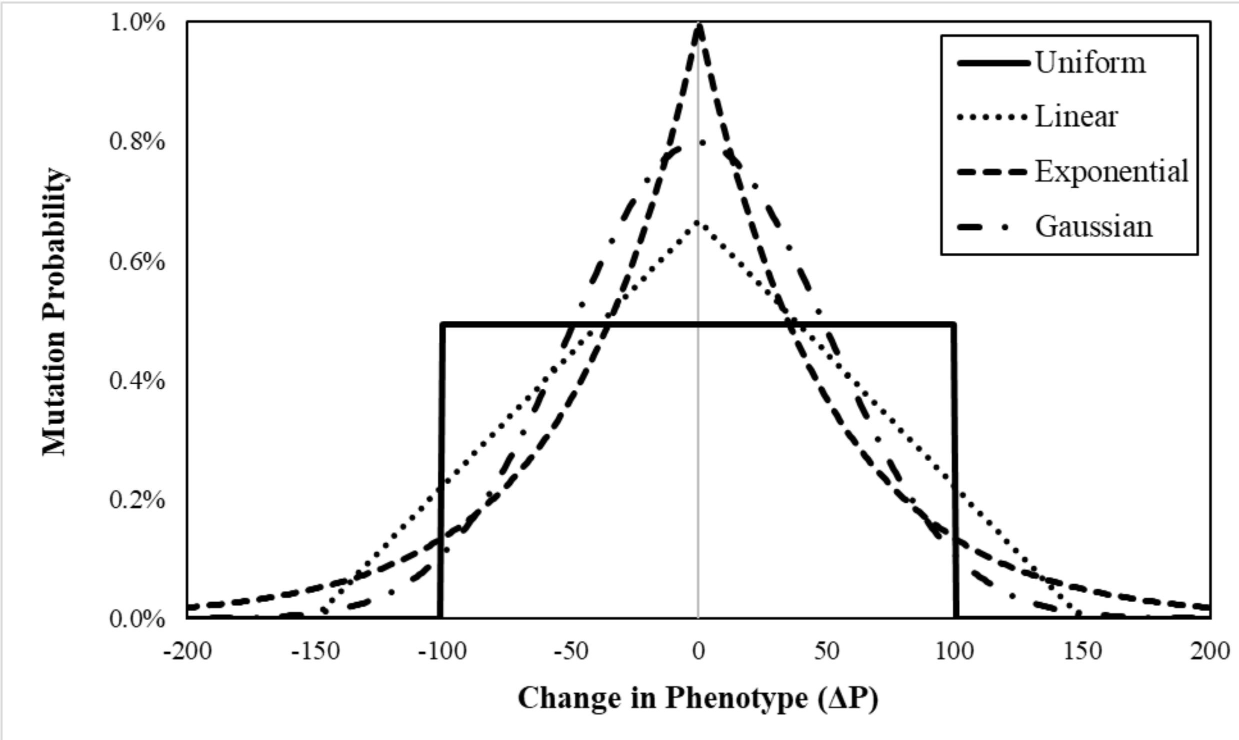


Figure 2-5. Plots of the probability density functions of phenotypic variation methods

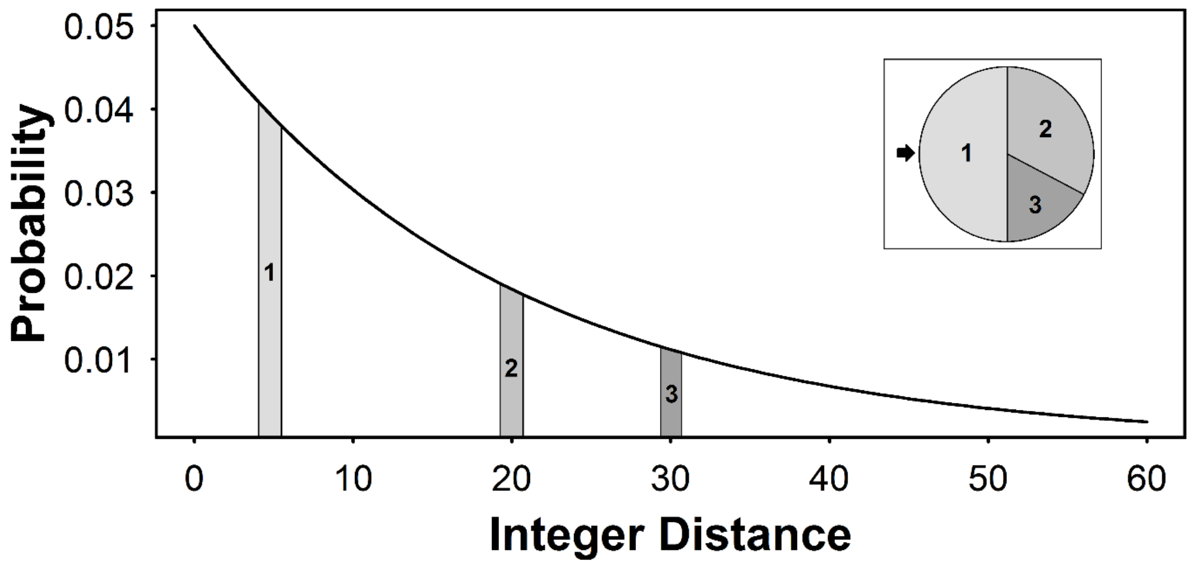


Figure 2-6. A simplified example of roulette-wheel selection

Table 3-1.

The Twelve Simulated Creature Types

	Algorithm Methods		
Abbreviated Creature Names	Selection	Reproduction	Variation
ETBD-based			
Linear-Bitwise-Bitflip	Continuous Linear[a]	Bitwise[c]	Bitflip-by-Individual[e]
Exponential-Bitwise-Bitflip	Continuous Exponential[a]	Bitwise[c]	Bitflip-by-Individual[e]
TNGS-based (Genotypic)			
Linear-Clone-Bitflip	Roulette-Continuous Linear[b]	Cloning[d]	Bitflip-by-Individual[e]
Exponential-Clone-Bitflip	Roulette-Continuous Exponential[b]	Cloning[d]	Bitflip-by-Individual[e]
TNGS-based (Phenotypic)			
Linear-Clone-Pheno-Uniform	Roulette-Continuous Linear[b]	Cloning[d]	Uniform Continuous[f]
Linear-Clone-Pheno-Linear	Roulette-Continuous Linear[b]	Cloning[d]	Linear Continuous[f]
Linear-Clone-Pheno-Exponential	Roulette-Continuous Linear[b]	Cloning[d]	Exponential Continuous[f]
Linear-Clone-Pheno-Gaussian	Roulette-Continuous Linear[b]	Cloning[d]	Gaussian Continuous[f]
Exponential-Clone-Pheno-Uniform	Roulette-Continuous Exponential[b]	Cloning[d]	Uniform Continuous[f]
Exponential-Clone-Pheno-Linear	Roulette-Continuous Exponential[b]	Cloning[d]	Linear Continuous[f]
Exponential-Clone-Pheno-Exponential	Roulette-Continuous Exponential[b]	Cloning[d]	Exponential Continuous[f]
Exponential-Clone-Pheno-Gaussian	Roulette-Continuous Exponential[b]	Cloning[d]	Gaussian Continuous[f]

[a] Section 2.1.2
[b] Section 2.2.3
[c] Section 2.1.3
[d] Section 2.2.1
[e] Section 2.1.4
[f] Section 2.2.2

Table 3-2.

Scheduled random-interval means of the two reinforcing target classes

Schedule Number	Target Class 1	Target Class 2	Schedule Number	Target Class 1	Target Class 2
1	2.50	2.50	27	13.33	10.00
2	2.50	3.33	28	13.33	13.33
3	2.50	5.00	29	13.33	20.00
4	2.50	10.00	30	13.33	40.00
5	3.33	2.50	31	20.00	5.00
6	3.33	3.33	32	20.00	6.67
7	3.33	5.00	33	20.00	10.00
8	3.33	10.00	34	20.00	13.33
9	5.00	2.50	35	20.00	20.00
10	5.00	3.33	36	20.00	26.67
11	5.00	5.00	37	20.00	40.00
12	5.00	6.67	38	20.00	80.00
13	5.00	10.00	39	26.67	20.00
14	5.00	20.00	40	26.67	26.67
15	6.67	5.00	41	26.67	40.00
16	6.67	6.67	42	26.67	80.00
17	6.67	10.00	43	40.00	10.00
18	6.67	20.00	44	40.00	13.33
19	10.00	2.50	45	40.00	20.00
20	10.00	3.33	46	40.00	26.67
21	10.00	5.00	47	40.00	40.00
22	10.00	6.67	48	40.00	80.00
23	10.00	10.00	49	80.00	20.00
24	10.00	13.33	50	80.00	26.67
25	10.00	20.00	51	80.00	40.00
26	10.00	40.00	52	80.00	80.00

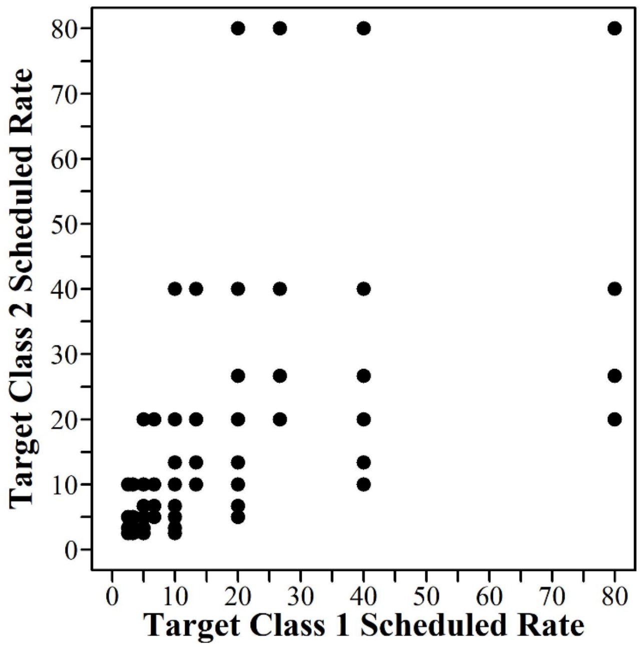


Figure 3-1. Scatterplot of scheduled reinforcement rates

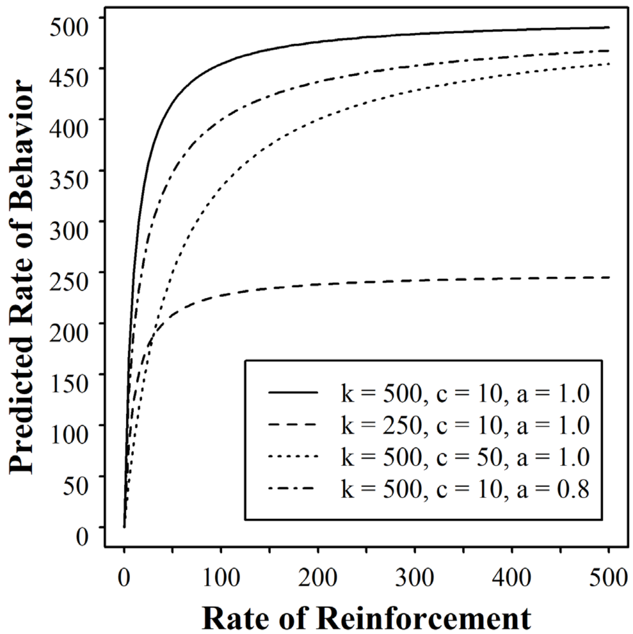


Figure 3-2. Effects of the parameters *k*, *c*, and *a* on the predicted rate of behavior

Table 3-2.

Model parameter restrictions

Model	Description	Parameters	a	k	c_1	c_2
1	Modern Algebraic	16	*	*	*	*
2	Modern Algebraic w/ No Bias	12	*	*	*	E
3	Modern Algebraic w/ Constant Exponent	9	C	*	*	E
4	Modern Algebraic w/ Constant k	6	C	C	*	E
5	Modern Response Strength	3	C	C	C	E
6	Classic Algebraic	8	1	*	*	E
7	Classic Algebraic w/ Constant k	5	1	C	*	E
8	Classic Response Strength	2	1	C	C	E

* = Varies with each magnitude pair, C = Constant across magnitude pairs, E = equal to c_1 at each magnitude pair, and a specific value means that is what the value is set to across all magnitude pairs

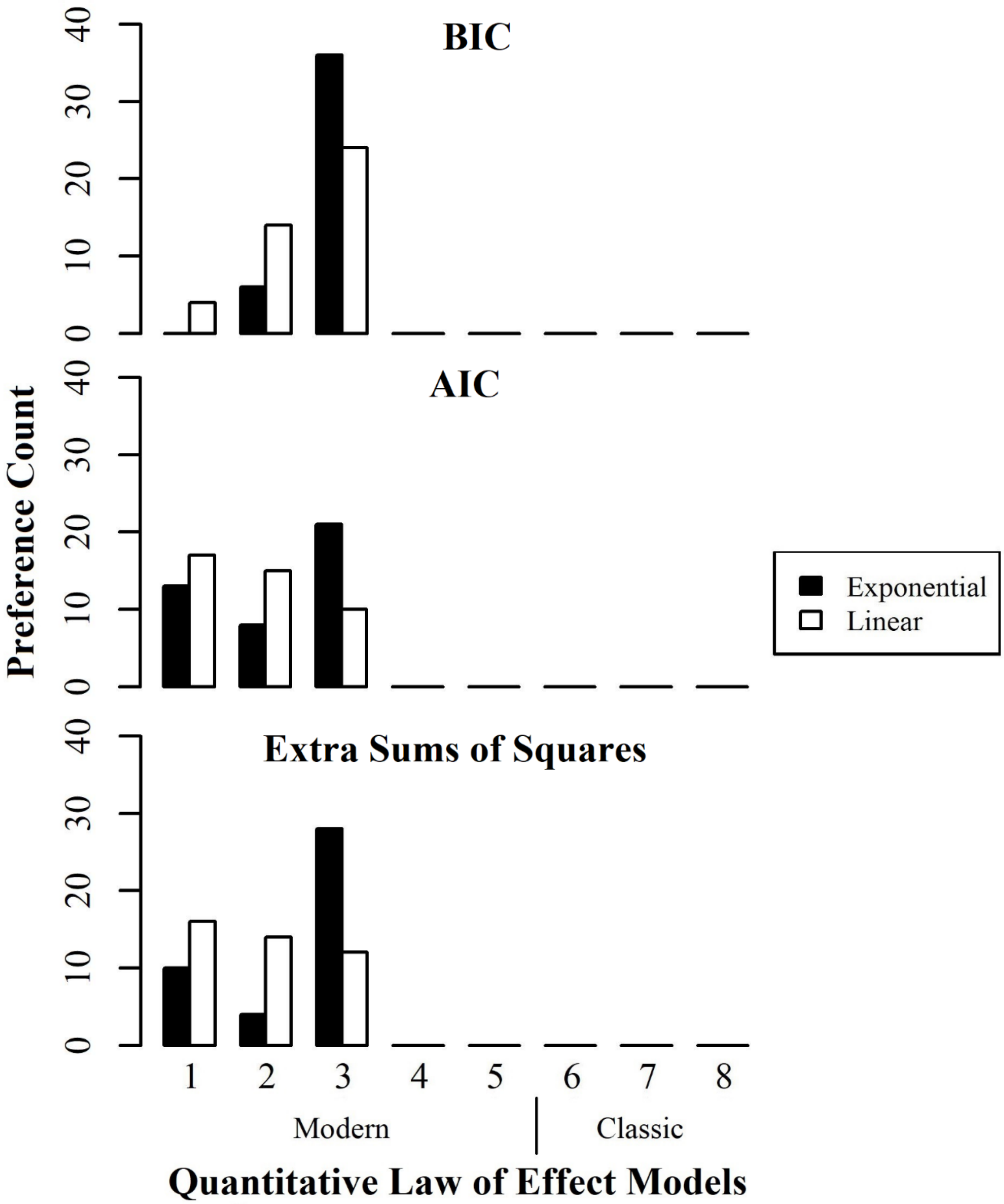


Figure 3-3. Summary of model preferences by the BIC, AIC, and extra sums of squares difference tests

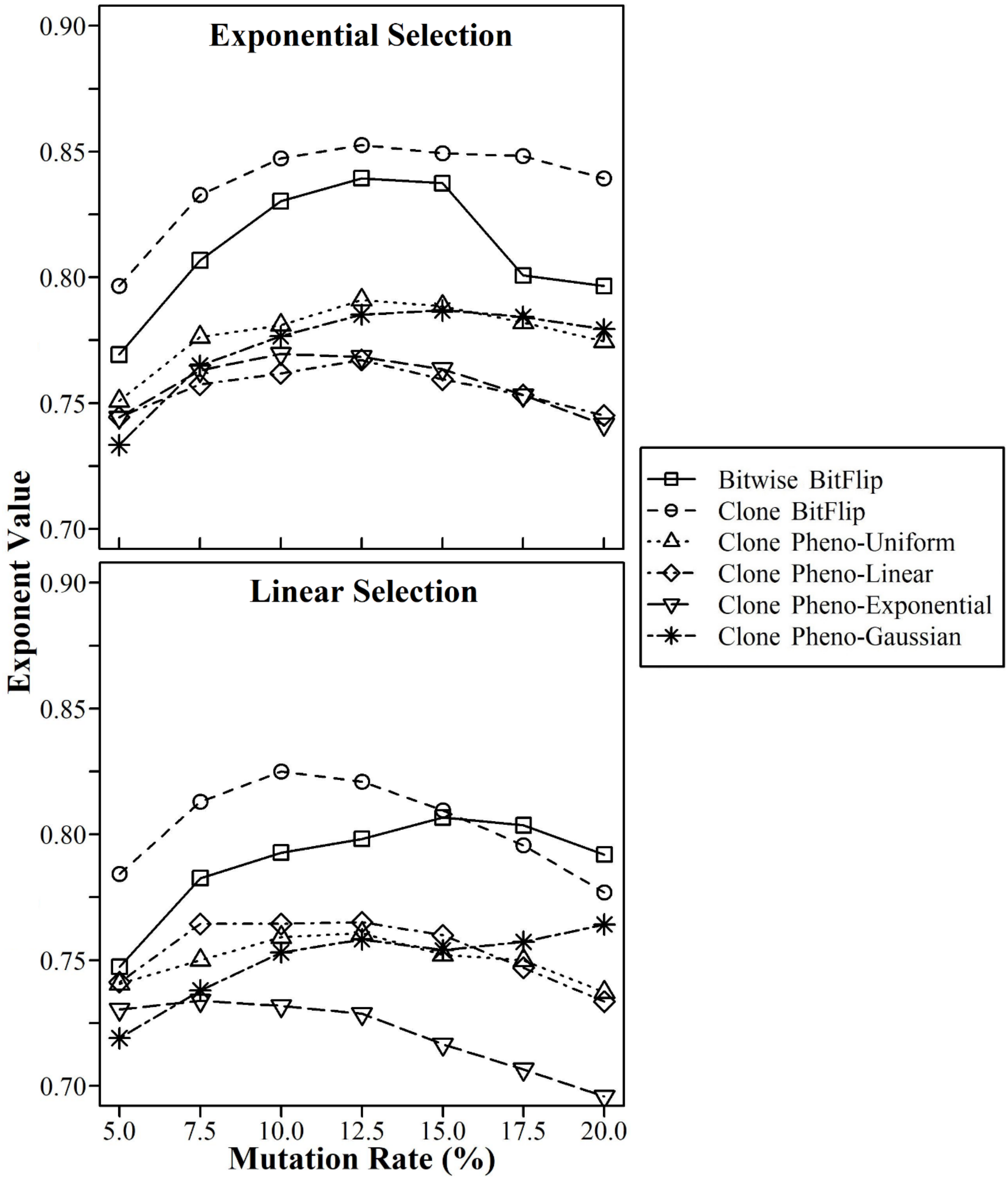


Figure 3-4. Exponent (*a*) parameter values of model 3 fits to simulated creature behavior

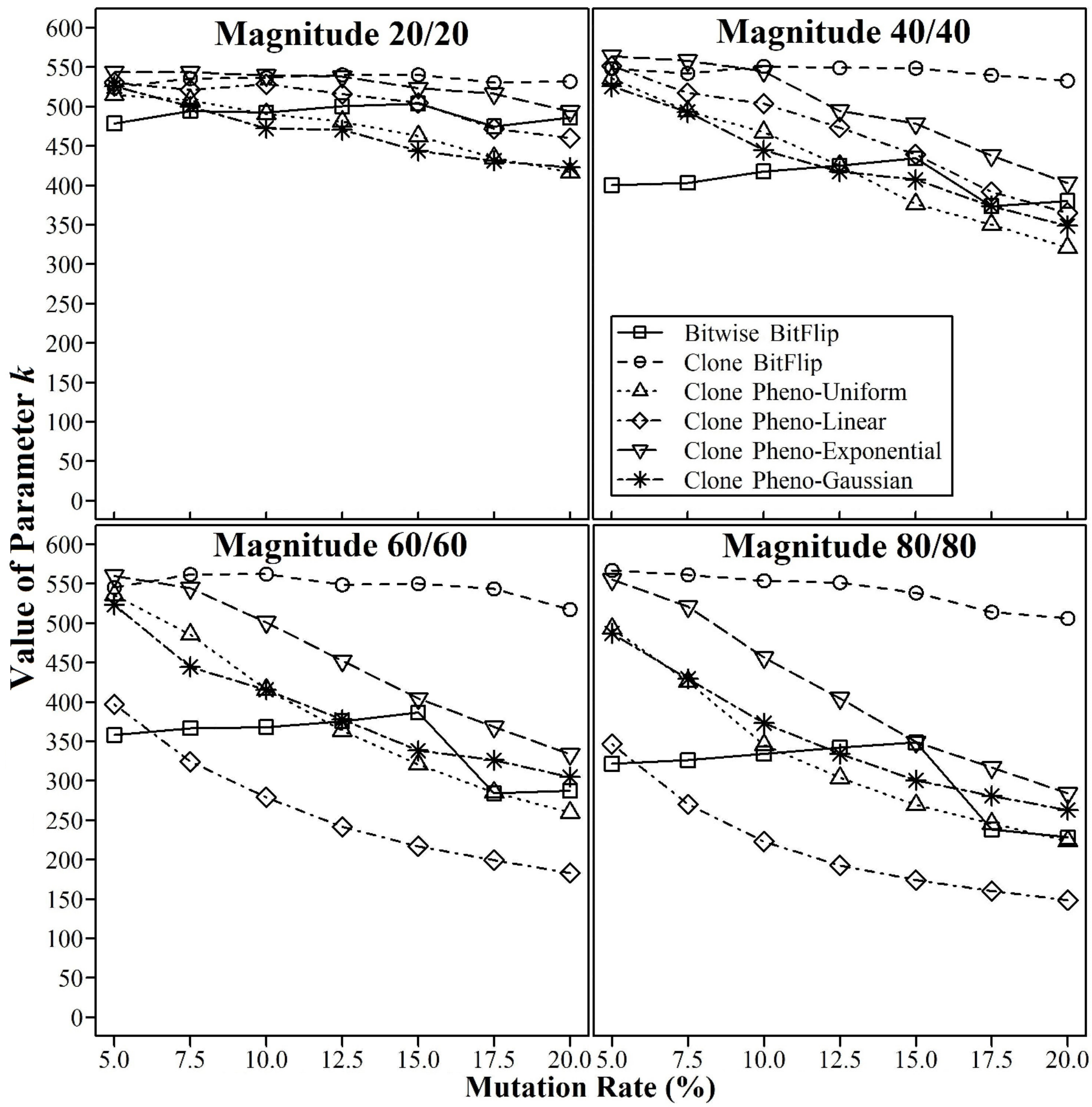


Figure 3-5. *k* parameter values of model 3 fits to the behavior of simulated creatures that used an exponential selection function

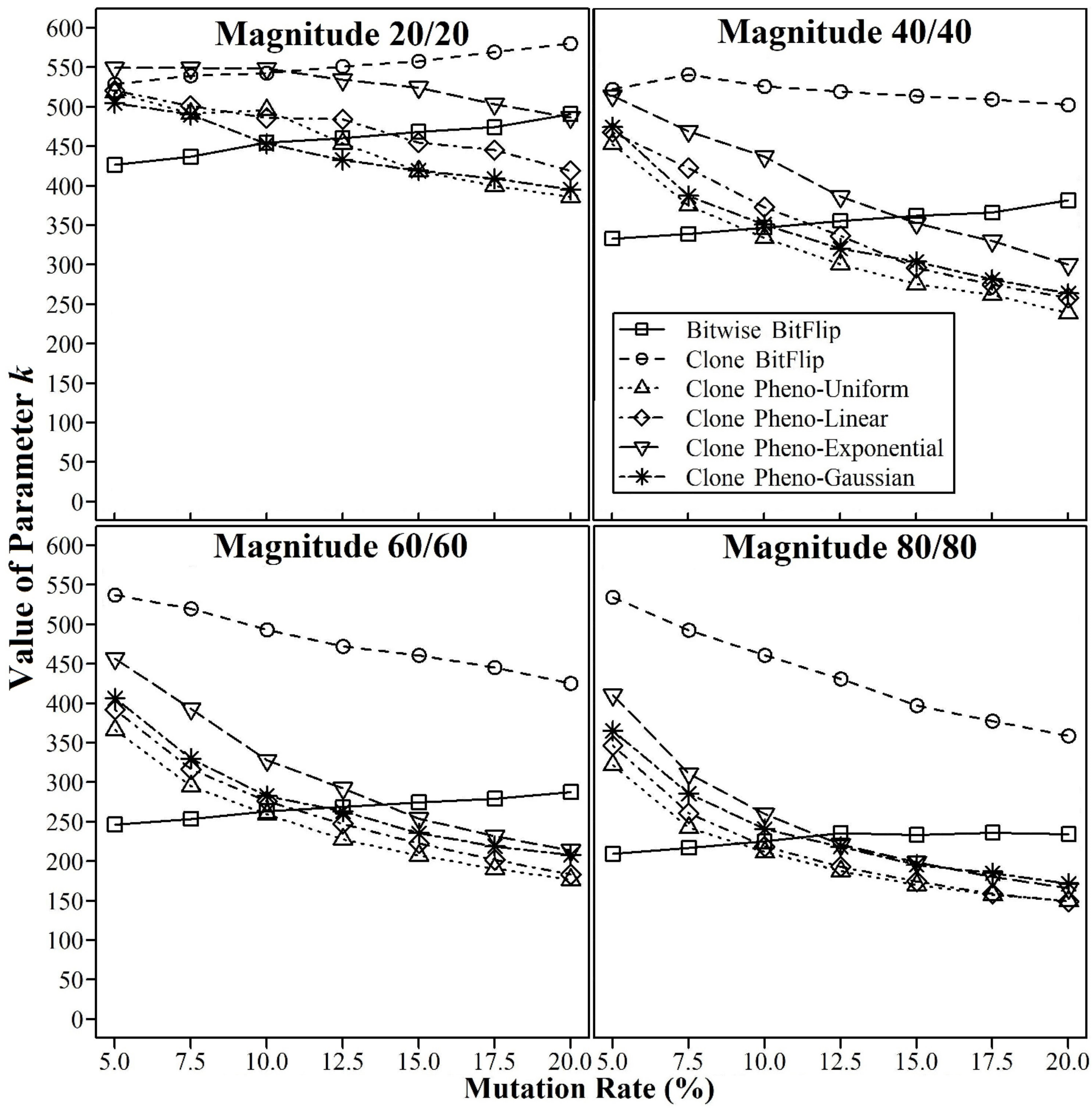


Figure 3-6. ***k*** **parameter values of model 3 fits to the behavior of simulated creatures that used a linear selection function**

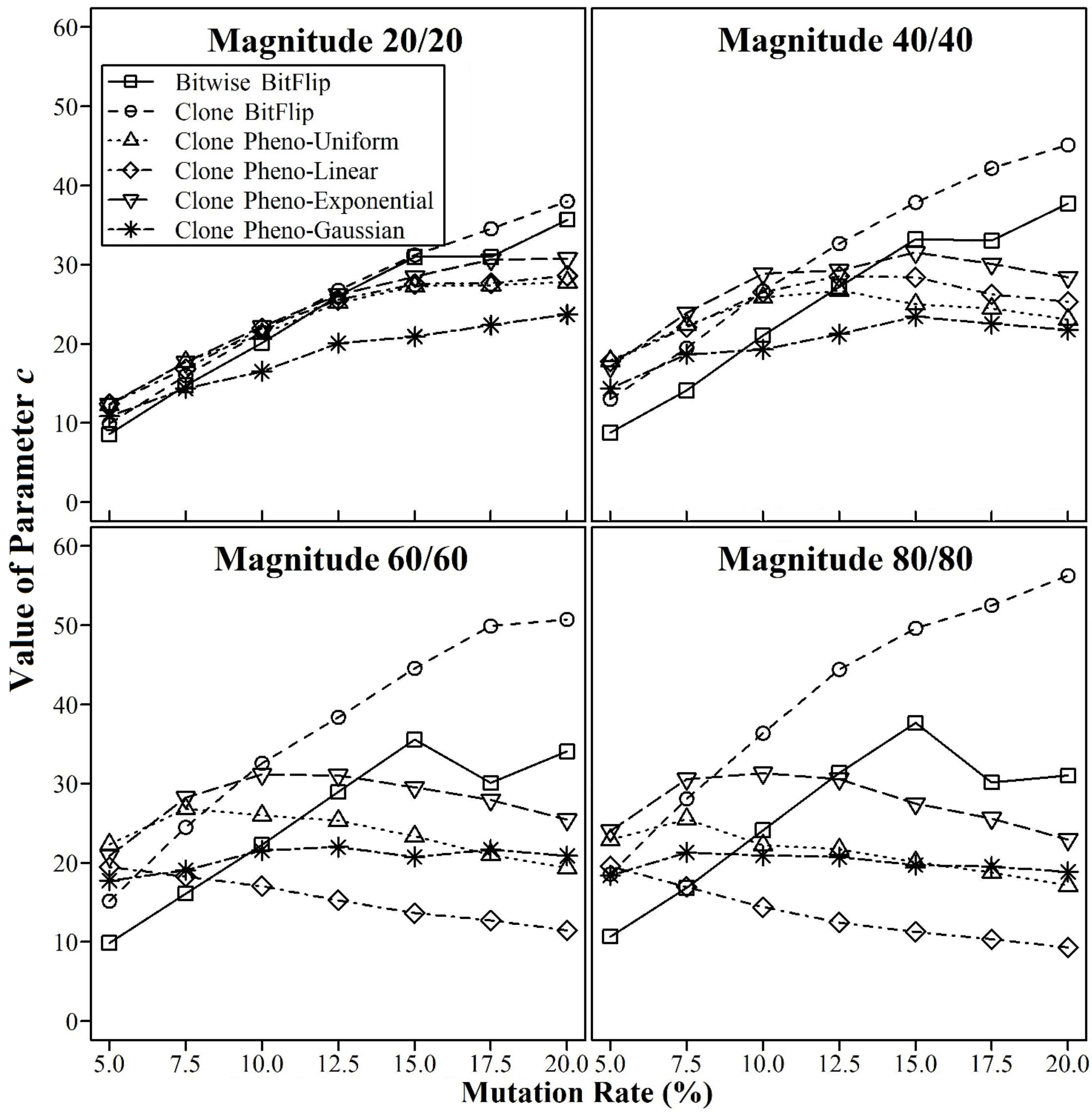


Figure 3-7. ***c*** **parameter values of model 3 fits to the behavior of simulated creatures that used an exponential selection function**

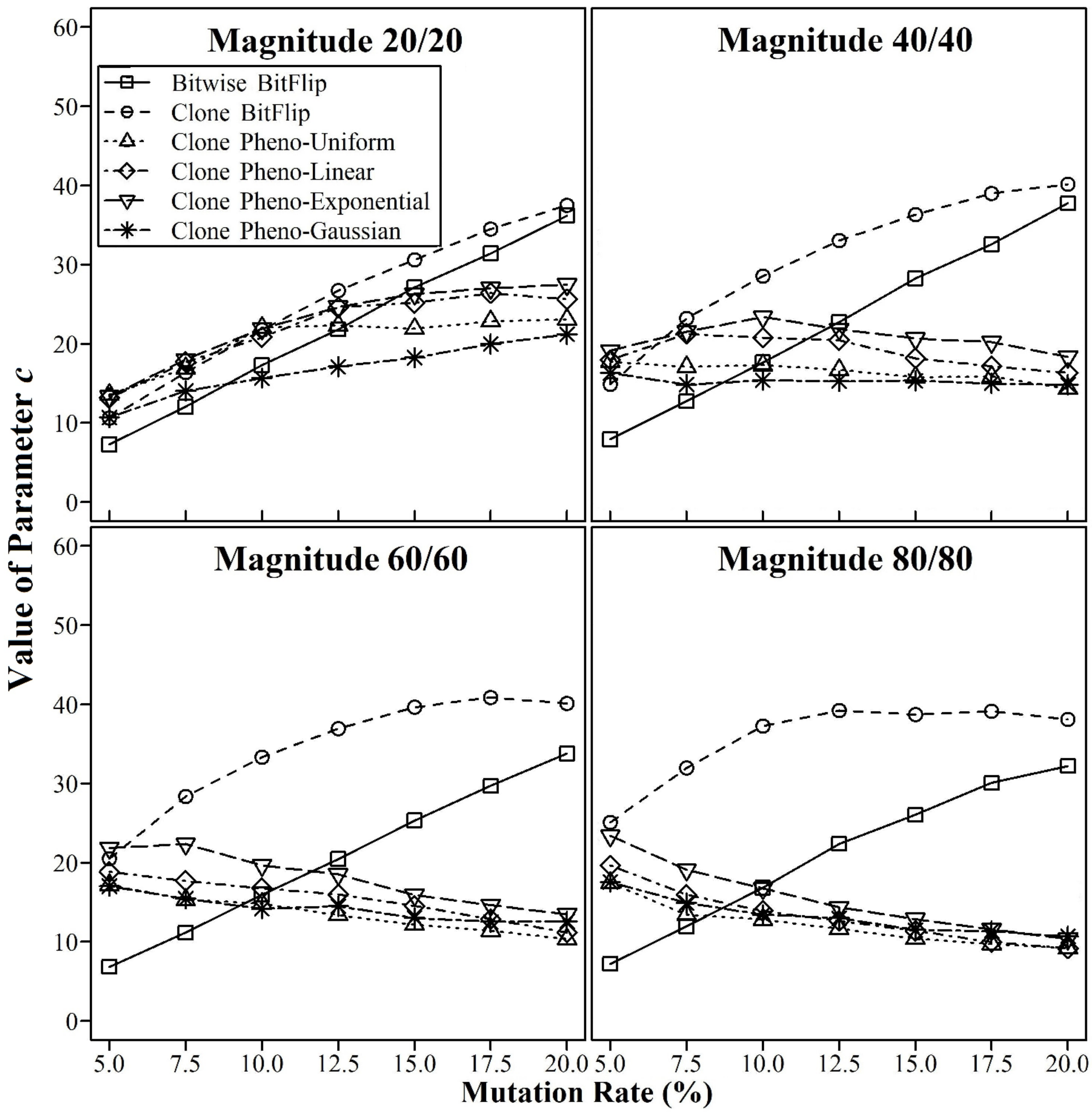
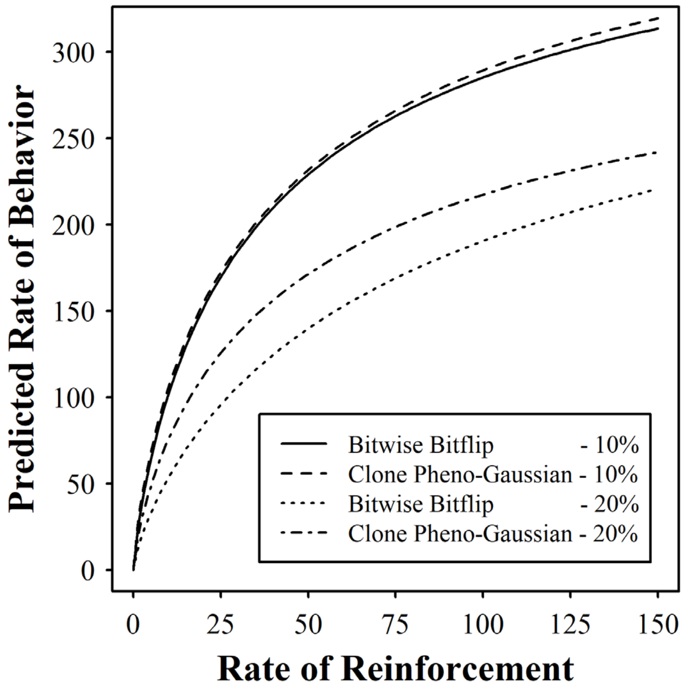


Figure 3-8. ***c*** **parameter values of model 3 fits to the behavior of simulated creatures that used a linear selection function**



Note: The parameter values of the fits can be found in Appendices A.3 and F.3 at the reinforcer magnitude pair of 40 & 40

Figure 3-9. Predicted rates of behavior for exponential-bitwise-bitflip and exponential-clone-pheno-Gaussian creature types at 10% and 20% mutation

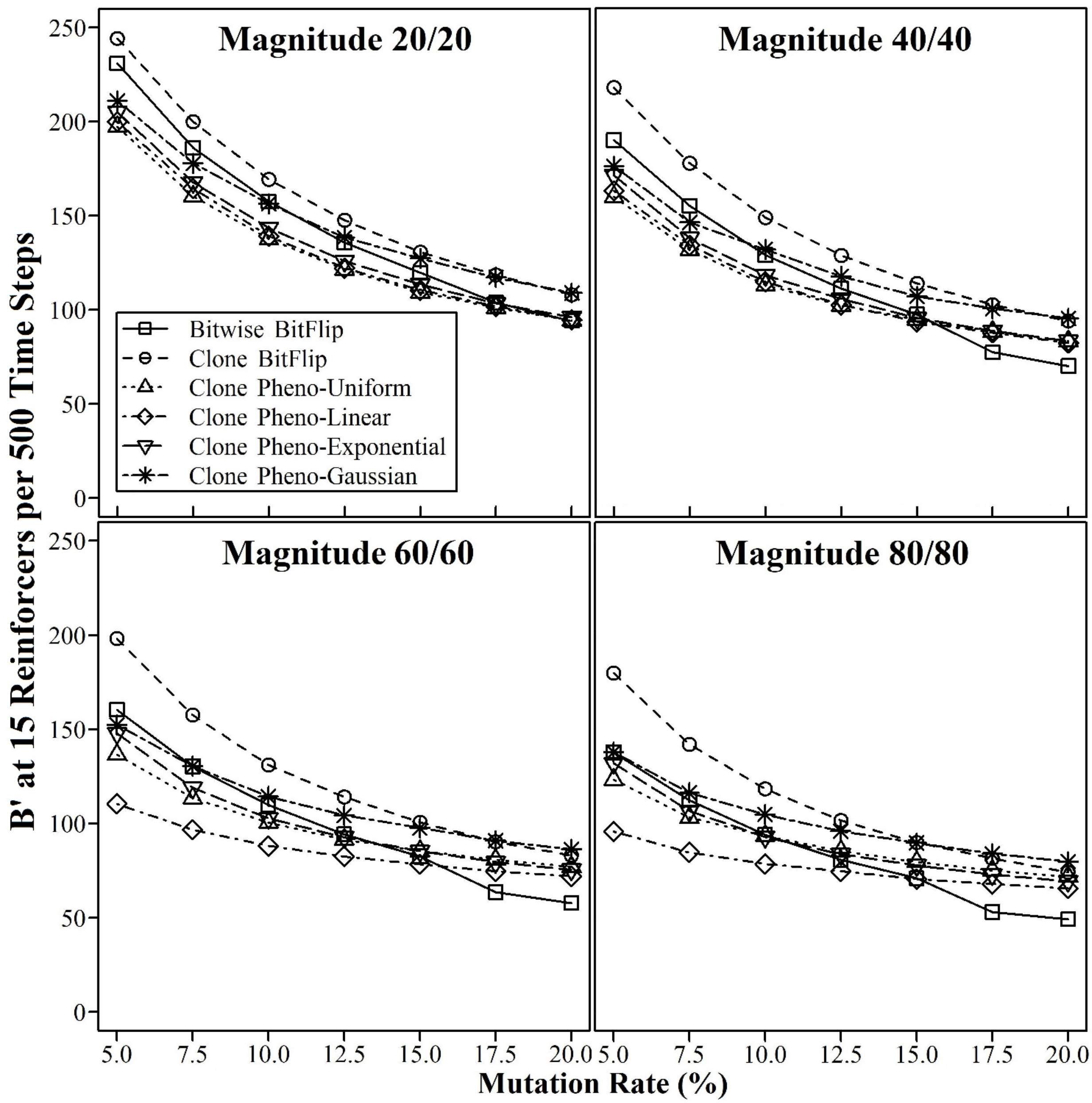


Figure 3-10. Predicted rate of behavior at 15 reinforcers per 500 time steps of simulated creatures that used an exponential selection function

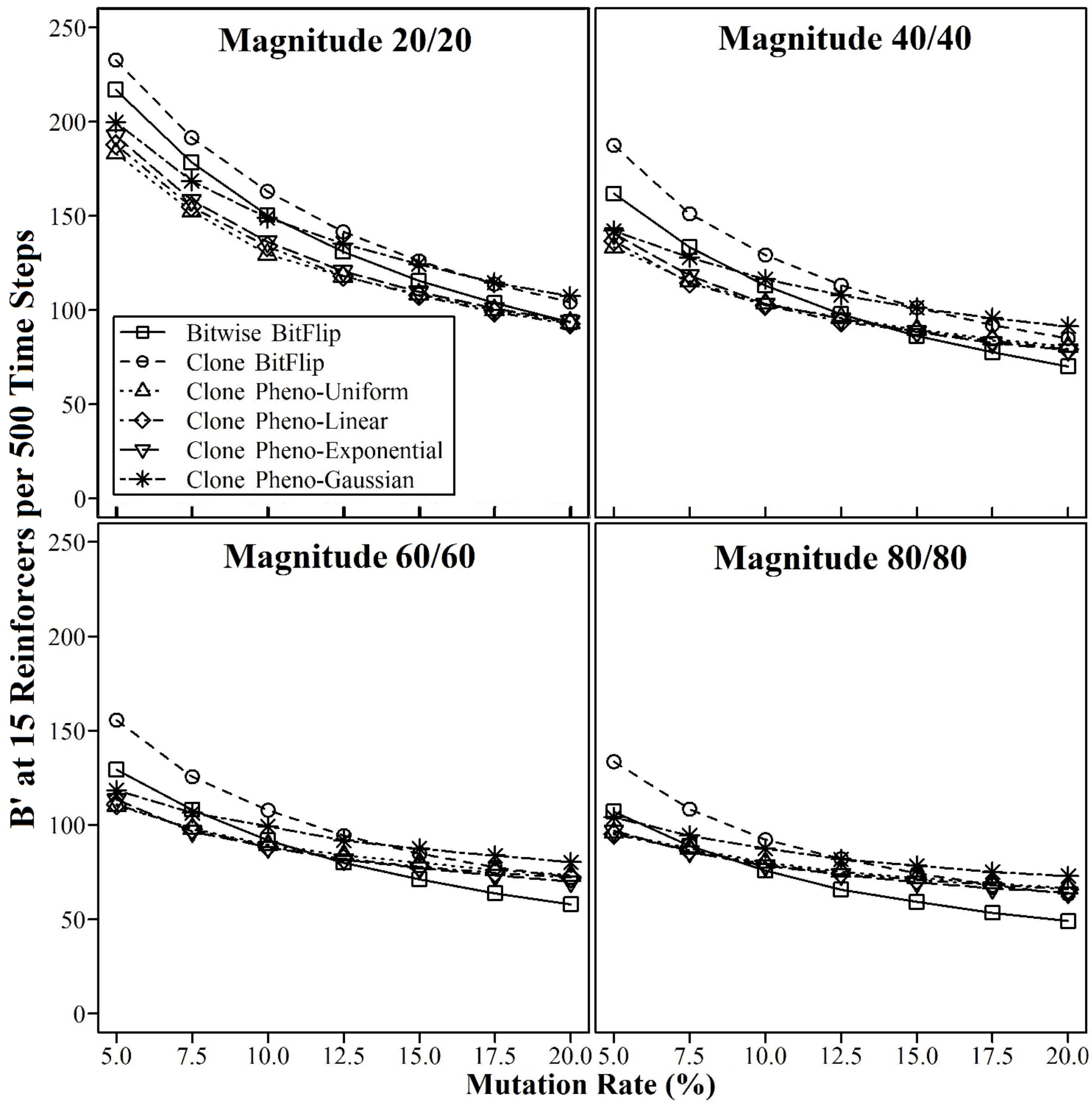


Figure 3-11. Predicted rate of behavior at 15 reinforcers per 500 time steps of simulated creatures that used a linear selection function

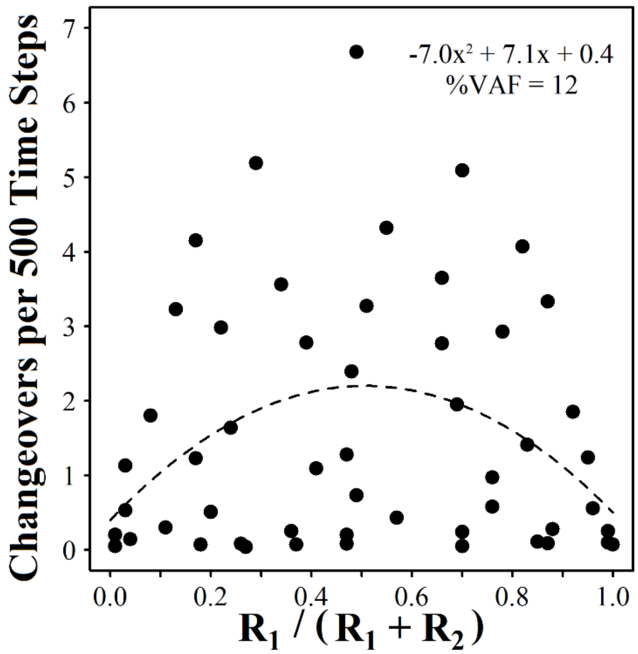
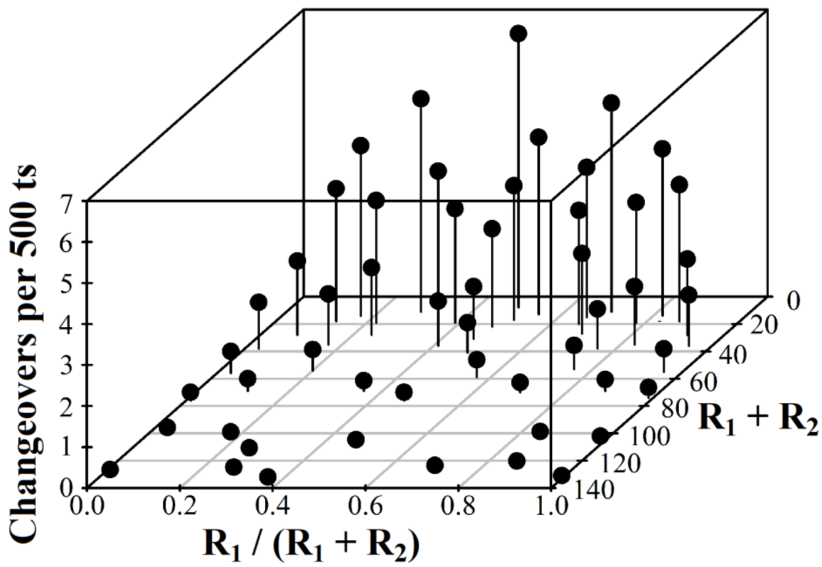
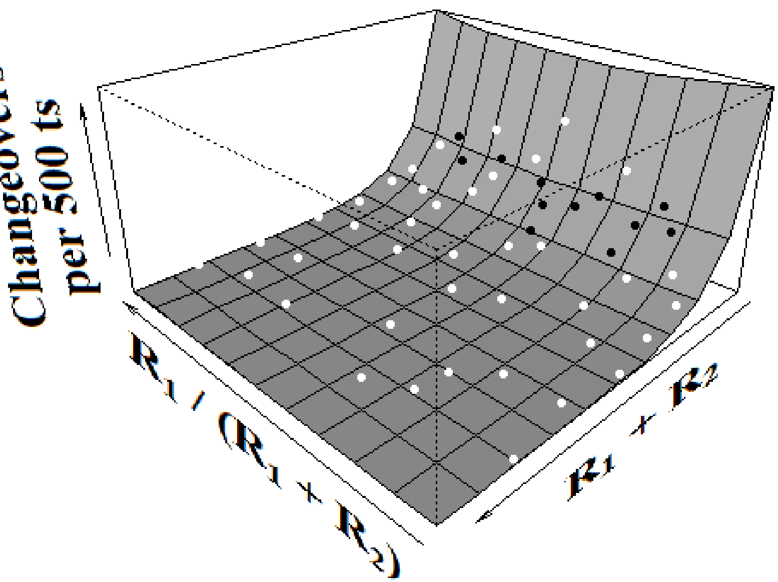


Figure 3-12. Quadratic fit to changeovers per 500 time steps of exponential-bitwise-bitflip creature type behavior at 10% mutation



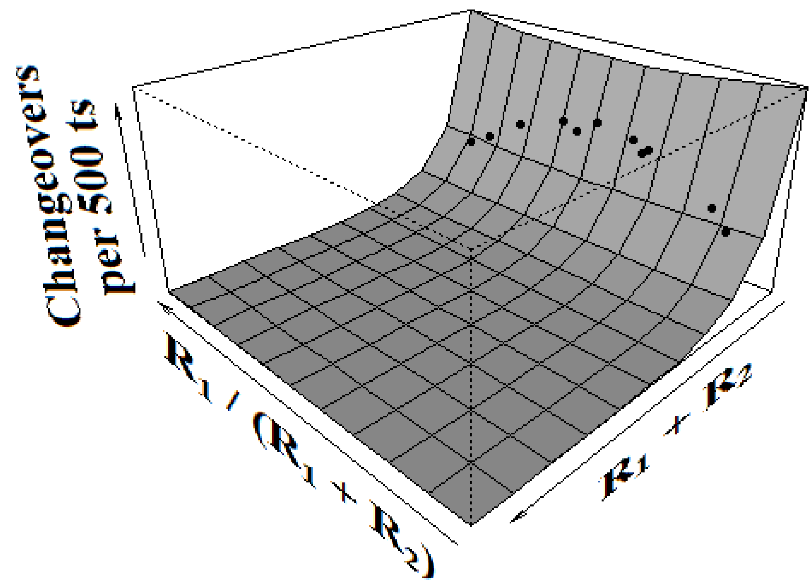
Note: The (R_1+R_2)-axis is reversed for display purposes.

Figure 3-13. Changeovers per 500 time steps (ts) as a function of total and proportional reinforcement of the exponential-bitwise-bitflip creature type at 10% mutation



Note: White dots are datapoints that are below the function's predicted values and black dots are above. The arrows on the axes indicate the direction of increasing value.

Figure 3-14. Quadratic-exponential fit to changeovers per 500 time steps (ts) of the exponential-bitwise-bitflip creature type at 10% mutation



Note: The arrows on the axes indicate the direction of increasing value.

Figure 3-15. Quadratic-exponential fit to changeovers per 500 time steps (ts) of the exponential-bitwise-bitflip creature type at 10% mutation on a typical 11 schedule experiment

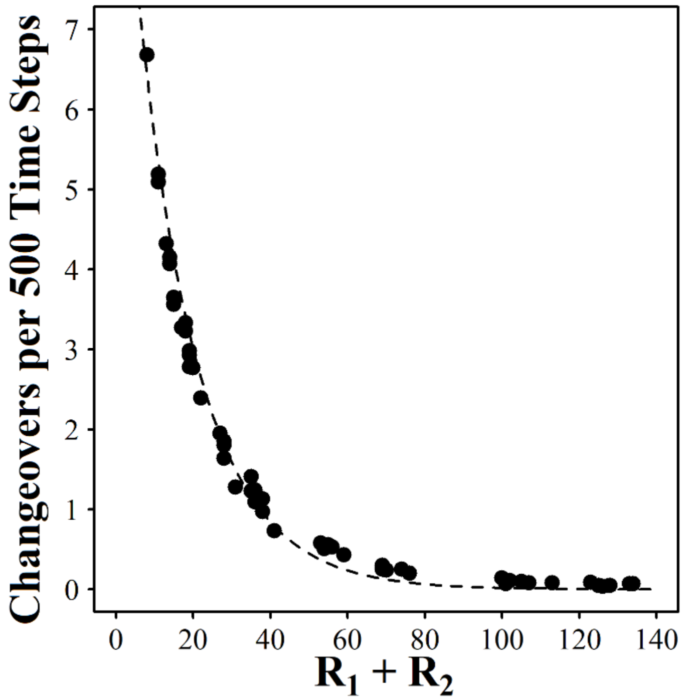


Figure 3-16. Exponential fit to changeovers per 500 time steps of the exponential-bitwise-bitflip creature type at 10% mutation

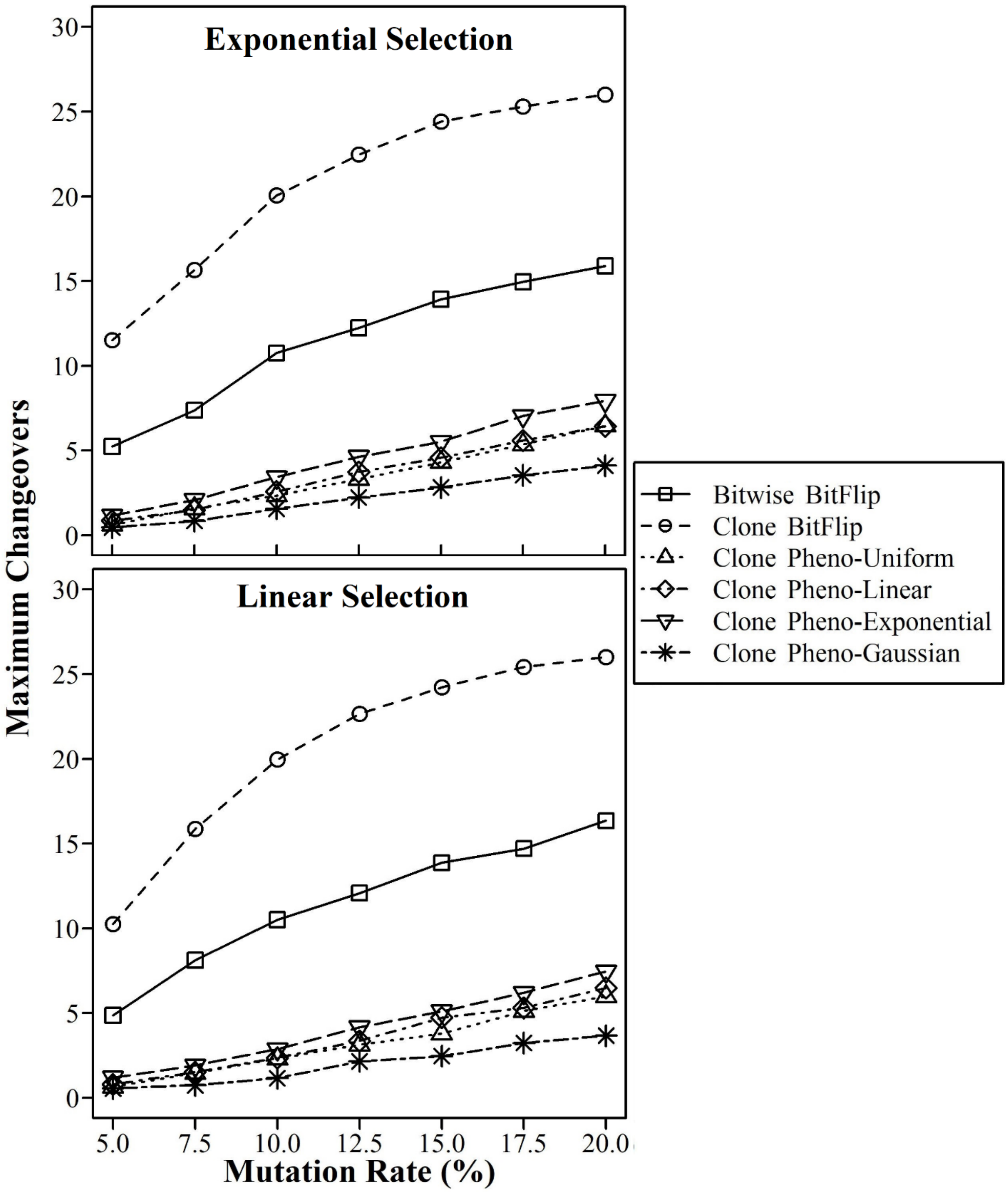


Figure 3-17. Averaged maximum changeovers (C_{Max}) predicted by the quadratic-exponential fits to simulated creature behavior

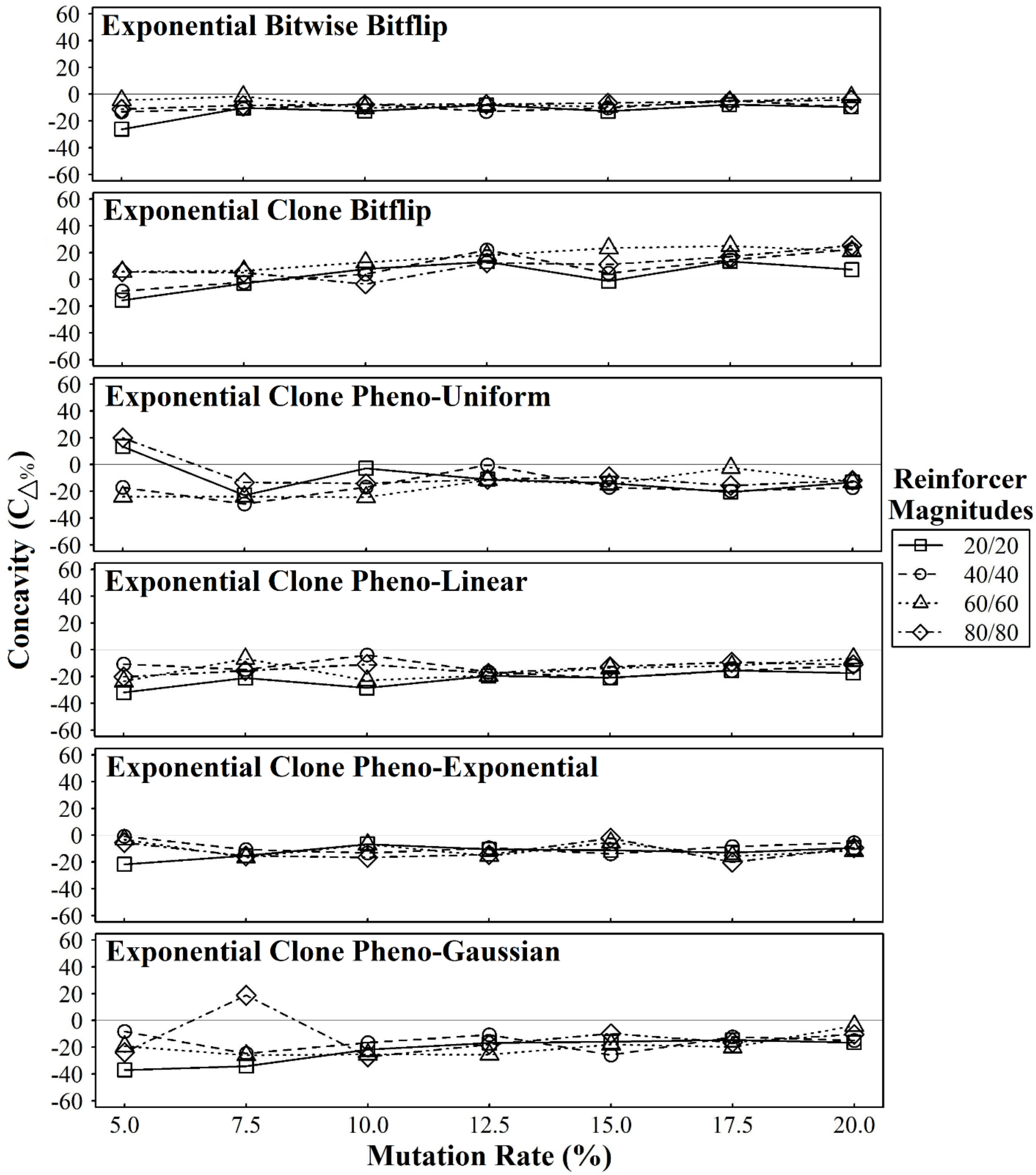


Figure 3-18. The concavity ($C_{\Delta\%}$) of the best fitting quadratic-exponential to the changeover behavior of simulated creatures that used an exponential selection function

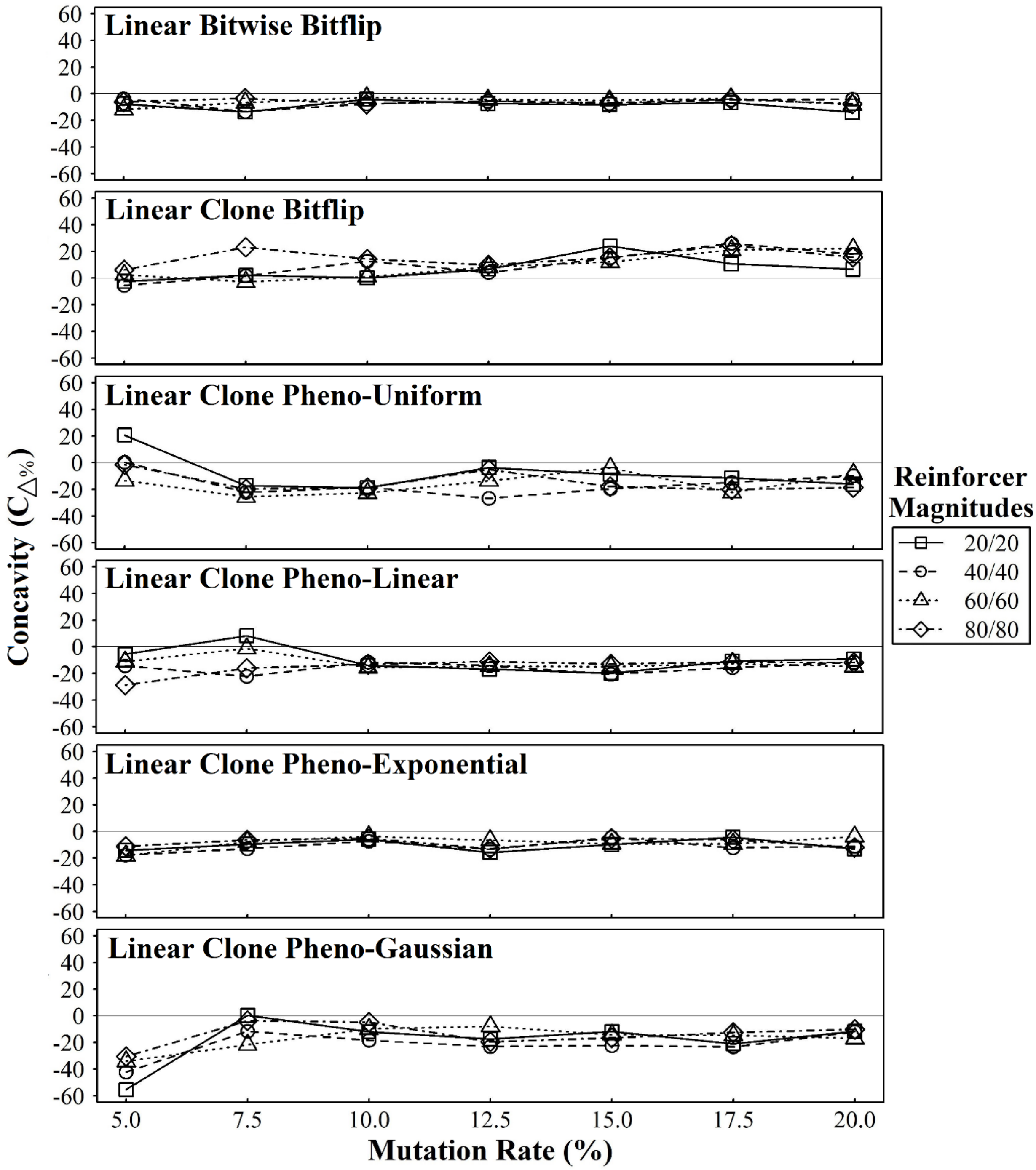
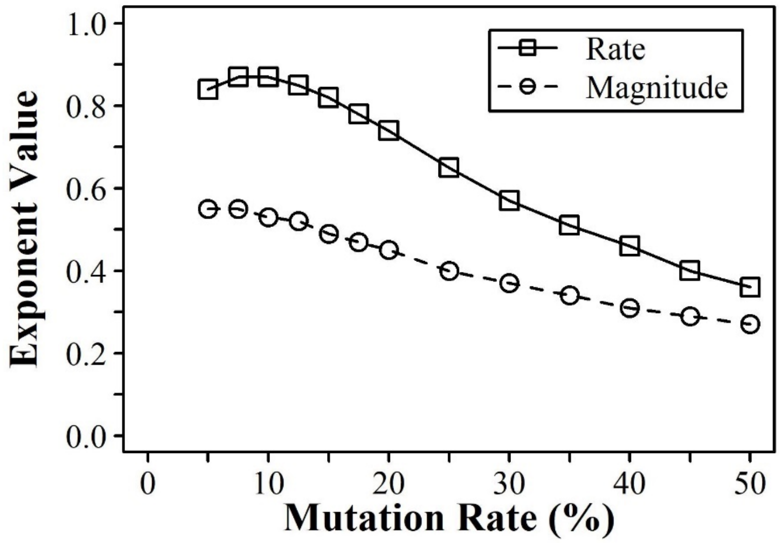


Figure 3-19. The concavity ($C_{\Delta\%}$) of the best fitting quadratic-exponential to the changeover behavior of simulated creatures that used a linear selection function

Table 4-1.

Scheduled random-interval rate means and reinforcer magnitudes of the two reinforcing components

Schedule Number	Component Rates		Component Magnitudes	
	1	2	1	2
1	15	180	15	90
2	15	180	34	71
3	15	180	52	52
4	15	180	71	34
5	15	180	90	15
6	56	139	15	90
7	56	139	34	71
8	56	139	52	52
9	56	139	71	34
10	56	139	90	15
11	98	98	15	90
12	98	98	34	71
13	98	98	52	52
14	98	98	71	34
15	98	98	90	15
16	139	56	15	90
17	139	56	34	71
18	139	56	52	52
19	139	56	71	34
20	139	56	90	15
21	180	15	15	90
22	180	15	34	71
23	180	15	52	52
24	180	15	71	34
25	180	15	90	15



Note: Mutation rates of 0.5, 1.0, and 2.5% are omitted because they could not be successfully run.

Figure 4-1. Bivariate matching fit exponents of exponential-bitwise-bitflip simulated creature behavior

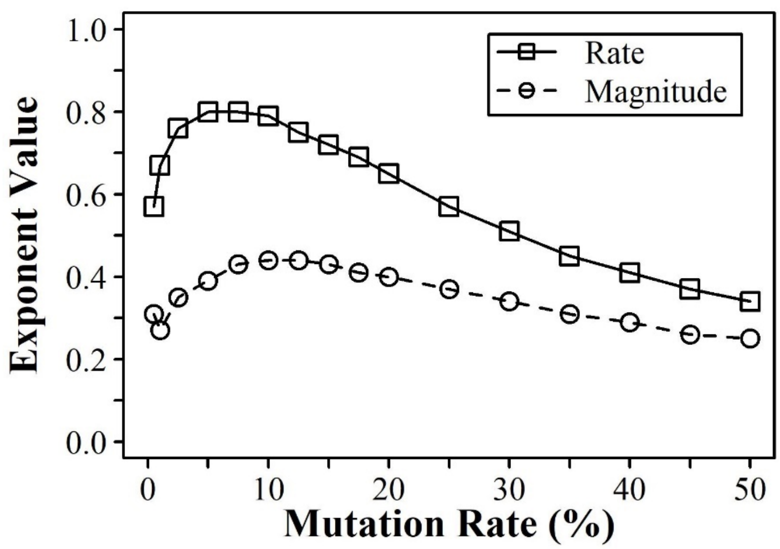


Figure 4-2. Bivariate matching fit exponents of exponential-clone-bitflip simulated creature behavior

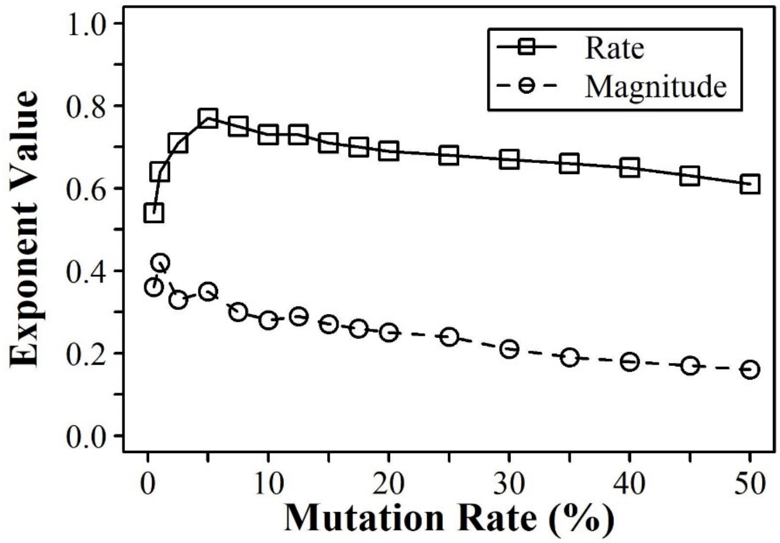


Figure 4-3. Bivariate matching fit exponents of exponential-clone-pheno-uniform simulated creature behavior

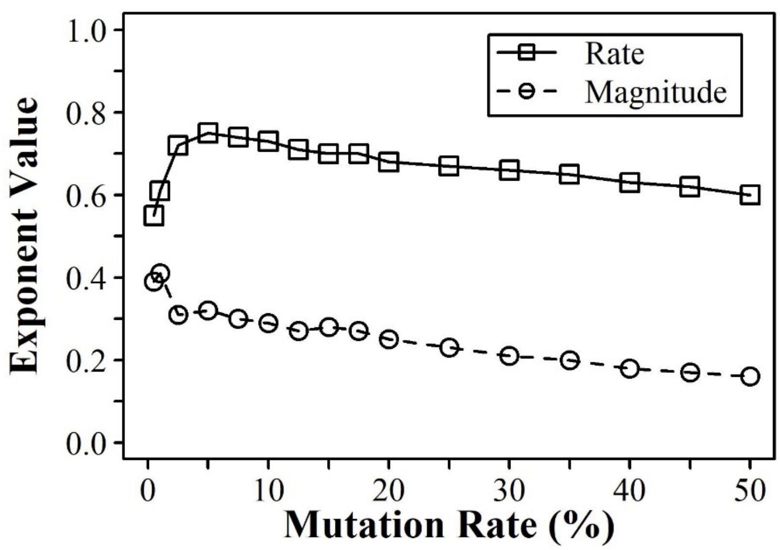


Figure 4-4. Bivariate matching fit exponents of exponential-clone-pheno-linear simulated creature behavior

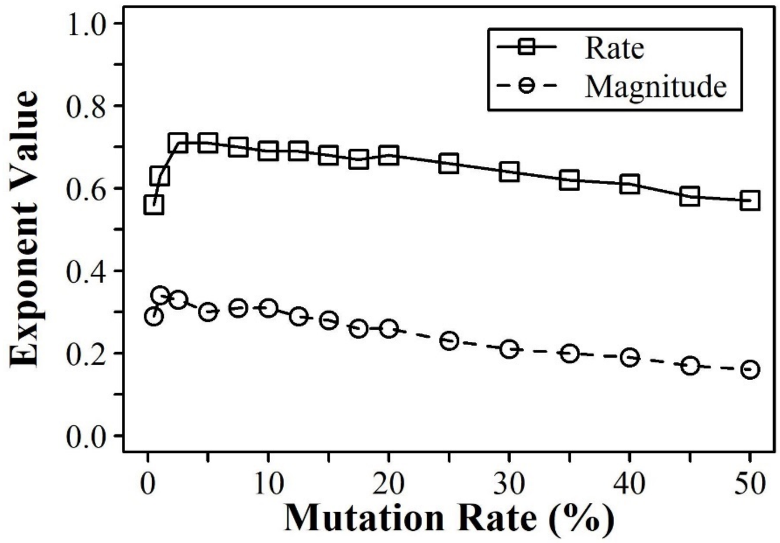


Figure 4-5. Bivariate matching fit exponents of exponential-clone-pheno-exponential simulated creature behavior

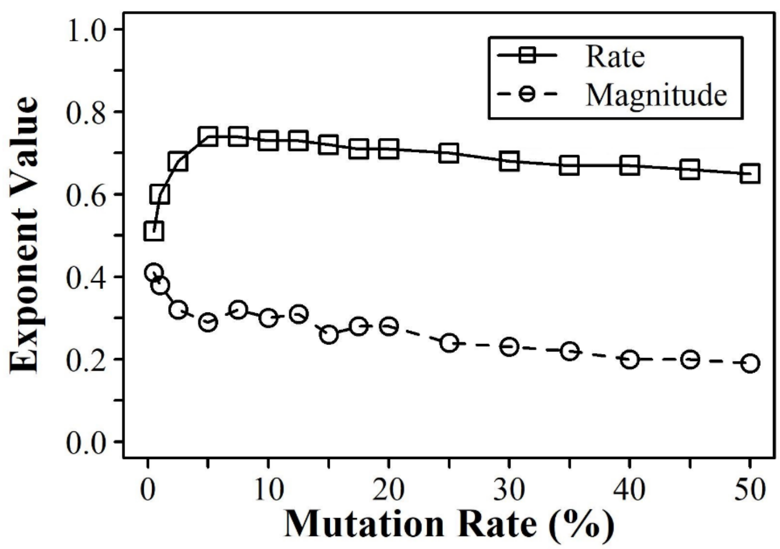
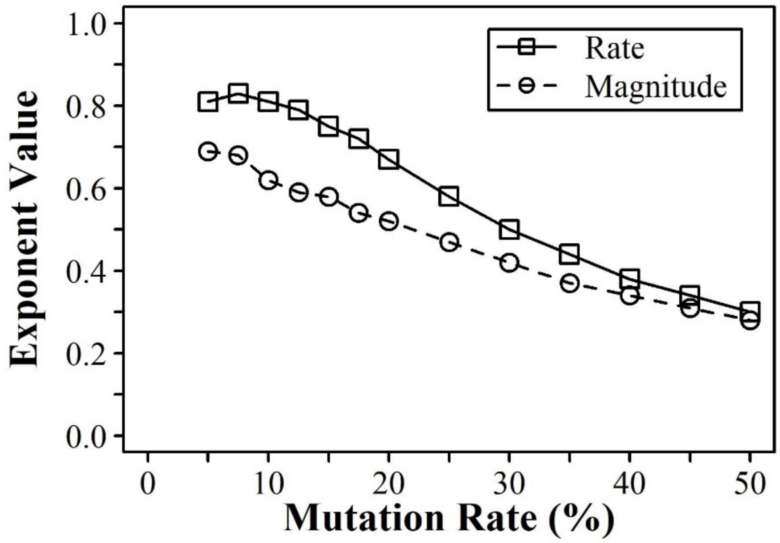


Figure 4-6. Bivariate matching fit exponents of exponential-clone-pheno-Gaussian simulated creature behavior



Note: Mutation rates of 0.5, 1.0, and 2.5% are omitted because they could not be successfully run.

Figure 4-7. Bivariate matching fit exponents of linear-bitwise-bitflip simulated creature behavior

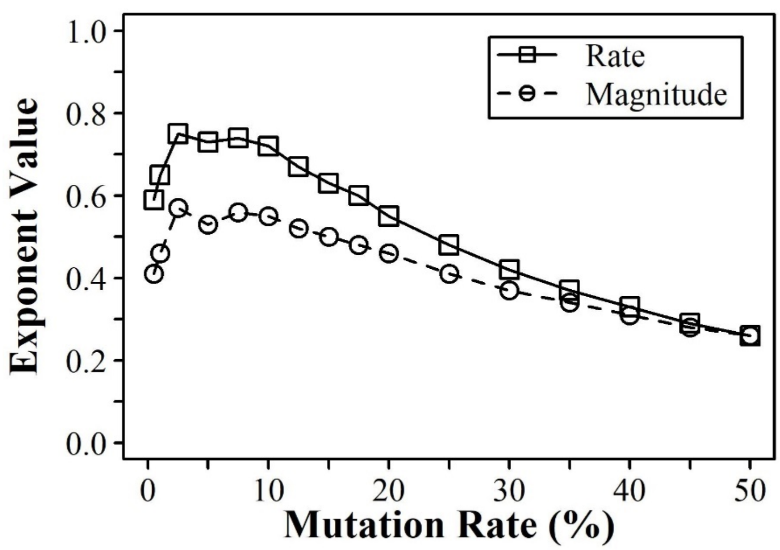


Figure 4-8. Bivariate matching fit exponents of linear-clone-bitflip simulated creature behavior

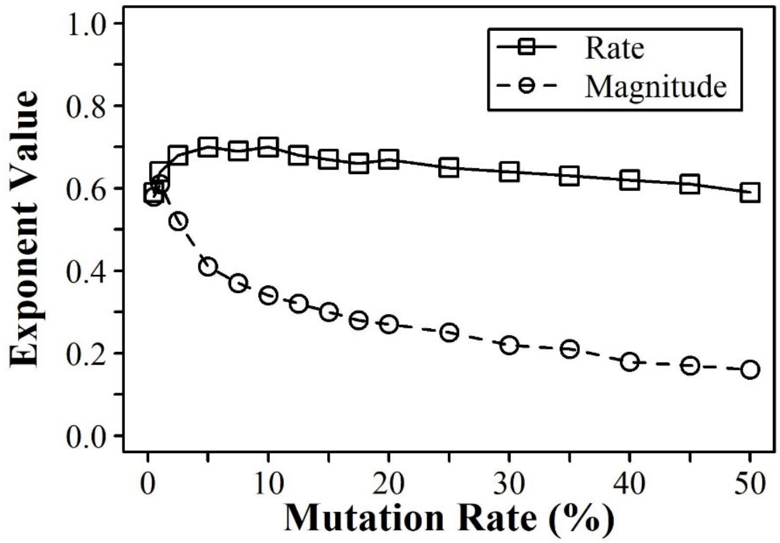


Figure 4-9. Bivariate matching fit exponents of linear-clone-pheno-uniform simulated creature behavior

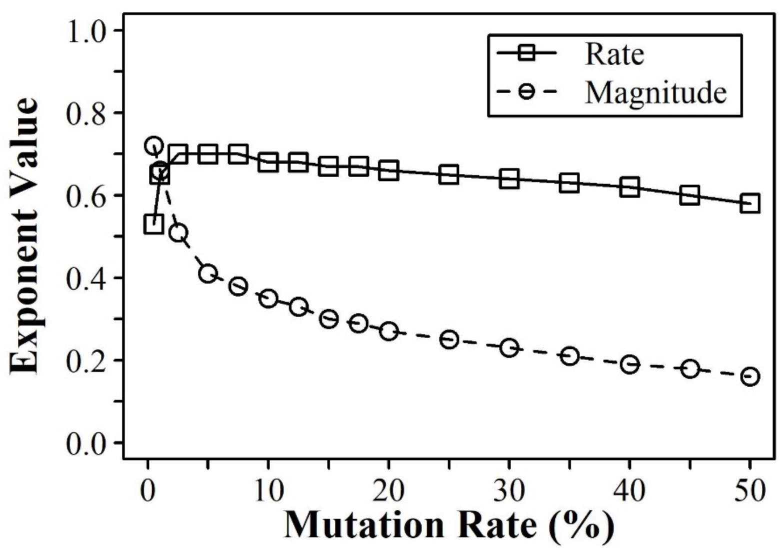


Figure 4-10. Bivariate matching fit exponents of linear-clone-pheno-linear simulated creature behavior

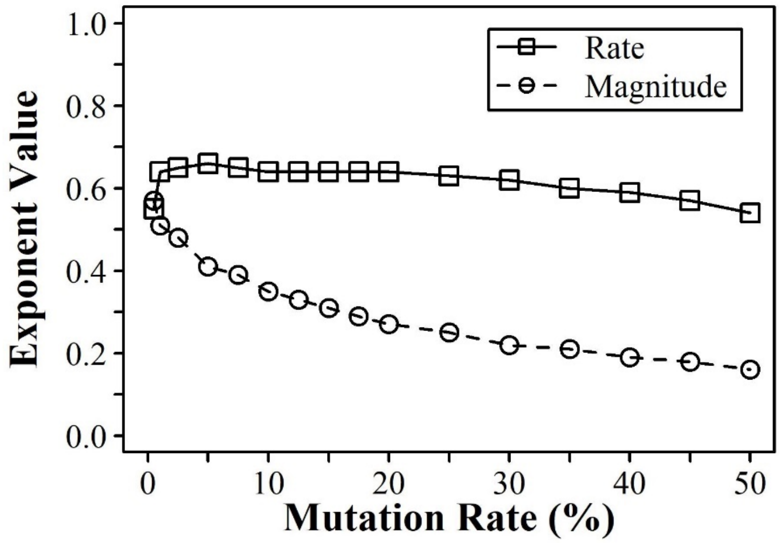


Figure 4-11. Bivariate matching fit exponents of linear-clone-pheno-exponential simulated creature behavior

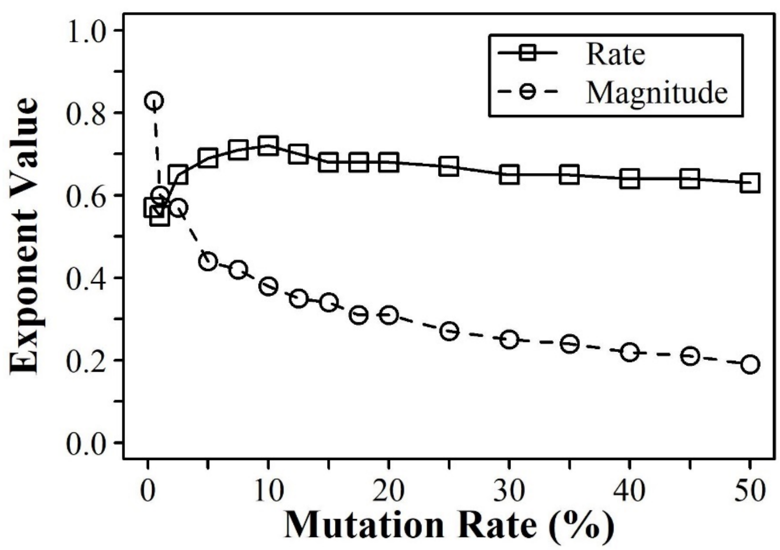


Figure 4-12. Bivariate matching fit exponents of linear-clone-pheno-Gaussian simulated creature behavior

APPENDICES

Appendix A: Experiment 1 Fitting Measures of the Exponential-Bitwise-Bitflip Creature Type

Table A.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	478	8.5	8.7	0.77	97	99
	40/40	400	8.7	8.9	0.77	99	99
	60/60	358	10.0	9.8	0.77	99	99
	80/80	322	10.6	10.8	0.77	98	99
7.5	20/20	494	14.7	14.8	0.81	99	99
	40/40	406	14.1	13.9	0.80	99	99
	60/60	364	16.3	16.2	0.81	99	100
	80/80	326	16.8	16.9	0.81	99	100
10.0	20/20	496	20.0	19.9	0.82	100	100
	40/40	416	21.1	21.3	0.83	100	100
	60/60	368	22.3	22.4	0.83	100	100
	80/80	332	24.1	24.2	0.83	100	100
12.5	20/20	503	26.0	25.8	0.83	100	100
	40/40	423	27.4	27.2	0.84	100	100
	60/60	372	28.9	29.2	0.85	100	100
	80/80	344	31.3	31.4	0.84	100	100
15.0	20/20	510	30.9	30.7	0.83	100	100
	40/40	433	33.3	33.3	0.84	100	100
	60/60	381	35.8	35.6	0.85	100	100
	80/80	350	37.7	37.7	0.84	100	100
17.5	20/20	454	31.3	31.2	0.82	100	100
	40/40	357	33.0	33.0	0.82	100	100
	60/60	285	30.1	30.2	0.80	100	100
	80/80	259	31.0	30.9	0.76	100	99
20.0	20/20	455	35.8	35.7	0.83	100	100
	40/40	360	37.2	37.5	0.82	100	100
	60/60	290	34.1	34.2	0.79	100	100
	80/80	253	32.2	32.2	0.75	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table A.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	478	8.6	0.77	97	99
	40/40	400	8.8	0.77	99	99
	60/60	358	9.9	0.77	99	99
	80/80	322	10.7	0.77	98	99
7.5	20/20	494	14.8	0.81	99	99
	40/40	406	14.0	0.80	99	99
	60/60	364	16.3	0.81	99	100
	80/80	326	16.9	0.81	99	100
10.0	20/20	496	20.0	0.82	100	100
	40/40	416	21.2	0.83	100	100
	60/60	368	22.3	0.83	100	100
	80/80	332	24.2	0.83	100	100
12.5	20/20	503	25.9	0.83	100	100
	40/40	423	27.3	0.84	100	100
	60/60	372	29.1	0.85	100	100
	80/80	344	31.4	0.84	100	100
15.0	20/20	510	30.8	0.83	100	100
	40/40	433	33.3	0.84	100	100
	60/60	381	35.7	0.85	100	100
	80/80	350	37.7	0.84	100	100
17.5	20/20	454	31.2	0.82	100	100
	40/40	357	33.0	0.82	100	100
	60/60	285	30.1	0.80	100	100
	80/80	259	30.9	0.76	100	99
20.0	20/20	455	35.7	0.83	100	100
	40/40	360	37.4	0.82	100	100
	60/60	290	34.2	0.79	100	100
	80/80	253	32.2	0.75	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table A.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	479	8.6	0.77	97	99
	40/40	400	8.9		99	99
	60/60	358	9.9		99	99
	80/80	322	10.7		98	99
7.5	20/20	495	14.7	0.81	99	99
	40/40	403	14.2		99	99
	60/60	367	16.1		99	100
	80/80	326	16.8		99	100
10.0	20/20	492	20.1	0.83	100	100
	40/40	417	21.1		100	100
	60/60	368	22.3		100	100
	80/80	334	24.1		100	100
12.5	20/20	500	26.1	0.84	100	100
	40/40	425	27.3		100	100
	60/60	376	29.0		100	100
	80/80	342	31.4		100	100
15.0	20/20	504	31.0	0.84	100	100
	40/40	434	33.3		100	100
	60/60	387	35.6		100	100
	80/80	349	37.7		100	100
17.5	20/20	475	31.0	0.80	100	100
	40/40	373	33.1		100	100
	60/60	284	30.1		100	100
	80/80	238	30.2		99	99
20.0	20/20	486	35.7	0.79	100	100
	40/40	380	37.8		100	100
	60/60	287	34.1		100	100
	80/80	228	31.0		99	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table A.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF	
					QLOE	ML
5.0	20/20	384	10.6	0.77	74	99
	40/40		9.9		96	99
	60/60		11.0		98	99
	80/80		11.5		85	98
7.5	20/20	398	17.5	0.80	80	99
	40/40		16.6		96	99
	60/60		18.1		99	100
	80/80		19.5		88	99
10.0	20/20	413	25.5	0.83	82	100
	40/40		23.7		98	100
	60/60		26.2		99	100
	80/80		28.9		90	99
12.5	20/20	372	28.3	0.85	79	100
	40/40		27.4		96	100
	60/60		28.5		100	100
	80/80		31.1		93	99
15.0	20/20	458	44.2	0.83	82	100
	40/40		41.3		98	100
	60/60		45.6		99	100
	80/80		49.3		91	99
17.5	20/20	474	64.3	0.79	59	100
	40/40		57.4		92	99
	60/60		64.7		98	100
	80/80		71.3		82	97
20.0	20/20	532	81.0	0.79	58	100
	40/40		72.2		91	99
	60/60		81.2		97	100
	80/80		88.9		81	96

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table A.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	378	10.3	0.77	73	99
	40/40				95	99
	60/60				98	99
	80/80				84	99
7.5	20/20	390	17.1	0.81	79	99
	40/40				95	99
	60/60				99	100
	80/80				87	100
10.0	20/20	403	25.0	0.83	81	100
	40/40				97	100
	60/60				99	100
	80/80				89	100
12.5	20/20	421	33.8	0.84	81	100
	40/40				97	100
	60/60				99	100
	80/80				89	100
15.0	20/20	443	43.1	0.84	81	100
	40/40				96	100
	60/60				99	100
	80/80				89	100
17.5	20/20	434	59.6	0.80	57	100
	40/40				88	100
	60/60				98	100
	80/80				79	99
20.0	20/20	481	74.6	0.80	56	100
	40/40				87	100
	60/60				98	100
	80/80				78	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table A.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	423	12.5	95	91
	40/40	351	12.5	97	90
	60/60	312	13.9	97	90
	80/80	277	14.7	97	90
7.5	20/20	433	19.9	98	94
	40/40	352	18.9	97	93
	60/60	314	20.8	99	94
	80/80	277	21.3	98	94
10.0	20/20	427	25.5	99	95
	40/40	359	26.4	99	96
	60/60	312	27.1	99	95
	80/80	279	28.6	99	96
12.5	20/20	428	32.1	99	96
	40/40	357	32.7	99	96
	60/60	312	34.0	99	96
	80/80	278	35.5	99	96
15.0	20/20	418	37.0	99	96
	40/40	353	38.6	99	96
	60/60	309	40.2	99	96
	80/80	272	40.9	99	96
17.5	20/20	365	36.8	99	95
	40/40	275	36.4	99	95
	60/60	210	32.2	98	93
	80/80	174	31.3	96	89
20.0	20/20	358	40.7	99	95
	40/40	268	39.8	99	95
	60/60	203	34.9	98	92
	80/80	164	31.6	96	88

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table A.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	347	5.2	91	91
	40/40		12.0	97	90
	60/60		19.8	96	90
	80/80		29.1	93	90
7.5	20/20	352	9.8	95	94
	40/40		18.9	97	93
	60/60		28.9	98	94
	80/80		40.2	96	94
10.0	20/20	355	14.6	97	95
	40/40		25.6	99	96
	60/60		37.6	98	95
	80/80		50.4	97	96
12.5	20/20	356	19.5	98	96
	40/40		32.4	99	96
	60/60		46.2	99	96
	80/80		60.5	97	96
15.0	20/20	351	23.8	98	96
	40/40		38.2	99	96
	60/60		53.1	99	96
	80/80		68.4	97	96
17.5	20/20	273	17.3	95	95
	40/40		35.8	99	95
	60/60		55.4	96	93
	80/80		73.3	91	89
20.0	20/20	264	19.3	95	95
	40/40		38.8	99	95
	60/60		58.7	96	92
	80/80		76.2	90	88

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table A.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	ML
5.0	20/20	327	14	71	91
	40/40			93	90
	60/60			96	90
	80/80			82	90
7.5	20/20	332	22	78	94
	40/40			94	93
	60/60			98	94
	80/80			86	94
10.0	20/20	336	30	80	95
	40/40			96	96
	60/60			99	95
	80/80			88	96
12.5	20/20	340	39	81	96
	40/40			96	96
	60/60			99	96
	80/80			88	96
15.0	20/20	341	47	80	96
	40/40			96	96
	60/60			99	96
	80/80			88	96
17.5	20/20	267	54	56	95
	40/40			87	95
	60/60			96	93
	80/80			76	89
20.0	20/20	266	60	55	95
	40/40			86	95
	60/60			96	92
	80/80			74	88

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table A.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	214	114	4	403	2
3	Constant a, $c_1 = c_2$	9	116	113	7	406	1
4	Constant a & c	6	29940	842	10	409	36*
5	Constant a, c & k	3	24275	875	13	412	28*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	6875	246	8	407	28*
7	Constant k, $a = 1$, $c_1 = c_2$	5	10199	384	11	410	27*
8	Constant k & c, $a = 1$,	2	26297	1001	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table A.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	16	50	4	403	0
3	Constant a, $c_1 = c_2$	9	25	50	7	406	1
4	Constant a & c	6	25397	670	10	409	38*
5	Constant a, c & k	3	20945	709	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2904	106	8	407	27*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6212	215	11	410	29*
8	Constant k & c, $a = 1$,	2	21335	772	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table A.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	4	19	4	403	0
3	Constant a, $c_1 = c_2$	9	-2	19	7	406	<0
4	Constant a & c	6	20765	527	10	409	39*
5	Constant a, c & k	3	17556	573	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1886	56	8	407	33*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3921	124	11	410	32*
8	Constant k & c, $a = 1$,	2	17475	611	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model. Model 3 had a lower residual sum of squares than Model 1, which made the test invalid because the F-value was less than 0.

Table A.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	21	9	4	403	2
3	Constant a, $c_1 = c_2$	9	13	9	7	406	1
4	Constant a & c	6	21031	523	10	409	40*
5	Constant a, c & k	3	15207	489	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1434	37	8	407	39*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2899	87	11	410	33*
8	Constant k & c, $a = 1$,	2	15106	521	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table A.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	5	5	4	403	1
3	Constant a, $c_1 = c_2$	9	2	5	7	406	0
4	Constant a & c	6	14751	366	10	409	40*
5	Constant a, c & k	3	12649	404	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1310	31	8	407	42*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2160	63	11	410	34*
8	Constant k & c, $a = 1$,	2	12609	433	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table A.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	0	3	4	403	0
3	Constant a, $c_1 = c_2$	9	46	4	7	406	12*
4	Constant a & c	6	21184	521	10	409	41*
5	Constant a, c & k	3	17888	568	13	412	32*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1110	25	8	407	44*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2856	80	11	410	36*
8	Constant k & c, $a = 1$,	2	17397	593	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table A.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	2	3	4	403	1
3	Constant a, $c_1 = c_2$	9	54	3	7	406	16*
4	Constant a & c	6	18030	443	10	409	41*
5	Constant a, c & k	3	15181	481	13	412	32*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	987	22	8	407	45*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2404	67	11	410	36*
8	Constant k & c, $a = 1$,	2	14785	504	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table A.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	1981	1643	1253	934	708	497	398
2	$c_1 = c_2$	12	1981	1636	1246	935	704	490	393
3	Constant a, $c_1 = c_2$	9	1974	1633	1238	929	696	577	517
4	Constant a & c	6	2807	2712	2612	2609	2460	2607	2540
5	Constant a, c & k	3	2820	2733	2644	2578	2499	2640	2572
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2297	1948	1684	1510	1435	1345	1290
7	Constant k, $a = 1$, $c_1 = c_2$	5	2479	2239	2010	1860	1728	1825	1753
8	Constant k & c, $a = 1$	2	2875	2767	2670	2603	2526	2657	2589

Table A.17. Akaike Information Criteria (AIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1083	-1218	-1323	-1469	-1530	-1512	-1517
2	$c_1 = c_2$	8	-1089	-1225	-1330	-1476	-1537	-1520	-1523
3, 4, 5	Constant a & $c_1 = c_2$	2	-1101	-1236	-1340	-1486	-1542	-1485	-1478
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-659	-730	-789	-839	-882	-902	-931

Table A.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2045	1708	1317	998	772	562	463
2	$c_1 = c_2$	12	2029	1685	1294	983	752	538	442
3	Constant a, $c_1 = c_2$	9	2011	1669	1274	966	732	614	553
4	Constant a & c	6	2831	2736	2636	2633	2484	2632	2564
5	Constant a, c & k	3	2832	2745	2656	2590	2511	2652	2584
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2329	1980	1716	1543	1467	1377	1322
7	Constant k, $a = 1$, $c_1 = c_2$	5	2499	2259	2030	1880	1748	1846	1773
8	Constant k & c, $a = 1$	2	2883	2775	2678	2611	2534	2665	2597

Table A.19. Bayes Information Criteria (BIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1043	-1178	-1283	-1429	-1490	-1472	-1477
2	$c_1 = c_2$	8	-1063	-1199	-1304	-1450	-1510	-1494	-1496
3, 4, 5	Constant a & $c_1 = c_2$	2	-1095	-1230	-1333	-1479	-1535	-1478	-1471
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-659	-730	-789	-839	-882	-902	-931

Table A.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	-0.4	0.3	0.3	0.3	0.1	1
	40/40	-1.1	1.1	0.3	0.5	0.3	3
	60/60	-1.4	1.4	0.3	0.7	0.4	3
	80/80	-1.6	1.5	0.5	0.9	0.4	2
7.5	20/20	-2.4	2.4	0.3	0.9	0.6	6
	40/40	-2.6	2.6	0.5	1.2	0.7	4
	60/60	-5.6	5.6	0.4	1.8	1.4	11
	80/80	-5.5	5.5	0.6	2.0	1.4	7
10.0	20/20	-5.2	5.2	0.3	1.6	1.3	11
	40/40	-7.0	7.1	0.4	2.2	1.8	12
	60/60	-8.9	8.9	0.6	2.8	2.2	13
	80/80	-10.0	9.9	0.9	3.3	2.4	13
12.5	20/20	-7.8	8.0	0.3	2.4	2.0	14
	40/40	-10.6	10.7	0.5	3.3	2.7	16
	60/60	-12.3	12.0	0.9	3.9	2.9	15
	80/80	-14.5	14.1	1.1	4.5	3.5	16
15.0	20/20	-10.6	10.7	0.5	3.1	2.7	16
	40/40	-13.7	13.7	0.7	4.2	3.4	16
	60/60	-15.6	15.9	0.9	5.0	4.1	15
	80/80	-17.7	17.5	1.3	5.7	4.4	15
17.5	20/20	-13.4	13.5	0.7	4.1	3.4	16
	40/40	-18.6	18.6	1.1	5.8	4.7	16
	60/60	-19.3	19.5	1.9	6.8	4.9	12
	80/80	-20.2	20.1	2.8	7.8	5.0	9
20.0	20/20	-15.6	15.7	0.9	4.9	3.9	17
	40/40	-21.9	21.8	1.3	6.8	5.4	16
	60/60	-22.4	22.4	2.3	7.9	5.6	12
	80/80	-18.7	18.8	4.2	8.9	4.7	6

Note. %VAF = Percentage of Variance Accounted For.

Table A.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	5.1	-4.8	4.3	0.043	4.3	-26%	99
	40/40	2.8	-2.8	5.3	0.041	5.3	-13%	99
	60/60	1.4	-1.2	5.2	0.035	5.2	-5%	99
	80/80	2.3	-2.5	6.1	0.032	6.1	-11%	99
7.5	20/20	4.0	-3.3	6.2	0.034	6.2	-10%	99
	40/40	3.6	-3.4	7.5	0.030	7.5	-11%	99
	60/60	1.1	-0.8	8.4	0.029	8.4	-2%	99
	80/80	4.1	-3.6	9.3	0.026	9.3	-8%	99
10.0	20/20	5.2	-4.9	9.2	0.030	9.2	-13%	99
	40/40	3.2	-3.1	10.7	0.028	10.7	-7%	99
	60/60	4.2	-4.4	11.3	0.024	11.3	-10%	99
	80/80	2.9	-3.3	11.9	0.021	11.9	-8%	99
12.5	20/20	2.8	-3.0	10.1	0.025	10.1	-8%	99
	40/40	7.1	-6.8	12.4	0.022	12.4	-13%	99
	60/60	3.6	-3.8	12.9	0.020	12.9	-8%	99
	80/80	4.1	-4.1	13.6	0.018	13.6	-8%	99
15.0	20/20	5.8	-5.9	11.7	0.021	11.7	-13%	99
	40/40	4.0	-4.8	13.9	0.019	13.9	-10%	99
	60/60	6.2	-5.9	15.1	0.017	15.1	-9%	99
	80/80	5.2	-4.6	15.0	0.015	15.0	-7%	99
17.5	20/20	4.2	-4.1	12.7	0.018	12.7	-8%	99
	40/40	3.8	-3.2	14.7	0.015	14.7	-5%	99
	60/60	4.3	-4.0	16.1	0.013	16.1	-6%	99
	80/80	3.7	-3.6	16.3	0.011	16.3	-5%	99
20.0	20/20	5.5	-5.4	14.0	0.016	14.0	-10%	99
	40/40	3.2	-3.5	16.2	0.013	16.2	-6%	99
	60/60	2.0	-1.7	16.3	0.011	16.3	-2%	99
	80/80	3.0	-3.0	17.1	0.010	17.1	-4%	99

Note. %VAF = Percentage of Variance Accounted For.

Appendix B: Experiment 1 Fitting Measures of the Exponential-Clone-Bitflip Creature Type

Table B.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	534	9.7	9.4	0.77	99	99
	40/40	549	13.0	13.1	0.79	99	99
	60/60	545	15.1	15.3	0.80	99	99
	80/80	550	19.3	19.2	0.83	100	100
7.5	20/20	543	15.4	15.9	0.82	100	100
	40/40	544	19.5	19.4	0.83	99	100
	60/60	554	24.5	24.9	0.84	100	100
	80/80	553	28.3	28.4	0.84	100	100
10.0	20/20	550	20.8	20.9	0.82	100	100
	40/40	549	26.7	26.9	0.85	100	100
	60/60	553	33.0	32.9	0.86	100	100
	80/80	544	36.7	36.8	0.86	100	100
12.5	20/20	548	26.4	26.5	0.84	100	100
	40/40	549	32.8	32.6	0.85	100	100
	60/60	542	38.6	38.5	0.86	100	100
	80/80	547	44.4	44.6	0.86	100	100
15.0	20/20	553	30.9	30.9	0.83	100	100
	40/40	543	38.0	38.1	0.85	100	100
	60/60	538	44.8	44.6	0.86	100	100
	80/80	539	49.4	49.8	0.85	100	100
17.5	20/20	543	34.4	34.1	0.83	100	100
	40/40	530	42.1	42.5	0.86	100	100
	60/60	525	49.9	49.9	0.86	100	100
	80/80	526	52.8	52.7	0.84	100	99
20.0	20/20	535	38.0	38.0	0.84	100	100
	40/40	520	45.0	45.3	0.85	100	100
	60/60	518	50.7	50.8	0.84	100	100
	80/80	517	56.7	56.6	0.83	100	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table B.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	534	9.6	0.77	98	99
	40/40	549	13.0	0.79	99	99
	60/60	544	15.2	0.80	99	99
	80/80	550	19.3	0.83	100	100
7.5	20/20	543	15.7	0.82	100	100
	40/40	544	19.4	0.83	99	100
	60/60	555	24.8	0.84	100	100
	80/80	553	28.4	0.84	100	100
10.0	20/20	550	20.9	0.82	100	100
	40/40	549	26.8	0.85	100	100
	60/60	553	33.0	0.86	100	100
	80/80	544	36.7	0.86	100	100
12.5	20/20	548	26.5	0.84	100	100
	40/40	549	32.7	0.85	100	100
	60/60	542	38.6	0.86	100	100
	80/80	547	44.5	0.86	100	100
15.0	20/20	553	30.9	0.83	100	100
	40/40	543	38.0	0.85	100	100
	60/60	538	44.7	0.86	100	100
	80/80	539	49.6	0.85	100	100
17.5	20/20	543	34.3	0.83	100	100
	40/40	530	42.3	0.86	100	100
	60/60	525	49.9	0.86	100	100
	80/80	526	52.7	0.84	100	99
20.0	20/20	535	38.0	0.84	100	100
	40/40	520	45.2	0.85	100	100
	60/60	518	50.8	0.84	100	100
	80/80	517	56.6	0.83	100	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table B.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	ML
5.0	20/20	524	9.9	0.80	98	99
	40/40	548	13.1		99	99
	60/60	546	15.2		99	99
	80/80	567	18.6		100	99
7.5	20/20	536	16.0	0.83	100	100
	40/40	542	19.5		99	100
	60/60	562	24.5		100	100
	80/80	561	28.1		100	100
10.0	20/20	536	21.5	0.85	100	100
	40/40	551	26.7		100	100
	60/60	562	32.6		100	100
	80/80	554	36.4		100	100
12.5	20/20	540	26.8	0.85	100	100
	40/40	549	32.7		100	100
	60/60	549	38.4		100	100
	80/80	551	44.4		100	100
15.0	20/20	541	31.2	0.85	100	100
	40/40	548	37.9		100	100
	60/60	550	44.6		100	100
	80/80	538	49.6		100	100
17.5	20/20	531	34.5	0.85	100	100
	40/40	540	42.2		100	100
	60/60	544	49.9		100	100
	80/80	514	52.5		100	99
20.0	20/20	532	38.0	0.84	100	100
	40/40	532	45.2		100	100
	60/60	518	50.8		100	100
	80/80	506	56.3		100	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table B.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	543	13.7	0.80	97	99
	40/40		13.4		99	99
	60/60		13.8		99	99
	80/80		14.6		98	99
7.5	20/20	546	21.4	0.83	97	100
	40/40		21.0		99	100
	60/60		21.6		100	100
	80/80		22.8		98	100
10.0	20/20	550	29.1	0.85	97	100
	40/40		28.0		100	100
	60/60		29.9		100	100
	80/80		31.4		98	100
12.5	20/20	550	36.0	0.85	97	100
	40/40		35.0		100	100
	60/60		37.0		100	100
	80/80		38.8		97	100
15.0	20/20	553	42.4	0.85	96	100
	40/40		40.8		99	100
	60/60		43.5		100	100
	80/80		45.4		97	99
17.5	20/20	543	46.9	0.85	95	100
	40/40		44.9		99	100
	60/60		48.0		100	100
	80/80		50.7		96	99
20.0	20/20	539	51.3	0.84	94	100
	40/40		49.0		99	100
	60/60		52.2		99	100
	80/80		55.0		96	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table B.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	542	13.7	0.80	97	99
	40/40				98	99
	60/60				99	99
	80/80				98	99
7.5	20/20	544	21.3	0.83	97	100
	40/40				99	100
	60/60				100	100
	80/80				98	100
10.0	20/20	548	29.1	0.85	97	100
	40/40				99	100
	60/60				100	100
	80/80				97	100
12.5	20/20	547	36.0	0.85	96	100
	40/40				99	100
	60/60				100	100
	80/80				97	100
15.0	20/20	547	42.2	0.85	96	100
	40/40				99	100
	60/60				100	100
	80/80				96	100
17.5	20/20	537	46.7	0.85	95	100
	40/40				99	100
	60/60				100	100
	80/80				96	99
20.0	20/20	531	50.9	0.84	94	100
	40/40				99	100
	60/60				100	100
	80/80				95	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table B.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF	
				QLOE	ML
5.0	20/20	470	13.9	97	91
	40/40	482	18.2	98	92
	60/60	473	20.9	98	93
	80/80	479	25.1	99	95
7.5	20/20	476	20.8	99	94
	40/40	477	25.3	98	95
	60/60	481	30.9	99	96
	80/80	472	34.8	99	96
10.0	20/20	474	27.1	99	95
	40/40	475	32.9	99	97
	60/60	475	39.5	99	97
	80/80	461	43.4	99	97
12.5	20/20	467	32.4	99	96
	40/40	464	39.1	99	97
	60/60	455	44.9	99	97
	80/80	444	50.3	99	97
15.0	20/20	457	37.2	99	96
	40/40	452	44.3	99	97
	60/60	440	50.3	99	97
	80/80	421	54.6	99	96
17.5	20/20	441	40.5	99	96
	40/40	434	47.8	99	97
	60/60	422	54.4	99	97
	80/80	391	55.6	99	96
20.0	20/20	427	43.5	99	96
	40/40	412	49.8	99	97
	60/60	390	54.1	99	96
	80/80	368	57.4	99	95

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table B.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	ML
5.0	20/20	475	14.5	97	91
	40/40		17.4	98	92
	60/60		21.3	98	93
	80/80		24.5	99	95
7.5	20/20	476	20.8	99	94
	40/40		25.3	98	95
	60/60		30.2	99	96
	80/80		35.8	99	96
10.0	20/20	472	26.7	99	95
	40/40		32.4	99	97
	60/60		38.9	99	97
	80/80		45.9	99	97
12.5	20/20	459	31.0	99	96
	40/40		38.0	99	97
	60/60		45.9	99	97
	80/80		54.2	99	97
15.0	20/20	445	34.8	99	96
	40/40		42.7	99	97
	60/60		51.6	99	97
	80/80		61.2	99	96
17.5	20/20	425	37.1	99	96
	40/40		45.8	99	97
	60/60		55.3	99	97
	80/80		65.8	99	96
20.0	20/20	403	38.1	99	96
	40/40		47.5	99	97
	60/60		58.1	99	96
	80/80		68.6	98	95

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table B.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	474	19	95	91
	40/40			98	92
	60/60			98	93
	80/80			97	95
7.5	20/20	473	27	97	94
	40/40			98	95
	60/60			99	96
	80/80			97	96
10.0	20/20	469	36	96	95
	40/40			99	97
	60/60			99	97
	80/80			97	97
12.5	20/20	457	42	96	96
	40/40			99	97
	60/60			99	97
	80/80			97	97
15.0	20/20	443	48	95	96
	40/40			99	97
	60/60			99	97
	80/80			96	96
17.5	20/20	423	52	94	96
	40/40			98	97
	60/60			99	97
	80/80			95	96
20.0	20/20	401	54	93	96
	40/40			98	97
	60/60			99	96
	80/80			94	95

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table B.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	151	131	4	403	1
3	Constant a, $c_1 = c_2$	9	245	133	7	406	2
4	Constant a & c	6	4674	242	10	409	19*
5	Constant a, c & k	3	4016	254	13	412	16*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	7327	273	8	407	27*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5363	271	11	410	20*
8	Constant k & c, $a = 1$,	2	7808	391	14	413	20*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table B.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	177	50	4	403	4*
3	Constant a, $c_1 = c_2$	9	134	51	7	406	3*
4	Constant a & c	6	5474	182	10	409	30*
5	Constant a, c & k	3	4651	194	13	412	24*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3666	120	8	407	31*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2674	119	11	410	22*
8	Constant k & c, $a = 1$,	2	6267	260	14	413	24*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table B.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	9	23	4	403	0
3	Constant a, $c_1 = c_2$	9	15	23	7	406	1
4	Constant a & c	6	5375	154	10	409	35*
5	Constant a, c & k	3	4811	174	13	412	28*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2839	78	8	407	36*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2083	78	11	410	27*
8	Constant k & c, $a = 1$,	2	5978	225	14	413	27*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table B.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	11	10	4	403	1
3	Constant a, $c_1 = c_2$	9	5	10	7	406	1
4	Constant a & c	6	5679	149	10	409	38*
5	Constant a, c & k	3	4996	167	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2318	56	8	407	42*
7	Constant k, $a = 1$, $c_1 = c_2$	5	1723	56	11	410	31*
8	Constant k & c, $a = 1$,	2	5881	209	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table B.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	5	10	4	403	0
3	Constant a, $c_1 = c_2$	9	6	10	7	406	1
4	Constant a & c	6	5444	143	10	409	38*
5	Constant a, c & k	3	4789	161	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2164	53	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	1636	54	11	410	30*
8	Constant k & c, $a = 1$,	2	5616	200	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table B.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	13	9	4	403	1
3	Constant a, $c_1 = c_2$	9	13	9	7	406	1
4	Constant a & c	6	5025	132	10	409	38*
5	Constant a, c & k	3	4495	151	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1967	47	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	1522	50	11	410	31*
8	Constant k & c, $a = 1$,	2	5249	187	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table B.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	2	9	4	403	0
3	Constant a, $c_1 = c_2$	9	4	9	7	406	0
4	Constant a & c	6	4927	130	10	409	38*
5	Constant a, c & k	3	4344	146	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1782	44	8	407	40*
7	Constant k, $a = 1$, $c_1 = c_2$	5	1418	47	11	410	30*
8	Constant k & c, $a = 1$,	2	4996	178	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table B.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2043	1634	1318	979	982	929	943
2	$c_1 = c_2$	12	2040	1641	1312	976	976	927	936
3	Constant a, $c_1 = c_2$	9	2043	1640	1309	969	972	925	932
4	Constant a & c	6	2289	2169	2100	2086	2070	2035	2028
5	Constant a, c & k	3	2305	2194	2148	2132	2116	2088	2075
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2340	1999	1821	1678	1655	1613	1582
7	Constant k, $a = 1$, $c_1 = c_2$	5	2335	1994	1818	1679	1662	1628	1606
8	Constant k & c, $a = 1$	2	2484	2314	2254	2224	2206	2176	2157

Table B.17. Akaike Information Criteria (AIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1125	-1305	-1378	-1437	-1427	-1396	-1379
2	$c_1 = c_2$	8	-1130	-1307	-1385	-1445	-1435	-1402	-1387
3, 4, 5	Constant a & $c_1 = c_2$	2	-1124	-1305	-1358	-1443	-1429	-1394	-1394
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-661	-741	-780	-825	-863	-895	-915

Table B.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2108	1699	1383	1044	1046	993	1007
2	$c_1 = c_2$	12	2088	1689	1360	1024	1024	975	984
3	Constant a, $c_1 = c_2$	9	2079	1676	1345	1005	1008	961	968
4	Constant a & c	6	2313	2193	2124	2110	2094	2059	2053
5	Constant a, c & k	3	2317	2206	2160	2144	2128	2100	2087
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2372	2031	1853	1710	1687	1645	1615
7	Constant k, $a = 1$, $c_1 = c_2$	5	2355	2014	1838	1700	1682	1648	1627
8	Constant k & c, $a = 1$	2	2492	2322	2262	2232	2214	2184	2165

Table B.19. Bayes Information Criteria (BIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1085	-1265	-1338	-1397	-1387	-1356	-1339
2	$c_1 = c_2$	8	-1103	-1281	-1358	-1418	-1408	-1376	-1360
3, 4, 5	Constant a & $c_1 = c_2$	2	-1118	-1298	-1351	-1437	-1422	-1388	-1388
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-661	-741	-780	-825	-863	-895	-915

Table B.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	-2.0	2.0	0.5	1.0	0.5	2
	40/40	-4.3	4.4	0.8	1.9	1.1	4
	60/60	-6.5	6.4	1.1	2.7	1.6	5
	80/80	-10.8	10.9	0.7	3.5	2.7	13
7.5	20/20	-8.8	8.7	0.8	3.0	2.1	10
	40/40	-10.8	10.2	2.0	4.4	2.4	8
	60/60	-22.4	21.9	1.1	6.5	5.4	22
	80/80	-23.2	23.0	1.3	7.0	5.7	21
10.0	20/20	-15.9	15.8	0.9	4.9	3.9	16
	40/40	-29.3	29.0	1.2	8.3	7.2	26
	60/60	-32.5	32.2	1.7	9.7	8.0	27
	80/80	-31.3	31.1	2.3	10.0	7.7	23
12.5	20/20	-27.0	26.7	0.7	7.3	6.6	30
	40/40	-40.8	41.2	0.7	11.1	10.4	32
	60/60	-43.2	42.8	2.1	12.7	10.6	31
	80/80	-47.8	48.1	1.8	13.8	12.1	36
15.0	20/20	-31.6	31.2	1.2	8.9	7.7	27
	40/40	-45.0	45.2	1.7	13.1	11.3	30
	60/60	-52.9	53.6	1.7	15.3	13.6	37
	80/80	-49.3	48.8	3.5	15.6	12.1	31
17.5	20/20	-35.4	35.4	1.3	10.1	8.9	27
	40/40	-52.7	52.2	2.3	15.2	13.0	34
	60/60	-56.8	57.2	2.7	17.1	14.4	39
	80/80	-54.7	54.1	4.5	17.9	13.4	35
20.0	20/20	-39.9	39.8	1.7	11.6	9.9	29
	40/40	-57.3	57.8	2.4	17.0	14.6	36
	60/60	-56.1	56.1	4.4	18.4	14.0	32
	80/80	-56.2	56.4	5.3	19.4	14.1	35

Note. %VAF = Percentage of Variance Accounted For.

Table B.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	7.0	-6.4	9.4	0.038	9.4	-16%	98
	40/40	1.1	-2.6	11.5	0.028	11.5	-9%	99
	60/60	-2.3	2.5	12.0	0.025	12.7	6%	98
	80/80	-2.8	2.7	12.0	0.023	12.6	5%	98
7.5	20/20	2.8	-2.1	12.5	0.025	12.5	-3%	99
	40/40	-1.5	0.1	16.9	0.021	16.9	-2%	99
	60/60	-4.7	4.4	16.5	0.018	17.6	6%	98
	80/80	-2.8	3.1	16.7	0.016	17.6	5%	99
10.0	20/20	-8.1	6.4	15.2	0.020	16.4	8%	99
	40/40	-6.8	5.0	20.2	0.016	21.0	4%	99
	60/60	-9.8	9.8	19.1	0.013	21.5	13%	98
	80/80	1.6	-2.3	21.4	0.011	21.4	-3%	97
12.5	20/20	-9.0	8.7	16.0	0.016	18.1	13%	99
	40/40	-16.9	17.0	19.5	0.013	23.8	22%	98
	60/60	-17.6	16.1	20.6	0.010	24.3	18%	96
	80/80	-12.1	11.2	21.1	0.009	23.7	12%	96
15.0	20/20	0.4	-0.7	20.5	0.014	20.5	-1%	99
	40/40	-5.4	4.9	24.4	0.011	25.5	5%	97
	60/60	-19.8	19.8	21.3	0.008	26.2	23%	96
	80/80	-10.6	10.3	22.9	0.007	25.4	11%	95
17.5	20/20	-9.8	9.9	18.6	0.012	21.1	13%	98
	40/40	-14.7	14.2	23.5	0.009	26.9	14%	96
	60/60	-19.9	20.7	21.6	0.007	27.0	25%	94
	80/80	-16.8	16.0	22.4	0.006	26.2	17%	92
20.0	20/20	-7.3	6.7	20.9	0.010	22.5	7%	98
	40/40	-19.0	19.5	22.3	0.007	27.3	22%	95
	60/60	-17.5	18.4	22.8	0.006	27.6	21%	91
	80/80	-21.0	21.3	21.3	0.005	26.7	25%	87

Note. %VAF = Percentage of Variance Accounted For.

Appendix C: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Uniform Creature Type

Table C.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	ML
5.0	20/20	524	11.3	12.3	0.73	94	96
	40/40	541	17.3	18.0	0.74	94	96
	60/60	529	21.6	22.8	0.76	97	98
	80/80	491	21.6	23.2	0.75	98	98
7.5	20/20	514	17.1	17.7	0.76	96	98
	40/40	499	22.3	22.3	0.77	98	99
	60/60	475	26.9	27.2	0.79	99	99
	80/80	423	25.4	25.7	0.78	98	99
10.0	20/20	496	21.2	21.0	0.77	98	99
	40/40	469	25.4	26.2	0.78	98	99
	60/60	408	25.0	26.3	0.79	99	99
	80/80	346	22.3	22.1	0.78	98	99
12.5	20/20	480	25.1	25.3	0.79	100	100
	40/40	423	26.7	27.0	0.79	99	100
	60/60	363	25.3	25.4	0.79	99	100
	80/80	306	21.4	21.9	0.79	99	100
15.0	20/20	458	27.1	27.6	0.79	99	100
	40/40	377	24.8	25.2	0.79	99	100
	60/60	320	22.7	23.5	0.79	99	99
	80/80	271	20.1	19.9	0.78	99	99
17.5	20/20	430	27.4	27.6	0.79	100	100
	40/40	346	24.4	24.7	0.79	99	100
	60/60	289	20.9	21.0	0.77	99	99
	80/80	247	18.7	18.8	0.78	99	100
20.0	20/20	402	28.0	27.9	0.79	99	100
	40/40	320	23.3	23.0	0.78	99	100
	60/60	262	19.2	19.4	0.77	99	100
	80/80	228	17.0	17.1	0.76	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table C.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	520	12.1	0.74	93	96
	40/40	539	17.8	0.74	94	96
	60/60	527	22.5	0.76	96	98
	80/80	488	23.0	0.76	97	98
7.5	20/20	513	17.6	0.77	96	97
	40/40	499	22.3	0.77	98	99
	60/60	475	27.1	0.79	99	99
	80/80	423	25.6	0.78	98	99
10.0	20/20	496	21.1	0.77	98	99
	40/40	468	25.9	0.78	98	99
	60/60	409	26.2	0.79	99	99
	80/80	346	22.2	0.78	98	99
12.5	20/20	480	25.2	0.79	99	100
	40/40	423	26.8	0.79	99	100
	60/60	363	25.3	0.79	99	100
	80/80	306	21.7	0.79	99	100
15.0	20/20	458	27.4	0.79	99	100
	40/40	377	25.0	0.79	99	100
	60/60	321	23.4	0.79	99	99
	80/80	271	20.0	0.78	99	99
17.5	20/20	430	27.5	0.79	100	100
	40/40	346	24.6	0.79	99	100
	60/60	289	21.0	0.77	99	99
	80/80	247	18.8	0.78	99	100
20.0	20/20	402	27.9	0.79	99	100
	40/40	320	23.1	0.78	99	100
	60/60	262	19.3	0.77	99	100
	80/80	228	17.1	0.76	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table C.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	515	12.3	0.75	93	96
	40/40	535	17.9		94	96
	60/60	536	22.3		96	98
	80/80	493	22.9		97	98
7.5	20/20	508	17.8	0.78	96	97
	40/40	494	22.4		98	99
	60/60	486	26.8		99	99
	80/80	426	25.5		98	99
10.0	20/20	491	21.3	0.78	98	99
	40/40	467	25.9		98	99
	60/60	416	26.0		99	99
	80/80	345	22.3		98	99
12.5	20/20	481	25.2	0.79	99	100
	40/40	425	26.8		99	100
	60/60	364	25.3		99	100
	80/80	304	21.7		99	100
15.0	20/20	462	27.3	0.79	99	100
	40/40	376	25.1		99	100
	60/60	321	23.3		99	99
	80/80	269	20.1		99	99
17.5	20/20	435	27.4	0.78	100	100
	40/40	350	24.5		99	99
	60/60	285	21.0		99	99
	80/80	246	18.8		99	100
20.0	20/20	416	27.8	0.77	99	100
	40/40	321	23.1		99	100
	60/60	260	19.3		99	100
	80/80	223	17.1		99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table C.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	523	19.4	0.75	80	96
	40/40		18.2		93	96
	60/60		19.1		96	98
	80/80		19.4		90	98
7.5	20/20	487	24.2	0.77	84	97
	40/40		23.3		97	99
	60/60		24.8		98	99
	80/80		26.5		91	99
10.0	20/20	448	26.7	0.77	84	99
	40/40		24.8		97	99
	60/60		26.7		98	99
	80/80		30.0		91	98
12.5	20/20	410	28.7	0.79	86	100
	40/40		27.0		98	99
	60/60		29.6		98	99
	80/80		31.5		92	99
15.0	20/20	372	27.8	0.78	85	100
	40/40		26.2		98	99
	60/60		28.1		98	99
	80/80		31.1		92	99
17.5	20/20	340	26.7	0.78	85	100
	40/40		25.0		98	99
	60/60		27.4		98	99
	80/80		29.2		92	99
20.0	20/20	311	25.1	0.77	84	100
	40/40		24.1		98	99
	60/60		25.6		98	100
	80/80		27.2		92	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table C.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	518	18.9	0.75	80	96
	40/40				92	96
	60/60				96	98
	80/80				90	98
7.5	20/20	479	23.8	0.77	83	97
	40/40				97	99
	60/60				98	99
	80/80				90	99
10.0	20/20	438	26.2	0.78	83	99
	40/40				96	99
	60/60				98	99
	80/80				89	99
12.5	20/20	401	28.1	0.79	85	100
	40/40				97	100
	60/60				98	100
	80/80				91	100
15.0	20/20	365	27.5	0.79	84	100
	40/40				97	100
	60/60				98	99
	80/80				90	99
17.5	20/20	332	26.1	0.78	84	100
	40/40				97	99
	60/60				98	99
	80/80				91	100
20.0	20/20	304	24.6	0.77	83	100
	40/40				97	100
	60/60				99	100
	80/80				91	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table C.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	439	18.5	88	86
	40/40	434	25.5	90	85
	60/60	412	29.7	93	89
	80/80	381	31.2	94	89
7.5	20/20	421	24.3	93	89
	40/40	392	29.3	95	91
	60/60	373	34.2	97	92
	80/80	327	32.1	96	92
10.0	20/20	400	28.6	95	91
	40/40	362	32.5	96	91
	60/60	320	32.3	97	92
	80/80	271	27.9	96	91
12.5	20/20	382	32.2	98	93
	40/40	336	34.1	97	93
	60/60	285	31.2	98	93
	80/80	241	26.5	98	92
15.0	20/20	360	34.0	98	93
	40/40	298	31.7	97	92
	60/60	251	28.3	97	92
	80/80	213	24.1	97	92
17.5	20/20	333	33.8	98	93
	40/40	269	29.7	98	92
	60/60	223	25.4	97	91
	80/80	194	22.6	97	92
20.0	20/20	310	33.5	98	93
	40/40	244	27.8	97	91
	60/60	201	23.0	97	91
	80/80	175	20.2	97	90

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table C.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	421	16.4	88	86
	40/40		23.7	90	85
	60/60		31.4	93	89
	80/80		39.5	93	89
7.5	20/20	387	19.1	93	89
	40/40		28.4	95	91
	60/60		37.2	97	92
	80/80		47.1	95	92
10.0	20/20	349	19.9	94	91
	40/40		29.8	96	91
	60/60		39.8	97	92
	80/80		50.0	94	91
12.5	20/20	320	20.1	96	93
	40/40		30.4	97	93
	60/60		41.1	97	93
	80/80		51.1	95	92
15.0	20/20	289	19.1	96	93
	40/40		29.4	97	92
	60/60		39.5	97	92
	80/80		48.7	94	92
17.5	20/20	260	17.8	95	93
	40/40		27.3	98	92
	60/60		36.7	96	91
	80/80		44.9	94	92
20.0	20/20	235	16.2	95	93
	40/40		25.3	97	91
	60/60		33.8	96	91
	80/80		41.1	94	90

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table C.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	413	26	76	86
	40/40			88	85
	60/60			93	89
	80/80			86	89
7.5	20/20	374	31	80	89
	40/40			94	91
	60/60			97	92
	80/80			87	92
10.0	20/20	335	33	80	91
	40/40			94	91
	60/60			97	92
	80/80			86	91
12.5	20/20	307	34	84	93
	40/40			95	93
	60/60			97	93
	80/80			88	92
15.0	20/20	276	33	82	93
	40/40			95	92
	60/60			97	92
	80/80			88	92
17.5	20/20	249	30	82	93
	40/40			95	92
	60/60			96	91
	80/80			88	92
20.0	20/20	225	28	81	93
	40/40			95	91
	60/60			96	91
	80/80			88	90

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table C.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	2435	267	4	403	9*
3	Constant a, $c_1 = c_2$	9	1475	267	7	406	6*
4	Constant a & c	6	13499	569	10	409	24*
5	Constant a, c & k	3	10606	572	13	412	19*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	11553	468	8	407	25*
7	Constant k, $a = 1$, $c_1 = c_2$	5	8662	471	11	410	18*
8	Constant k & c, $a = 1$,	2	15635	767	14	413	20*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table C.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	233	119	4	403	2
3	Constant a, $c_1 = c_2$	9	181	119	7	406	2
4	Constant a & c	6	10896	382	10	409	29*
5	Constant a, c & k	3	9193	405	13	412	23*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	5711	228	8	407	25*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4753	243	11	410	20*
8	Constant k & c, $a = 1$,	2	11911	518	14	413	23*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table C.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	187	75	4	403	3*
3	Constant a, $c_1 = c_2$	9	129	74	7	406	2
4	Constant a & c	6	9930	314	10	409	32*
5	Constant a, c & k	3	8547	341	13	412	25*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3916	149	8	407	26*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3878	176	11	410	22*
8	Constant k & c, $a = 1$,	2	10509	427	14	413	25*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table C.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	26	26	4	403	1
3	Constant a, $c_1 = c_2$	9	13	26	7	406	0
4	Constant a & c	6	9900	267	10	409	37*
5	Constant a, c & k	3	8379	290	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2891	82	8	407	35*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3477	119	11	410	29*
8	Constant k & c, $a = 1$,	2	9619	351	14	413	27*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table C.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	89	26	4	403	3*
3	Constant a, $c_1 = c_2$	9	51	26	7	406	2
4	Constant a & c	6	8317	228	10	409	36*
5	Constant a, c & k	3	7086	248	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2237	69	8	407	33*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3115	108	11	410	29*
8	Constant k & c, $a = 1$,	2	8186	302	14	413	27*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table C.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	11	15	4	403	1
3	Constant a, $c_1 = c_2$	9	7	14	7	406	0
4	Constant a & c	6	7054	187	10	409	38*
5	Constant a, c & k	3	5960	202	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1999	54	8	407	37*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2866	91	11	410	31*
8	Constant k & c, $a = 1$,	2	6859	247	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table C.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	10	12	4	403	1
3	Constant a, $c_1 = c_2$	9	16	12	7	406	1
4	Constant a & c	6	6332	167	10	409	38*
5	Constant a, c & k	3	5248	178	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1784	47	8	407	38*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2731	85	11	410	32*
8	Constant k & c, $a = 1$,	2	6055	217	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table C.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2304	2000	1802	1370	1359	1130	1063
2	$c_1 = c_2$	12	2335	2000	1805	1366	1365	1125	1058
3	Constant a, $c_1 = c_2$	9	2331	1997	1801	1360	1359	1119	1058
4	Constant a & c	6	2644	2478	2397	2330	2264	2180	2134
5	Constant a, c & k	3	2643	2499	2428	2360	2296	2211	2157
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2564	2266	2089	1842	1767	1663	1611
7	Constant k, $a = 1$, $c_1 = c_2$	5	2565	2288	2154	1991	1952	1881	1854
8	Constant k & c, $a = 1$	2	2764	2601	2521	2439	2376	2292	2239

Table C.17. Akaike Information Criteria (AIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-966	-1084	-1131	-1292	-1278	-1342	-1384
2	$c_1 = c_2$	8	-966	-1091	-1132	-1298	-1280	-1348	-1390
3, 4, 5	Constant a & c	2	-977	-1101	-1144	-1308	-1290	-1355	-1387
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-679	-701	-713	-724	-738	-746	-756

Table C.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2368	2065	1867	1435	1423	1194	1127
2	$c_1 = c_2$	12	2384	2049	1853	1415	1414	1173	1107
3	Constant a, $c_1 = c_2$	9	2368	2034	1837	1396	1396	1156	1095
4	Constant a & c	6	2668	2502	2421	2354	2288	2205	2158
5	Constant a, c & k	3	2656	2511	2440	2372	2308	2223	2169
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2597	2298	2121	1874	1799	1695	1643
7	Constant k, $a = 1$, $c_1 = c_2$	5	2585	2309	2174	2011	1973	1901	1874
8	Constant k & c, $a = 1$	2	2772	2609	2529	2447	2385	2300	2248

Table C.19. Bayes Information Criteria (BIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-925	-1044	-1091	-1252	-1238	-1302	-1344
2	$c_1 = c_2$	8	-939	-1064	-1106	-1271	-1254	-1322	-1364
3, 4, 5	Constant a & c	2	-971	-1094	-1137	-1301	-1284	-1348	-1380
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-679	-701	-713	-724	-738	-746	-756

Table C.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	0.1	-0.1	0.0	0.0	0.0	3
	40/40	0.1	-0.1	0.1	0.0	0.0	2
	60/60	0.0	-0.1	0.0	0.0	0.0	1
	80/80	0.0	0.0	0.1	0.0	0.0	0
7.5	20/20	0.0	0.0	0.1	0.1	0.0	0
	40/40	-0.1	0.1	0.1	0.1	0.0	0
	60/60	-0.2	0.2	0.1	0.1	0.0	1
	80/80	-0.2	0.2	0.1	0.1	0.0	1
10.0	20/20	-0.1	0.1	0.1	0.1	0.0	0
	40/40	-0.2	0.2	0.1	0.2	0.0	1
	60/60	-0.6	0.5	0.1	0.2	0.1	5
	80/80	-0.6	0.6	0.1	0.3	0.2	2
12.5	20/20	-0.8	0.8	0.1	0.3	0.2	5
	40/40	-0.6	0.6	0.1	0.3	0.2	3
	60/60	-0.9	0.9	0.1	0.4	0.2	4
	80/80	-1.2	1.2	0.2	0.5	0.3	4
15.0	20/20	-0.9	0.9	0.2	0.4	0.2	4
	40/40	-0.7	0.7	0.2	0.4	0.2	2
	60/60	-1.4	1.3	0.2	0.5	0.3	6
	80/80	-1.9	1.9	0.2	0.7	0.5	5
17.5	20/20	-1.5	1.4	0.2	0.6	0.4	5
	40/40	-1.5	1.5	0.2	0.6	0.4	5
	60/60	-1.9	1.8	0.3	0.7	0.4	5
	80/80	-2.3	2.2	0.3	0.9	0.5	5
20.0	20/20	-2.3	2.3	0.2	0.8	0.6	7
	40/40	-2.1	2.1	0.3	0.8	0.5	5
	60/60	-2.7	2.6	0.3	0.9	0.6	6
	80/80	-3.0	3.0	0.4	1.1	0.7	5

Note. %VAF = Percentage of Variance Accounted For.

Table C.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	-0.2	0.2	0.4	0.052	0.4	13%	93
	40/40	0.6	-0.5	0.7	0.060	0.7	-17%	96
	60/60	0.4	-0.5	0.7	0.055	0.7	-24%	95
	80/80	-0.4	0.4	0.5	0.050	0.6	20%	94
7.5	20/20	1.1	-1.2	1.4	0.058	1.4	-23%	97
	40/40	1.7	-1.8	1.6	0.059	1.6	-29%	98
	60/60	1.9	-1.8	1.7	0.056	1.7	-24%	98
	80/80	0.6	-0.8	1.7	0.051	1.7	-13%	98
10.0	20/20	0.4	-0.3	1.7	0.048	1.7	-3%	98
	40/40	2.1	-1.8	2.1	0.051	2.1	-17%	98
	60/60	2.7	-2.6	2.5	0.047	2.5	-24%	98
	80/80	1.3	-1.5	3.1	0.051	3.1	-14%	98
12.5	20/20	1.1	-1.1	2.5	0.043	2.5	-11%	99
	40/40	0.3	-0.2	2.7	0.047	2.7	0%	98
	60/60	1.4	-1.6	3.7	0.050	3.7	-12%	97
	80/80	1.7	-1.9	4.4	0.048	4.4	-11%	97
15.0	20/20	2.3	-2.1	3.6	0.042	3.6	-14%	98
	40/40	2.8	-2.7	3.7	0.042	3.7	-17%	99
	60/60	2.7	-2.7	4.5	0.044	4.5	-15%	98
	80/80	2.4	-2.2	5.4	0.044	5.4	-9%	98
17.5	20/20	4.1	-4.1	4.9	0.041	4.9	-21%	98
	40/40	4.3	-4.1	4.9	0.039	4.9	-20%	99
	60/60	0.6	-0.5	4.9	0.040	4.9	-2%	98
	80/80	4.4	-4.3	6.7	0.041	6.7	-16%	98
20.0	20/20	2.4	-2.7	5.7	0.039	5.7	-13%	98
	40/40	3.8	-4.0	6.1	0.038	6.1	-17%	98
	60/60	2.5	-2.9	6.3	0.037	6.3	-13%	97
	80/80	3.3	-3.5	7.8	0.038	7.8	-12%	98

Note. %VAF = Percentage of Variance Accounted For.

Appendix D: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Linear Creature Type

Table D.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	535	11.9	12.4	0.73	94	97
	40/40	541	17.5	18.4	0.76	95	97
	60/60	404	18.5	19.6	0.73	98	99
	80/80	347	19.4	19.9	0.74	98	99
7.5	20/20	519	16.8	17.0	0.76	98	98
	40/40	507	22.1	22.6	0.77	98	99
	60/60	326	17.7	18.5	0.75	99	99
	80/80	275	16.4	17.0	0.74	99	99
10.0	20/20	514	22.2	22.7	0.78	99	100
	40/40	489	27.0	26.8	0.78	99	100
	60/60	281	17.0	17.0	0.76	99	99
	80/80	231	14.1	14.3	0.73	99	99
12.5	20/20	500	25.6	26.0	0.78	99	99
	40/40	446	28.2	29.1	0.80	99	99
	60/60	246	14.9	15.3	0.75	99	99
	80/80	200	12.2	12.4	0.73	99	99
15.0	20/20	475	27.7	28.2	0.79	100	100
	40/40	411	28.7	28.6	0.79	99	100
	60/60	221	13.6	13.6	0.74	99	99
	80/80	182	11.1	11.1	0.71	99	99
17.5	20/20	447	28.1	27.6	0.78	100	100
	40/40	371	26.5	26.3	0.78	99	100
	60/60	203	12.7	12.6	0.73	99	99
	80/80	166	10.2	10.2	0.72	99	99
20.0	20/20	420	28.6	28.7	0.79	100	100
	40/40	340	25.2	25.4	0.78	99	100
	60/60	188	11.3	11.4	0.72	99	100
	80/80	155	9.2	9.1	0.70	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table D.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	534	12.3	0.74	94	97
	40/40	540	18.2	0.76	95	97
	60/60	402	19.3	0.73	97	98
	80/80	346	19.6	0.74	98	99
7.5	20/20	519	16.9	0.76	98	98
	40/40	507	22.4	0.77	98	99
	60/60	325	18.3	0.75	99	99
	80/80	275	16.8	0.74	99	99
10.0	20/20	514	22.5	0.78	99	99
	40/40	489	26.9	0.78	99	100
	60/60	281	17.0	0.76	99	99
	80/80	231	14.2	0.73	99	99
12.5	20/20	500	25.9	0.79	99	99
	40/40	446	28.9	0.80	99	99
	60/60	246	15.2	0.75	99	99
	80/80	200	12.3	0.73	99	99
15.0	20/20	475	28.0	0.79	100	100
	40/40	411	28.6	0.79	99	100
	60/60	221	13.6	0.74	99	99
	80/80	182	11.1	0.72	99	99
17.5	20/20	447	27.9	0.78	100	100
	40/40	371	26.4	0.78	99	100
	60/60	203	12.6	0.73	99	99
	80/80	166	10.2	0.72	99	99
20.0	20/20	420	28.7	0.79	100	100
	40/40	340	25.3	0.78	99	100
	60/60	188	11.4	0.72	99	100
	80/80	155	9.2	0.70	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table D.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	531	12.4	0.74	94	97
	40/40	551	17.8		95	97
	60/60	397	19.5		97	98
	80/80	347	19.6		98	99
7.5	20/20	521	16.8	0.76	98	98
	40/40	517	22.1		98	99
	60/60	324	18.3		99	99
	80/80	270	17.0		99	99
10.0	20/20	528	22.0	0.76	99	99
	40/40	503	26.6		99	100
	60/60	279	17.1		99	99
	80/80	223	14.4		99	99
12.5	20/20	516	25.5	0.76	99	99
	40/40	473	28.6		99	99
	60/60	242	15.3		99	99
	80/80	193	12.5		99	99
15.0	20/20	505	27.6	0.76	99	100
	40/40	439	28.5		99	99
	60/60	217	13.7		99	99
	80/80	174	11.3		99	99
17.5	20/20	472	27.7	0.75	100	100
	40/40	391	26.3		99	99
	60/60	199	12.7		99	99
	80/80	160	10.4		99	99
20.0	20/20	460	28.6	0.74	99	99
	40/40	365	25.4		99	99
	60/60	183	11.5		99	100
	80/80	148	9.3		99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table D.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	505	24.4	0.73	48	97
	40/40		20.0		79	95
	60/60		25.1		93	98
	80/80		28.0		76	97
7.5	20/20	466	30.1	0.75	54	98
	40/40		24.8		82	97
	60/60		31.2		95	99
	80/80		34.2		78	97
10.0	20/20	460	36.7	0.75	58	99
	40/40		30.5		83	98
	60/60		38.3		95	99
	80/80		41.7		77	98
12.5	20/20	398	33.8	0.75	58	99
	40/40		27.3		86	98
	60/60		34.7		95	99
	80/80		38.1		78	98
15.0	20/20	367	32.9	0.74	60	99
	40/40		27.7		84	98
	60/60		33.9		95	99
	80/80		37.0		77	98
17.5	20/20	325	29.1	0.74	60	99
	40/40		24.9		85	98
	60/60		30.0		95	99
	80/80		32.6		78	98
20.0	20/20	285	25.3	0.73	60	99
	40/40		21.9		84	98
	60/60		25.7		95	100
	80/80		28.0		78	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table D.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF	
					QLOE	ML
5.0	20/20	464	21.8	0.74	47	97
	40/40				70	97
	60/60				94	98
	80/80				71	99
7.5	20/20	421	26.3	0.75	52	98
	40/40				74	99
	60/60				96	99
	80/80				74	99
10.0	20/20	397	30.4	0.76	55	99
	40/40				75	99
	60/60				96	99
	80/80				75	99
12.5	20/20	353	29.3	0.76	55	99
	40/40				77	99
	60/60				96	99
	80/80				77	99
15.0	20/20	323	28.2	0.75	56	100
	40/40				77	99
	60/60				96	99
	80/80				77	99
17.5	20/20	291	25.5	0.75	57	100
	40/40				78	99
	60/60				96	99
	80/80				77	99
20.0	20/20	260	22.6	0.74	57	99
	40/40				78	99
	60/60				97	100
	80/80				77	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table D.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	450	18.7	89	86
	40/40	444	25.7	92	88
	60/60	305	25.8	93	86
	80/80	265	25.5	95	87
7.5	20/20	423	23.5	95	90
	40/40	403	29.9	95	91
	60/60	253	23.3	96	89
	80/80	212	21.4	96	87
10.0	20/20	418	30.2	97	92
	40/40	380	34.5	97	92
	60/60	219	21.2	97	89
	80/80	179	18.0	95	86
12.5	20/20	394	33.1	98	92
	40/40	346	34.9	98	93
	60/60	193	19.0	96	88
	80/80	157	15.3	96	86
15.0	20/20	370	34.9	98	93
	40/40	314	34.2	98	93
	60/60	172	16.8	96	87
	80/80	142	13.9	94	83
17.5	20/20	338	33.9	98	92
	40/40	281	31.8	98	92
	60/60	159	15.6	96	86
	80/80	131	12.8	94	84
20.0	20/20	318	34.2	98	92
	40/40	255	29.8	97	91
	60/60	146	14.2	95	84
	80/80	122	11.6	93	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table D.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	396	12.4	88	86
	40/40		18.8	91	88
	60/60		47.4	91	86
	80/80		62.3	89	87
7.5	20/20	351	13.4	92	90
	40/40		20.7	94	91
	60/60		50.9	92	89
	80/80		66.7	88	87
10.0	20/20	321	14.5	93	92
	40/40		22.5	96	92
	60/60		53.1	91	89
	80/80		67.7	84	86
12.5	20/20	287	13.9	92	92
	40/40		21.8	97	93
	60/60		49.9	91	88
	80/80		63.4	83	86
15.0	20/20	256	12.7	91	93
	40/40		20.4	96	93
	60/60		45.1	90	87
	80/80		57.2	80	83
17.5	20/20	230	11.7	90	92
	40/40		19.1	96	92
	60/60		40.3	89	86
	80/80		50.9	81	84
20.0	20/20	206	10.1	89	92
	40/40		16.9	95	91
	60/60		34.9	89	84
	80/80		44.1	79	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table D.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF	
				QLOE	ML
5.0	20/20	348	29	42	86
	40/40			67	88
	60/60			90	86
	80/80			67	87
7.5	20/20	303	31	49	90
	40/40			70	91
	60/60			93	89
	80/80			70	87
10.0	20/20	275	34	52	92
	40/40			72	92
	60/60			94	89
	80/80			71	86
12.5	20/20	244	32	52	92
	40/40			75	93
	60/60			94	88
	80/80			73	86
15.0	20/20	220	31	53	93
	40/40			75	93
	60/60			93	87
	80/80			72	83
17.5	20/20	200	28	54	92
	40/40			76	92
	60/60			93	86
	80/80			72	84
20.0	20/20	181	25	54	92
	40/40			76	91
	60/60			92	84
	80/80			71	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table D.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	976	222	4	403	4*
3	Constant a, $c_1 = c_2$	9	578	221	7	406	3*
4	Constant a & c	6	47626	1374	10	409	35*
5	Constant a, c & k	3	42383	1545	13	412	27*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	8906	385	8	407	23*
7	Constant k, $a = 1$, $c_1 = c_2$	5	9711	469	11	410	21*
8	Constant k & c, $a = 1$,	2	44836	1727	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table D.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	222	74	4	403	3*
3	Constant a, $c_1 = c_2$	9	86	73	7	406	1
4	Constant a & c	6	42728	1116	10	409	38*
5	Constant a, c & k	3	37688	1260	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	6056	190	8	407	32*
7	Constant k, $a = 1$, $c_1 = c_2$	5	8360	295	11	410	28*
8	Constant k & c, $a = 1$,	2	38851	1387	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table D.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	39	32	4	403	1
3	Constant a, $c_1 = c_2$	9	33	31	7	406	1
4	Constant a & c	6	38221	965	10	409	40*
5	Constant a, c & k	3	33861	1099	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3528	100	8	407	35*
7	Constant k, $a = 1$, $c_1 = c_2$	5	7424	230	11	410	32*
8	Constant k & c, $a = 1$,	2	34389	1196	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table D.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	97	24	4	403	4*
3	Constant a, $c_1 = c_2$	9	127	25	7	406	5*
4	Constant a & c	6	31083	783	10	409	40*
5	Constant a, c & k	3	28126	910	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2538	73	8	407	35*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6741	204	11	410	33*
8	Constant k & c, $a = 1$,	2	28413	986	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table D.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	25	14	4	403	2
3	Constant a, $c_1 = c_2$	9	96	15	7	406	6*
4	Constant a & c	6	26421	659	10	409	40*
5	Constant a, c & k	3	23339	750	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2320	59	8	407	39*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6557	189	11	410	35*
8	Constant k & c, $a = 1$,	2	23670	816	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table D.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	28	10	4	403	3*
3	Constant a, $c_1 = c_2$	9	68	11	7	406	6*
4	Constant a & c	6	20185	503	10	409	40*
5	Constant a, c & k	3	17652	567	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2104	51	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5606	160	11	410	35*
8	Constant k & c, $a = 1$,	2	18045	621	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table D.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	8	9	4	403	1
3	Constant a, $c_1 = c_2$	9	94	11	7	406	9*
4	Constant a & c	6	17253	431	10	409	40*
5	Constant a, c & k	3	14936	480	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1870	46	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5377	153	11	410	35*
8	Constant k & c, $a = 1$,	2	15199	524	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table D.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2248	1798	1449	1328	1103	974	936
2	$c_1 = c_2$	12	2258	1802	1446	1337	1102	978	932
3	Constant a, $c_1 = c_2$	9	2253	1792	1443	1352	1137	1007	991
4	Constant a & c	6	3011	2924	2864	2777	2705	2593	2528
5	Constant a, c & k	3	3057	2972	2915	2836	2756	2639	2570
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2484	2190	1923	1791	1703	1644	1597
7	Constant k, $a = 1$, $c_1 = c_2$	5	2563	2370	2266	2216	2185	2116	2097
8	Constant k & c, $a = 1$	2	3102	3011	2949	2869	2790	2677	2606

Table D.17. Akaike Information Criteria (AIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1002	-1150	-1275	-1298	-1372	-1390	-1434
2	$c_1 = c_2$	8	-1003	-1154	-1280	-1299	-1379	-1396	-1441
3, 4, 5	Constant a & $c_1 = c_2$	2	-1011	-1157	-1262	-1270	-1308	-1351	-1343
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-670	-693	-707	-721	-735	-745	-755

Table D.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2312	1862	1514	1393	1167	1039	1001
2	$c_1 = c_2$	12	2307	1851	1495	1385	1151	1026	980
3	Constant a, $c_1 = c_2$	9	2289	1828	1479	1388	1173	1043	1028
4	Constant a & c	6	3035	2948	2888	2801	2729	2617	2552
5	Constant a, c & k	3	3069	2984	2927	2849	2768	2651	2583
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2516	2223	1956	1824	1735	1676	1629
7	Constant k, $a = 1$, $c_1 = c_2$	5	2583	2390	2286	2236	2205	2136	2117
8	Constant k & c, $a = 1$	2	3110	3019	2957	2877	2798	2685	2614

Table D.19. Bayes Information Criteria (BIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-962	-1110	-1235	-1258	-1332	-1350	-1394
2	$c_1 = c_2$	8	-976	-1127	-1253	-1272	-1352	-1369	-1415
3, 4, 5	Constant a & $c_1 = c_2$	2	-1005	-1150	-1255	-1264	-1302	-1344	-1336
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-670	-693	-707	-721	-735	-745	-755

Table D.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	0.1	-0.1	0.1	0.0	0.0	1
	40/40	0.0	0.0	0.1	0.0	0.0	0
	60/60	0.0	0.0	0.1	0.0	0.0	1
	80/80	0.0	0.0	0.1	0.0	-0.1	0
7.5	20/20	-0.1	0.1	0.1	0.1	0.0	0
	40/40	-0.2	0.1	0.1	0.1	0.0	1
	60/60	-0.2	0.2	0.1	0.2	0.0	1
	80/80	-0.3	0.3	0.1	0.2	0.1	1
10.0	20/20	-0.3	0.2	0.1	0.2	0.1	1
	40/40	-0.4	0.5	0.1	0.2	0.1	2
	60/60	-0.5	0.5	0.1	0.3	0.1	2
	80/80	-0.4	0.4	0.2	0.3	0.1	1
12.5	20/20	-0.7	0.7	0.2	0.3	0.2	3
	40/40	-1.2	1.1	0.2	0.4	0.2	7
	60/60	-0.7	0.7	0.3	0.4	0.2	2
	80/80	-0.9	0.9	0.3	0.5	0.2	2
15.0	20/20	-1.5	1.5	0.2	0.6	0.4	6
	40/40	-1.6	1.6	0.2	0.6	0.4	6
	60/60	-1.5	1.5	0.3	0.6	0.4	4
	80/80	-1.3	1.3	0.4	0.7	0.3	2
17.5	20/20	-2.0	2.0	0.2	0.7	0.5	6
	40/40	-2.0	2.0	0.3	0.8	0.5	6
	60/60	-2.0	2.0	0.3	0.8	0.5	4
	80/80	-1.8	1.8	0.5	1.0	0.4	2
20.0	20/20	-2.9	2.9	0.2	1.0	0.7	8
	40/40	-3.1	3.0	0.3	1.0	0.7	8
	60/60	-2.3	2.2	0.5	1.0	0.5	3
	80/80	-1.6	1.6	0.7	1.2	0.4	1

Note. %VAF = Percentage of Variance Accounted For.

Table D.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	1.2	-1.2	1.0	0.062	1.0	-32%	97
	40/40	0.8	-0.6	0.7	0.054	0.7	-11%	98
	60/60	0.6	-0.7	0.9	0.051	0.9	-24%	95
	80/80	0.5	-0.6	0.9	0.043	0.9	-20%	97
7.5	20/20	0.7	-1.0	1.5	0.049	1.5	-21%	97
	40/40	0.9	-0.9	1.5	0.049	1.5	-15%	98
	60/60	0.3	-0.3	1.4	0.045	1.4	-7%	97
	80/80	1.2	-1.2	1.7	0.043	1.7	-16%	98
10.0	20/20	2.6	-2.9	2.8	0.047	2.8	-29%	98
	40/40	1.0	-0.7	2.1	0.044	2.1	-4%	98
	60/60	2.7	-2.7	2.9	0.046	2.9	-23%	98
	80/80	1.0	-1.1	2.5	0.039	2.5	-11%	97
12.5	20/20	3.0	-3.0	3.8	0.046	3.8	-19%	98
	40/40	2.0	-2.2	3.6	0.043	3.6	-16%	98
	60/60	2.9	-2.9	3.7	0.040	3.7	-19%	98
	80/80	2.4	-2.6	3.9	0.038	3.9	-17%	97
15.0	20/20	4.2	-4.1	4.7	0.041	4.7	-21%	98
	40/40	2.8	-3.3	4.6	0.038	4.6	-21%	98
	60/60	2.1	-2.2	4.4	0.037	4.4	-14%	97
	80/80	2.3	-2.3	4.7	0.035	4.7	-13%	97
17.5	20/20	3.1	-3.1	5.1	0.036	5.1	-16%	98
	40/40	3.0	-3.2	5.4	0.036	5.4	-16%	98
	60/60	2.3	-2.5	5.6	0.036	5.6	-12%	97
	80/80	2.1	-2.2	6.3	0.036	6.3	-9%	96
20.0	20/20	3.9	-4.2	6.4	0.035	6.4	-17%	97
	40/40	2.6	-2.8	6.4	0.035	6.4	-12%	98
	60/60	1.4	-1.4	6.0	0.033	6.0	-6%	98
	80/80	3.2	-3.1	6.9	0.032	6.9	-11%	96

Note. %VAF = Percentage of Variance Accounted For.

Appendix E: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Exponential Creature Type

Table E.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	560	11.9	12.1	0.71	97	98
	40/40	567	16.8	17.3	0.74	98	99
	60/60	551	20.6	21.4	0.76	98	98
	80/80	535	23.8	24.7	0.77	99	99
7.5	20/20	557	17.5	17.3	0.74	99	99
	40/40	559	24.0	23.9	0.76	99	99
	60/60	543	28.2	28.3	0.76	99	100
	80/80	500	30.6	30.8	0.78	100	100
10.0	20/20	551	21.9	22.1	0.75	100	100
	40/40	535	29.1	29.0	0.78	100	100
	60/60	501	31.0	31.2	0.77	99	100
	80/80	452	31.4	31.4	0.78	99	100
12.5	20/20	535	26.0	26.4	0.77	100	100
	40/40	498	29.3	29.2	0.76	100	100
	60/60	451	31.0	31.1	0.77	99	100
	80/80	405	30.8	30.3	0.77	99	100
15.0	20/20	522	28.3	28.6	0.77	100	100
	40/40	471	31.6	31.5	0.77	99	100
	60/60	402	29.5	29.6	0.77	99	100
	80/80	357	27.5	27.6	0.75	99	100
17.5	20/20	504	30.5	30.7	0.76	99	100
	40/40	436	30.1	30.1	0.75	99	100
	60/60	373	27.9	28.0	0.75	99	100
	80/80	321	25.6	25.8	0.75	99	100
20.0	20/20	480	30.7	30.6	0.75	99	100
	40/40	405	28.4	28.6	0.74	99	100
	60/60	336	25.5	25.5	0.74	99	100
	80/80	287	23.1	22.9	0.74	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table E.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	560	12.0	0.71	97	98
	40/40	567	17.1	0.74	98	99
	60/60	550	21.1	0.76	98	98
	80/80	535	24.4	0.77	99	99
7.5	20/20	557	17.4	0.74	99	99
	40/40	559	24.0	0.76	99	99
	60/60	543	28.3	0.76	99	100
	80/80	500	30.8	0.78	100	100
10.0	20/20	551	22.0	0.76	100	100
	40/40	535	29.0	0.78	100	100
	60/60	501	31.2	0.77	99	100
	80/80	452	31.4	0.78	99	100
12.5	20/20	535	26.2	0.77	100	100
	40/40	498	29.3	0.76	100	100
	60/60	451	31.1	0.77	99	100
	80/80	404	30.6	0.77	99	100
15.0	20/20	521	28.5	0.77	100	100
	40/40	471	31.6	0.77	99	100
	60/60	402	29.5	0.77	99	100
	80/80	357	27.5	0.75	99	100
17.5	20/20	504	30.6	0.76	99	100
	40/40	436	30.1	0.75	99	100
	60/60	373	28.0	0.75	99	100
	80/80	321	25.7	0.75	99	100
20.0	20/20	480	30.6	0.75	99	100
	40/40	405	28.5	0.74	99	100
	60/60	336	25.5	0.74	99	100
	80/80	287	23.0	0.74	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table E.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	544	12.4	0.74	97	98
	40/40	564	17.2		98	99
	60/60	560	20.9		98	98
	80/80	555	24.0		99	99
7.5	20/20	543	17.7	0.76	99	99
	40/40	558	24.0		99	99
	60/60	545	28.2		99	100
	80/80	521	30.6		100	100
10.0	20/20	540	22.2	0.77	100	100
	40/40	544	28.9		100	100
	60/60	501	31.2		99	100
	80/80	456	31.3		99	99
12.5	20/20	538	26.2	0.77	100	100
	40/40	494	29.3		100	100
	60/60	452	31.1		99	100
	80/80	405	30.6		99	100
15.0	20/20	523	28.5	0.76	100	100
	40/40	478	31.6		99	100
	60/60	404	29.5		99	100
	80/80	349	27.5		99	100
17.5	20/20	516	30.7	0.75	99	100
	40/40	437	30.1		99	100
	60/60	368	27.9		99	100
	80/80	317	25.6		99	100
20.0	20/20	494	30.8	0.74	99	100
	40/40	403	28.5		99	100
	60/60	334	25.5		99	100
	80/80	284	22.9		99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table E.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF	
					QLOE	ML
5.0	20/20	559	18.8	0.74	89	98
	40/40		17.8		98	99
	60/60		18.7		97	98
	80/80		19.5		94	99
7.5	20/20	551	26.0	0.76	90	99
	40/40		25.3		98	99
	60/60		26.7		99	100
	80/80		28.3		94	99
10.0	20/20	532	31.3	0.77	89	100
	40/40		30.0		98	99
	60/60		32.2		99	99
	80/80		34.6		93	99
12.5	20/20	501	33.6	0.76	88	100
	40/40		32.2		98	100
	60/60		34.5		99	99
	80/80		37.6		93	99
15.0	20/20	469	35.2	0.76	86	100
	40/40		33.6		98	99
	60/60		36.1		99	100
	80/80		38.4		91	99
17.5	20/20	439	34.6	0.75	84	100
	40/40		33.1		98	99
	60/60		35.4		98	100
	80/80		37.6		91	99
20.0	20/20	407	32.9	0.74	83	100
	40/40		31.3		98	99
	60/60		33.7		98	100
	80/80		35.9		90	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table E.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	554	18.4	0.74	89	98
	40/40				97	99
	60/60				97	98
	80/80				94	99
7.5	20/20	544	25.7	0.76	90	99
	40/40				98	99
	60/60				99	100
	80/80				93	100
10.0	20/20	521	30.8	0.77	88	100
	40/40				98	100
	60/60				99	100
	80/80				92	99
12.5	20/20	490	33.2	0.77	87	100
	40/40				98	100
	60/60				99	100
	80/80				91	100
15.0	20/20	458	34.5	0.76	85	100
	40/40				97	100
	60/60				99	100
	80/80				90	100
17.5	20/20	427	33.9	0.75	83	100
	40/40				97	100
	60/60				99	100
	80/80				90	100
20.0	20/20	394	32.0	0.74	82	100
	40/40				96	100
	60/60				99	100
	80/80				89	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table E.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	452	17.7	92	83
	40/40	449	24.0	96	86
	60/60	430	28.3	96	88
	80/80	415	31.8	97	90
7.5	20/20	438	23.7	96	87
	40/40	425	30.5	97	89
	60/60	405	35.5	97	90
	80/80	378	37.6	98	92
10.0	20/20	426	29.1	97	89
	40/40	406	36.1	98	91
	60/60	367	37.7	97	91
	80/80	331	37.5	98	91
12.5	20/20	409	33.0	98	91
	40/40	366	35.9	97	90
	60/60	325	36.4	97	91
	80/80	289	35.2	97	90
15.0	20/20	383	34.5	98	90
	40/40	339	36.9	97	91
	60/60	291	34.8	97	90
	80/80	251	31.5	97	89
17.5	20/20	361	35.8	97	90
	40/40	304	34.5	97	89
	60/60	259	31.8	96	88
	80/80	225	29.1	96	88
20.0	20/20	334	35.0	97	89
	40/40	276	32.3	96	87
	60/60	231	28.6	96	87
	80/80	201	25.8	95	87

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table E.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF	
				QLOE	ML
5.0	20/20	440	16.3	92	83
	40/40		22.7	96	86
	60/60		30.0	96	88
	80/80		36.9	97	90
7.5	20/20	418	20.6	96	87
	40/40		29.1	97	89
	60/60		38.2	97	90
	80/80		47.2	98	92
10.0	20/20	391	23.1	97	89
	40/40		32.9	98	91
	60/60		43.7	97	91
	80/80		54.1	97	91
12.5	20/20	357	23.1	97	91
	40/40		33.8	97	90
	60/60		45.0	97	91
	80/80		55.7	96	90
15.0	20/20	324	22.5	96	90
	40/40		33.2	97	91
	60/60		44.3	96	90
	80/80		55.0	94	89
17.5	20/20	294	21.2	95	90
	40/40		31.8	97	89
	60/60		42.5	96	88
	80/80		52.2	94	88
20.0	20/20	265	19.5	94	89
	40/40		29.5	96	87
	60/60		39.2	95	87
	80/80		48.1	92	87

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table E.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	434	25	84	83
	40/40			95	86
	60/60			95	88
	80/80			91	90
7.5	20/20	410	32	87	87
	40/40			96	89
	60/60			97	90
	80/80			92	92
10.0	20/20	381	37	86	89
	40/40			97	91
	60/60			97	91
	80/80			90	91
12.5	20/20	346	39	85	91
	40/40			95	90
	60/60			97	91
	80/80			89	90
15.0	20/20	315	39	83	90
	40/40			95	91
	60/60			96	90
	80/80			87	89
17.5	20/20	285	37	81	90
	40/40			94	89
	60/60			96	88
	80/80			86	88
20.0	20/20	256	34	79	89
	40/40			93	87
	60/60			95	87
	80/80			85	87

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table E.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	455	141	4	403	3*
3	Constant a, $c_1 = c_2$	9	433	143	7	406	3*
4	Constant a & c	6	10581	393	10	409	27*
5	Constant a, c & k	3	8635	406	13	412	21*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	10767	347	8	407	31*
7	Constant k, $a = 1$, $c_1 = c_2$	5	7992	348	11	410	23*
8	Constant k & c, $a = 1$,	2	14086	610	14	413	23*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table E.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	15	53	4	403	0
3	Constant a, $c_1 = c_2$	9	66	54	7	406	1
4	Constant a & c	6	10060	298	10	409	34*
5	Constant a, c & k	3	8628	324	13	412	27*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	6301	176	8	407	36*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4878	183	11	410	27*
8	Constant k & c, $a = 1$,	2	11613	445	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table E.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	10	24	4	403	0
3	Constant a, $c_1 = c_2$	9	27	24	7	406	1
4	Constant a & c	6	9978	268	10	409	37*
5	Constant a, c & k	3	8711	298	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	4740	117	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4049	132	11	410	31*
8	Constant k & c, $a = 1$,	2	10839	391	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table E.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	32	17	4	403	2
3	Constant a, $c_1 = c_2$	9	19	17	7	406	1
4	Constant a & c	6	9312	244	10	409	38*
5	Constant a, c & k	3	8166	274	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	4015	95	8	407	42*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3825	119	11	410	32*
8	Constant k & c, $a = 1$,	2	10081	358	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table E.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	10	15	4	403	1
3	Constant a, $c_1 = c_2$	9	10	15	7	406	1
4	Constant a & c	6	8852	231	10	409	38*
5	Constant a, c & k	3	7594	254	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3381	81	8	407	42*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3484	108	11	410	32*
8	Constant k & c, $a = 1$,	2	9072	322	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table E.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	3	14	4	403	0
3	Constant a, $c_1 = c_2$	9	10	14	7	406	1
4	Constant a & c	6	7713	202	10	409	38*
5	Constant a, c & k	3	6552	220	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3012	73	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3299	102	11	410	32*
8	Constant k & c, $a = 1$,	2	7940	282	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table E.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	3	11	4	403	0
3	Constant a, $c_1 = c_2$	9	10	11	7	406	1
4	Constant a & c	6	6443	168	10	409	38*
5	Constant a, c & k	3	5515	184	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2744	64	8	407	43*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3080	93	11	410	33*
8	Constant k & c, $a = 1$,	2	6800	241	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table E.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2063	1671	1341	1186	1141	1104	1001
2	$c_1 = c_2$	12	2069	1664	1335	1186	1136	1097	994
3	Constant a, $c_1 = c_2$	9	2072	1666	1335	1180	1132	1095	993
4	Constant a & c	6	2490	2375	2330	2292	2269	2213	2136
5	Constant a, c & k	3	2500	2407	2372	2337	2306	2246	2172
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2440	2159	1988	1903	1836	1790	1740
7	Constant k, $a = 1$, $c_1 = c_2$	5	2439	2171	2036	1992	1952	1927	1890
8	Constant k & c, $a = 1$	2	2669	2538	2484	2447	2403	2349	2282

Table E.17. Akaike Information Criteria (AIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1100	-1271	-1351	-1398	-1428	-1453	-1504
2	$c_1 = c_2$	8	-1103	-1278	-1358	-1401	-1435	-1460	-1511
3, 4, 5	Constant a & $c_1 = c_2$	2	-1106	-1279	-1364	-1412	-1443	-1467	-1518
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-671	-705	-725	-748	-762	-777	-788

Table E.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2128	1735	1406	1251	1205	1169	1065
2	$c_1 = c_2$	12	2117	1712	1383	1234	1184	1146	1042
3	Constant a, $c_1 = c_2$	9	2108	1702	1372	1217	1168	1132	1030
4	Constant a & c	6	2514	2399	2354	2316	2293	2237	2161
5	Constant a, c & k	3	2512	2419	2385	2349	2318	2258	2184
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2472	2191	2020	1935	1868	1822	1772
7	Constant k, $a = 1$, $c_1 = c_2$	5	2459	2191	2056	2012	1972	1948	1910
8	Constant k & c, $a = 1$	2	2677	2546	2492	2455	2411	2357	2290

Table E.19. Bayes Information Criteria (BIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1060	-1230	-1311	-1358	-1388	-1413	-1464
2	$c_1 = c_2$	8	-1077	-1251	-1331	-1374	-1408	-1433	-1484
3, 4, 5	Constant a & $c_1 = c_2$	2	-1099	-1272	-1357	-1406	-1436	-1460	-1511
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-671	-705	-725	-748	-762	-777	-788

Table E.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	0.0	0.0	0.1	0.1	0.0	0
	40/40	-0.1	0.1	0.1	0.1	0.0	0
	60/60	-0.2	0.2	0.1	0.2	0.0	1
	80/80	-0.4	0.3	0.1	0.2	0.1	2
7.5	20/20	-0.6	0.6	0.1	0.3	0.2	2
	40/40	-0.7	0.7	0.1	0.3	0.2	3
	60/60	-0.7	0.6	0.2	0.4	0.1	3
	80/80	-1.2	1.2	0.2	0.5	0.3	5
10.0	20/20	-1.2	1.2	0.2	0.5	0.3	4
	40/40	-1.7	1.6	0.2	0.6	0.4	7
	60/60	-1.5	1.5	0.3	0.6	0.4	5
	80/80	-1.7	1.7	0.4	0.8	0.4	5
12.5	20/20	-2.1	2.1	0.2	0.8	0.5	7
	40/40	-2.0	2.0	0.3	0.8	0.5	5
	60/60	-2.5	2.6	0.3	0.9	0.7	6
	80/80	-3.2	3.3	0.3	1.1	0.8	7
15.0	20/20	-3.2	3.2	0.3	1.1	0.8	8
	40/40	-3.5	3.6	0.3	1.2	0.9	9
	60/60	-3.1	3.1	0.5	1.2	0.8	6
	80/80	-4.0	4.0	0.5	1.5	1.0	6
17.5	20/20	-4.1	4.0	0.4	1.4	1.0	9
	40/40	-4.0	3.9	0.5	1.4	1.0	7
	60/60	-4.2	4.2	0.6	1.6	1.0	6
	80/80	-4.4	4.4	0.7	1.8	1.1	5
20.0	20/20	-5.3	5.4	0.4	1.7	1.4	9
	40/40	-4.7	4.7	0.6	1.8	1.2	6
	60/60	-5.2	5.2	0.6	1.9	1.3	6
	80/80	-5.7	5.8	0.8	2.3	1.5	5

Note. %VAF = Percentage of Variance Accounted For.

Table E.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	1.1	-1.1	1.2	0.037	1.2	-22%	95
	40/40	0.1	-0.1	1.0	0.036	1.0	-1%	95
	60/60	0.4	-0.3	1.0	0.033	1.0	-3%	98
	80/80	0.0	-0.2	1.4	0.035	1.4	-6%	97
7.5	20/20	1.3	-1.3	2.0	0.032	2.0	-15%	97
	40/40	0.8	-0.8	1.9	0.031	1.9	-11%	97
	60/60	1.4	-1.5	2.4	0.032	2.4	-17%	96
	80/80	2.4	-2.1	2.9	0.033	2.9	-15%	97
10.0	20/20	0.6	-0.7	2.9	0.030	2.9	-7%	96
	40/40	1.5	-1.6	3.3	0.032	3.3	-13%	96
	60/60	1.0	-1.0	3.2	0.029	3.2	-7%	97
	80/80	2.1	-2.4	4.2	0.029	4.2	-17%	97
12.5	20/20	2.0	-1.8	4.0	0.028	4.0	-11%	97
	40/40	1.5	-1.5	4.1	0.028	4.1	-9%	97
	60/60	3.5	-3.2	4.8	0.029	4.8	-15%	97
	80/80	3.6	-3.4	5.7	0.029	5.7	-14%	97
15.0	20/20	2.5	-2.4	5.3	0.028	5.3	-11%	96
	40/40	3.1	-3.0	5.3	0.026	5.3	-14%	97
	60/60	0.7	-0.9	5.4	0.026	5.4	-5%	97
	80/80	0.6	-0.6	6.2	0.026	6.2	-2%	96
17.5	20/20	3.4	-3.3	6.1	0.025	6.1	-13%	96
	40/40	2.2	-2.1	6.2	0.025	6.2	-9%	96
	60/60	4.1	-4.3	7.2	0.025	7.2	-16%	96
	80/80	5.9	-6.4	8.5	0.024	8.5	-20%	96
20.0	20/20	2.8	-2.8	7.3	0.025	7.3	-9%	96
	40/40	1.7	-1.6	7.1	0.024	7.1	-5%	95
	60/60	4.0	-3.9	8.2	0.024	8.2	-12%	95
	80/80	3.7	-3.6	9.2	0.024	9.2	-9%	96

Note. %VAF = Percentage of Variance Accounted For.

Appendix F: Experiment 1 Fitting Measures of the Exponential-Clone-Pheno-Gaussian Creature Type

Table F.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	533	10.2	10.8	0.71	92	94
	40/40	529	13.9	14.6	0.73	93	95
	60/60	523	17.5	18.0	0.73	96	97
	80/80	483	17.9	18.9	0.74	95	97
7.5	20/20	502	13.4	14.6	0.76	95	97
	40/40	491	18.2	19.1	0.77	96	97
	60/60	446	18.2	19.4	0.76	97	98
	80/80	434	21.3	21.1	0.76	98	99
10.0	20/20	476	15.8	16.6	0.77	96	98
	40/40	442	19.4	19.5	0.78	98	99
	60/60	416	21.3	21.9	0.78	98	99
	80/80	372	20.8	21.1	0.78	98	99
12.5	20/20	471	19.6	20.3	0.78	98	99
	40/40	413	20.6	21.7	0.79	98	99
	60/60	378	21.9	22.1	0.78	98	99
	80/80	338	20.3	20.8	0.78	99	99
15.0	20/20	442	20.4	21.2	0.79	99	99
	40/40	404	22.9	23.8	0.79	99	99
	60/60	339	20.3	21.0	0.78	99	99
	80/80	304	19.4	19.8	0.78	99	99
17.5	20/20	429	22.4	22.4	0.79	99	99
	40/40	370	21.7	22.8	0.79	99	99
	60/60	322	21.6	21.9	0.79	99	100
	80/80	288	19.3	19.3	0.77	99	100
20.0	20/20	417	23.9	23.7	0.79	100	100
	40/40	346	21.5	22.0	0.78	99	99
	60/60	300	21.1	20.8	0.79	99	100
	80/80	271	18.7	18.8	0.76	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table F.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	531	10.7	0.72	91	94
	40/40	526	14.4	0.73	92	95
	60/60	522	17.8	0.74	96	97
	80/80	480	18.6	0.75	95	97
7.5	20/20	499	14.4	0.77	95	97
	40/40	489	18.9	0.77	96	97
	60/60	444	19.1	0.77	97	98
	80/80	434	21.2	0.76	98	99
10.0	20/20	475	16.4	0.77	96	98
	40/40	442	19.4	0.78	98	99
	60/60	415	21.6	0.78	98	99
	80/80	373	20.9	0.78	98	99
12.5	20/20	471	20.1	0.78	98	99
	40/40	412	21.5	0.79	98	99
	60/60	378	22.0	0.78	98	99
	80/80	337	20.6	0.78	99	99
15.0	20/20	442	21.0	0.79	99	99
	40/40	404	23.6	0.79	99	99
	60/60	338	20.8	0.79	99	99
	80/80	304	19.6	0.78	99	99
17.5	20/20	429	22.4	0.79	99	99
	40/40	370	22.7	0.79	99	99
	60/60	322	21.8	0.79	99	100
	80/80	288	19.3	0.77	99	100
20.0	20/20	417	23.8	0.79	100	100
	40/40	346	21.9	0.78	99	99
	60/60	300	21.0	0.79	99	100
	80/80	271	18.8	0.76	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table F.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	526	10.9	0.73	91	94
	40/40	525	14.4		92	95
	60/60	524	17.8		96	97
	80/80	487	18.4		95	97
7.5	20/20	500	14.4	0.76	95	97
	40/40	492	18.7		96	97
	60/60	444	19.1		97	98
	80/80	429	21.3		98	99
10.0	20/20	472	16.5	0.78	95	98
	40/40	444	19.4		98	99
	60/60	416	21.6		98	99
	80/80	373	20.9		98	99
12.5	20/20	470	20.1	0.79	98	99
	40/40	417	21.3		98	99
	60/60	378	22.0		98	99
	80/80	334	20.7		99	99
15.0	20/20	444	20.9	0.79	99	99
	40/40	407	23.5		99	99
	60/60	338	20.8		99	99
	80/80	301	19.7		99	99
17.5	20/20	431	22.4	0.78	99	99
	40/40	373	22.6		99	99
	60/60	326	21.7		99	100
	80/80	281	19.5		99	100
20.0	20/20	423	23.7	0.78	100	100
	40/40	348	21.8		99	99
	60/60	305	20.9		99	100
	80/80	263	18.9		99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table F.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	518	15.9	0.73	79	94
	40/40		14.7		92	95
	60/60		15.9		96	97
	80/80		16.1		88	96
7.5	20/20	471	19.0	0.76	82	97
	40/40		17.6		95	97
	60/60		18.7		96	98
	80/80		20.9		92	98
10.0	20/20	431	20.7	0.77	83	98
	40/40		19.8		97	99
	60/60		21.0		97	99
	80/80		22.5		90	98
12.5	20/20	405	23.0	0.78	85	99
	40/40		21.1		97	99
	60/60		23.6		98	99
	80/80		24.7		92	99
15.0	20/20	378	23.7	0.78	85	99
	40/40		21.7		98	99
	60/60		23.8		98	99
	80/80		25.5		92	99
17.5	20/20	360	24.1	0.78	86	99
	40/40		22.0		98	99
	60/60		24.5		99	99
	80/80		26.4		92	99
20.0	20/20	344	24.3	0.78	87	100
	40/40		22.7		98	99
	60/60		25.1		99	100
	80/80		26.2		92	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table F.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	ML
5.0	20/20	514	15.6	0.73	80	94
	40/40				91	95
	60/60				96	97
	80/80				87	97
7.5	20/20	464	18.7	0.76	82	97
	40/40				95	97
	60/60				96	98
	80/80				91	99
10.0	20/20	425	20.5	0.78	82	98
	40/40				97	99
	60/60				97	99
	80/80				90	99
12.5	20/20	399	22.6	0.79	85	99
	40/40				96	99
	60/60				98	99
	80/80				91	99
15.0	20/20	373	23.3	0.79	85	99
	40/40				97	99
	60/60				98	99
	80/80				91	99
17.5	20/20	353	23.7	0.78	86	99
	40/40				97	99
	60/60				99	100
	80/80				91	100
20.0	20/20	336	23.8	0.78	86	100
	40/40				97	99
	60/60				99	100
	80/80				91	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table F.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	442	16.1	86	81
	40/40	429	21.4	87	83
	60/60	405	24.4	92	85
	80/80	382	26.3	91	87
7.5	20/20	422	20.6	92	89
	40/40	404	26.3	93	89
	60/60	363	26.9	94	90
	80/80	336	27.9	95	89
10.0	20/20	399	23.3	92	91
	40/40	359	25.6	96	92
	60/60	330	27.9	96	91
	80/80	298	27.3	96	91
12.5	20/20	383	26.3	96	91
	40/40	336	27.5	96	92
	60/60	301	27.8	97	91
	80/80	268	26.3	97	92
15.0	20/20	360	27.1	97	92
	40/40	321	29.5	98	92
	60/60	272	26.4	97	92
	80/80	242	24.6	97	91
17.5	20/20	342	28.4	97	92
	40/40	295	28.4	98	92
	60/60	260	27.3	97	93
	80/80	224	24.2	97	91
20.0	20/20	329	29.8	98	92
	40/40	273	27.2	97	92
	60/60	238	25.6	98	92
	80/80	207	22.8	97	89

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table F.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	419	13.5	86	81
	40/40		20.0	87	83
	60/60		26.7	92	85
	80/80		33.0	90	87
7.5	20/20	388	15.9	91	89
	40/40		23.6	93	89
	60/60		31.8	94	90
	80/80		39.5	94	89
10.0	20/20	353	16.4	91	91
	40/40		24.6	96	92
	60/60		33.1	96	91
	80/80		40.7	95	91
12.5	20/20	328	17.1	95	91
	40/40		25.9	96	92
	60/60		34.5	97	91
	80/80		42.8	95	92
15.0	20/20	305	17.2	96	92
	40/40		25.9	98	92
	60/60		35.1	96	92
	80/80		43.1	95	91
17.5	20/20	286	17.3	96	92
	40/40		26.1	98	92
	60/60		34.4	97	93
	80/80		43.0	95	91
20.0	20/20	267	16.7	96	92
	40/40		25.6	97	92
	60/60		33.9	97	92
	80/80		41.7	94	89

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table F.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	412	22	75	81
	40/40			86	83
	60/60			91	85
	80/80			83	87
7.5	20/20	376	26	79	89
	40/40			92	89
	60/60			93	90
	80/80			87	89
10.0	20/20	342	27	78	91
	40/40			95	92
	60/60			95	91
	80/80			87	91
12.5	20/20	317	29	83	91
	40/40			94	92
	60/60			96	91
	80/80			89	92
15.0	20/20	294	29	83	92
	40/40			96	92
	60/60			96	92
	80/80			89	91
17.5	20/20	275	29	84	92
	40/40			96	92
	60/60			97	93
	80/80			89	91
20.0	20/20	257	29	84	92
	40/40			95	92
	60/60			97	92
	80/80			89	89

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table F.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	1688	365	4	403	5*
3	Constant a, $c_1 = c_2$	9	978	362	7	406	3*
4	Constant a & c	6	12604	651	10	409	19*
5	Constant a, c & k	3	10122	660	13	412	15*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	13600	612	8	407	22*
7	Constant k, $a = 1$, $c_1 = c_2$	5	10369	620	11	410	17*
8	Constant k & c, $a = 1$,	2	16658	904	14	413	18*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table F.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	1454	180	4	403	8*
3	Constant a, $c_1 = c_2$	9	825	178	7	406	5*
4	Constant a & c	6	11958	455	10	409	26*
5	Constant a, c & k	3	10028	478	13	412	21*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	8022	321	8	407	25*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6625	340	11	410	19*
8	Constant k & c, $a = 1$,	2	13621	623	14	413	22*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table F.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	347	115	4	403	3*
3	Constant a, $c_1 = c_2$	9	218	115	7	406	2
4	Constant a & c	6	9997	354	10	409	28*
5	Constant a, c & k	3	8371	373	13	412	22*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	5766	224	8	407	26*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5056	245	11	410	21*
8	Constant k & c, $a = 1$,	2	11039	483	14	413	23*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table F.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	373	71	4	403	5*
3	Constant a, $c_1 = c_2$	9	213	70	7	406	3*
4	Constant a & c	6	9995	310	10	409	32*
5	Constant a, c & k	3	8469	333	13	412	25*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3694	139	8	407	27*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3895	170	11	410	23*
8	Constant k & c, $a = 1$,	2	9829	399	14	413	25*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table F.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	302	39	4	403	8*
3	Constant a, $c_1 = c_2$	9	175	39	7	406	4*
4	Constant a & c	6	9092	258	10	409	35*
5	Constant a, c & k	3	7637	277	13	412	28*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3034	96	8	407	32*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3468	129	11	410	27*
8	Constant k & c, $a = 1$,	2	8788	333	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table F.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	141	27	4	403	5*
3	Constant a, $c_1 = c_2$	9	86	27	7	406	3*
4	Constant a & c	6	7600	211	10	409	36*
5	Constant a, c & k	3	6548	231	13	412	28*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2576	76	8	407	34*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2991	105	11	410	28*
8	Constant k & c, $a = 1$,	2	7454	277	14	413	27*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table F.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	56	17	4	403	3*
3	Constant a, $c_1 = c_2$	9	39	17	7	406	2*
4	Constant a & c	6	6924	186	10	409	37*
5	Constant a, c & k	3	5871	202	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2230	61	8	407	37*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2889	94	11	410	31*
8	Constant k & c, $a = 1$,	2	6838	248	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table F.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2453	2144	1980	1768	1514	1362	1195
2	$c_1 = c_2$	12	2465	2171	1985	1782	1539	1377	1201
3	Constant a, $c_1 = c_2$	9	2459	2164	1980	1776	1533	1372	1198
4	Constant a & c	6	2700	2551	2447	2392	2315	2231	2179
5	Constant a, c & k	3	2703	2569	2466	2418	2341	2267	2210
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2676	2408	2258	2059	1904	1807	1714
7	Constant k, $a = 1$, $c_1 = c_2$	5	2679	2429	2293	2141	2025	1940	1895
8	Constant k & c, $a = 1$	2	2833	2678	2572	2492	2418	2341	2295

Table F.17. Akaike Information Criteria (AIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-909	-991	-1056	-1111	-1192	-1266	-1329
2	$c_1 = c_2$	8	-911	-987	-1060	-1114	-1192	-1264	-1335
3, 4, 5	Constant a & c	2	-922	-998	-1072	-1125	-1203	-1270	-1336
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-651	-679	-695	-701	-710	-718	-729

Table F.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2518	2208	2045	1832	1578	1427	1260
2	$c_1 = c_2$	12	2513	2219	2033	1830	1587	1425	1249
3	Constant a, $c_1 = c_2$	9	2495	2201	2017	1812	1570	1409	1234
4	Constant a & c	6	2724	2575	2471	2416	2339	2255	2203
5	Constant a, c & k	3	2715	2581	2478	2430	2353	2279	2222
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2708	2441	2290	2092	1936	1839	1746
7	Constant k, $a = 1$, $c_1 = c_2$	5	2699	2449	2313	2161	2045	1960	1915
8	Constant k & c, $a = 1$	2	2841	2686	2580	2500	2426	2349	2303

Table F.19. Bayes Information Criteria (BIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-868	-951	-1016	-1070	-1152	-1226	-1289
2	$c_1 = c_2$	8	-884	-960	-1033	-1088	-1165	-1238	-1308
3, 4, 5	Constant a & c	2	-915	-991	-1065	-1118	-1196	-1264	-1329
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-651	-679	-695	-701	-710	-718	-729

Table F.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	0.1	-0.1	0.0	0.0	0.0	2
	40/40	0.1	-0.1	0.0	0.0	0.0	4
	60/60	0.0	0.0	0.0	0.0	0.0	0
	80/80	0.0	0.0	0.0	0.0	0.0	1
7.5	20/20	0.0	-0.1	0.1	0.0	0.0	1
	40/40	0.1	-0.1	0.1	0.0	0.0	3
	60/60	0.1	-0.1	0.1	0.0	0.0	1
	80/80	-0.1	0.1	0.0	0.1	0.0	0
10.0	20/20	0.0	0.0	0.1	0.1	0.0	1
	40/40	-0.1	0.1	0.1	0.1	0.0	1
	60/60	0.0	0.0	0.1	0.1	0.0	0
	80/80	-0.1	0.1	0.1	0.1	0.0	0
12.5	20/20	-0.2	0.2	0.1	0.1	0.0	2
	40/40	-0.3	0.3	0.1	0.2	0.1	3
	60/60	-0.3	0.3	0.1	0.2	0.1	2
	80/80	-0.3	0.3	0.1	0.2	0.1	1
15.0	20/20	-0.4	0.4	0.1	0.2	0.1	3
	40/40	-0.5	0.5	0.1	0.2	0.1	4
	60/60	-0.5	0.4	0.2	0.3	0.1	2
	80/80	-0.6	0.6	0.2	0.3	0.2	2
17.5	20/20	-0.8	0.8	0.1	0.3	0.2	4
	40/40	-0.8	0.7	0.2	0.3	0.2	4
	60/60	-0.7	0.7	0.2	0.4	0.1	3
	80/80	-0.9	0.9	0.2	0.5	0.2	2
20.0	20/20	-1.1	1.1	0.1	0.4	0.3	5
	40/40	-1.2	1.0	0.2	0.4	0.2	5
	60/60	-1.6	1.6	0.1	0.5	0.4	6
	80/80	-1.5	1.5	0.2	0.6	0.4	4

Note. %VAF = Percentage of Variance Accounted For.

Table F.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	0.6	-0.7	0.5	0.069	0.5	-37%	93
	40/40	0.2	-0.2	0.3	0.056	0.3	-8%	95
	60/60	0.6	-0.4	0.4	0.057	0.4	-19%	97
	80/80	0.5	-0.6	0.6	0.061	0.6	-24%	96
7.5	20/20	1.1	-1.2	0.9	0.060	0.9	-34%	97
	40/40	0.5	-0.7	0.8	0.054	0.8	-25%	97
	60/60	0.8	-0.8	0.8	0.051	0.8	-26%	96
	80/80	-0.5	0.5	0.8	0.052	0.9	19%	96
10.0	20/20	1.0	-1.1	1.5	0.060	1.5	-22%	98
	40/40	0.8	-0.8	1.3	0.055	1.3	-16%	96
	60/60	1.2	-1.3	1.3	0.046	1.3	-25%	97
	80/80	2.2	-2.3	2.2	0.057	2.2	-27%	97
12.5	20/20	0.7	-0.9	1.7	0.050	1.7	-17%	98
	40/40	0.5	-0.7	1.9	0.053	1.9	-11%	98
	60/60	1.6	-2.2	2.6	0.053	2.6	-26%	99
	80/80	1.8	-1.9	2.7	0.050	2.7	-18%	98
15.0	20/20	2.2	-2.0	2.7	0.053	2.7	-16%	98
	40/40	2.8	-2.8	2.7	0.048	2.7	-26%	98
	60/60	2.1	-2.1	3.1	0.049	3.1	-18%	98
	80/80	1.6	-1.3	2.9	0.044	2.9	-10%	99
17.5	20/20	1.6	-1.7	2.9	0.045	2.9	-15%	98
	40/40	1.9	-1.7	3.2	0.046	3.2	-12%	98
	60/60	2.4	-2.7	3.8	0.046	3.8	-20%	98
	80/80	3.6	-3.2	4.3	0.044	4.3	-16%	98
20.0	20/20	1.9	-2.2	3.7	0.043	3.7	-16%	98
	40/40	1.4	-1.9	4.1	0.044	4.1	-15%	98
	60/60	0.8	-0.7	4.0	0.042	4.0	-4%	98
	80/80	2.6	-2.3	4.7	0.041	4.7	-10%	98

Note. %VAF = Percentage of Variance Accounted For.

Appendix G: Experiment 1 Fitting Measures of the Linear-Bitwise-Bitflip Creature Type

Table G.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	ML
5.0	20/20	422	7.5	7.4	0.76	98	99
	40/40	329	8.1	8.3	0.77	99	99
	60/60	248	6.8	6.7	0.74	99	99
	80/80	212	7.1	7.1	0.73	98	98
7.5	20/20	431	12.4	12.1	0.80	99	99
	40/40	335	13.1	13.0	0.80	99	100
	60/60	254	11.1	11.2	0.78	99	99
	80/80	222	11.8	11.8	0.76	99	99
10.0	20/20	440	17.8	17.8	0.82	100	100
	40/40	341	17.9	17.9	0.81	100	100
	60/60	264	15.9	16.0	0.79	100	99
	80/80	235	16.7	16.7	0.76	99	100
12.5	20/20	448	22.1	22.2	0.82	100	100
	40/40	349	23.0	22.9	0.81	100	100
	60/60	271	20.5	20.3	0.79	100	100
	80/80	245	22.3	22.5	0.78	100	100
15.0	20/20	454	27.5	27.3	0.83	100	100
	40/40	355	28.4	28.4	0.82	100	100
	60/60	275	25.3	25.4	0.80	100	100
	80/80	244	26.3	26.2	0.78	100	100
17.5	20/20	454	31.7	31.6	0.83	100	100
	40/40	357	32.7	32.5	0.82	100	100
	60/60	282	29.7	29.8	0.80	100	100
	80/80	250	30.5	30.6	0.78	100	99
20.0	20/20	462	36.1	36.2	0.82	100	100
	40/40	359	37.3	37.5	0.82	100	100
	60/60	291	33.9	34.0	0.79	100	99
	80/80	260	33.5	33.7	0.75	99	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table G.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	422	7.5	0.76	98	99
	40/40	329	8.2	0.77	98	99
	60/60	248	6.8	0.74	99	99
	80/80	212	7.1	0.73	98	98
7.5	20/20	431	12.3	0.80	99	99
	40/40	335	13.0	0.80	99	100
	60/60	254	11.2	0.78	99	99
	80/80	222	11.8	0.76	99	99
10.0	20/20	440	17.8	0.82	100	100
	40/40	341	17.9	0.81	100	100
	60/60	264	15.9	0.79	100	99
	80/80	235	16.7	0.76	99	100
12.5	20/20	448	22.2	0.82	100	100
	40/40	349	23.0	0.81	100	100
	60/60	271	20.4	0.79	100	100
	80/80	245	22.4	0.78	100	100
15.0	20/20	455	27.4	0.83	100	100
	40/40	355	28.4	0.82	100	100
	60/60	275	25.3	0.80	100	100
	80/80	244	26.2	0.78	100	100
17.5	20/20	454	31.7	0.83	100	100
	40/40	357	32.6	0.82	100	100
	60/60	282	29.7	0.80	100	100
	80/80	250	30.6	0.78	100	99
20.0	20/20	462	36.1	0.82	100	100
	40/40	359	37.4	0.82	100	100
	60/60	291	33.9	0.79	100	99
	80/80	260	33.6	0.75	99	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table G.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	ML
5.0	20/20	426	7.3	0.75	98	98
	40/40	333	8.0		98	99
	60/60	246	6.8		99	99
	80/80	209	7.2		98	98
7.5	20/20	436	12.1	0.78	99	99
	40/40	339	12.8		99	100
	60/60	253	11.2		99	99
	80/80	217	12.0		99	99
10.0	20/20	454	17.3	0.79	100	100
	40/40	347	17.7		100	100
	60/60	263	16.0		100	99
	80/80	225	16.8		99	99
12.5	20/20	460	21.8	0.80	100	100
	40/40	355	22.8		100	100
	60/60	269	20.5		100	100
	80/80	235	22.4		100	99
15.0	20/20	468	27.1	0.81	100	100
	40/40	362	28.3		100	100
	60/60	274	25.3		100	100
	80/80	233	26.1		100	99
17.5	20/20	474	31.4	0.80	100	100
	40/40	366	32.6		100	100
	60/60	279	29.7		100	100
	80/80	236	30.1		100	99
20.0	20/20	490	36.2	0.79	100	100
	40/40	382	37.8		100	100
	60/60	287	33.8		100	99
	80/80	234	32.2		99	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table G.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	291	10.2	0.74	38	98
	40/40		8.9		86	98
	60/60		10.5		97	99
	80/80		11.5		72	97
7.5	20/20	310	17.2	0.78	50	99
	40/40		15.2		88	99
	60/60		17.3		98	99
	80/80		19.2		78	98
10.0	20/20	340	26.3	0.79	57	100
	40/40		23.0		90	99
	60/60		26.4		98	99
	80/80		29.2		81	98
12.5	20/20	373	36.3	0.79	58	100
	40/40		32.2		91	99
	60/60		36.9		98	100
	80/80		40.3		82	98
15.0	20/20	413	48.6	0.80	61	100
	40/40		43.1		92	99
	60/60		49.0		98	100
	80/80		54.2		83	98
17.5	20/20	457	61.9	0.80	60	100
	40/40		55.6		92	99
	60/60		62.5		98	100
	80/80		68.4		82	97
20.0	20/20	539	81.9	0.79	59	100
	40/40		73.0		91	99
	60/60		82.2		97	99
	80/80		89.5		82	96

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table G.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	278	9.4	0.75	37	99
	40/40				82	99
	60/60				98	99
	80/80				71	98
7.5	20/20	296	16.0	0.78	48	99
	40/40				85	100
	60/60				98	99
	80/80				76	99
10.0	20/20	322	24.5	0.79	55	100
	40/40				87	100
	60/60				99	99
	80/80				79	99
12.5	20/20	348	33.6	0.80	56	100
	40/40				88	100
	60/60				98	100
	80/80				80	99
15.0	20/20	383	45.3	0.81	59	100
	40/40				88	100
	60/60				98	100
	80/80				80	99
17.5	20/20	421	57.7	0.80	58	100
	40/40				88	100
	60/60				98	100
	80/80				80	99
20.0	20/20	487	75.0	0.79	57	100
	40/40				87	100
	60/60				98	99
	80/80				78	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table G.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	ML
5.0	20/20	375	10.9	95	90
	40/40	287	11.4	96	90
	60/60	214	9.5	96	86
	80/80	180	9.6	94	85
7.5	20/20	378	16.6	98	93
	40/40	293	17.7	98	93
	60/60	217	14.5	98	92
	80/80	182	14.8	96	89
10.0	20/20	381	22.7	99	95
	40/40	287	22.3	99	94
	60/60	216	19.3	98	92
	80/80	183	19.8	97	89
12.5	20/20	376	27.5	99	95
	40/40	284	27.4	99	94
	60/60	216	24.2	98	93
	80/80	184	25.0	97	91
15.0	20/20	374	32.9	99	95
	40/40	283	33.0	99	95
	60/60	214	28.4	98	94
	80/80	179	28.0	97	92
17.5	20/20	367	37.1	99	95
	40/40	274	36.1	99	95
	60/60	209	31.9	98	93
	80/80	174	31.2	97	91
20.0	20/20	358	40.9	99	95
	40/40	268	40.0	99	95
	60/60	203	34.8	97	92
	80/80	165	32.2	96	87

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table G.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	271	1.4	83	90
	40/40		9.0	96	90
	60/60		21.4	91	86
	80/80		33.6	81	85
7.5	20/20	277	4.7	90	93
	40/40		14.8	98	93
	60/60		29.6	94	92
	80/80		44.2	87	89
10.0	20/20	277	7.7	92	95
	40/40		20.3	99	94
	60/60		37.0	95	92
	80/80		52.5	89	89
12.5	20/20	279	11.2	94	95
	40/40		26.2	99	94
	60/60		44.1	95	93
	80/80		60.9	92	91
15.0	20/20	279	14.6	95	95
	40/40		31.8	99	95
	60/60		50.8	96	94
	80/80		68.5	92	92
17.5	20/20	273	17.3	95	95
	40/40		35.9	99	95
	60/60		55.6	96	93
	80/80		73.3	92	91
20.0	20/20	265	19.5	95	95
	40/40		38.9	99	95
	60/60		58.6	96	92
	80/80		76.6	91	87

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table G.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF	
				QLOE	ML
5.0	20/20	235	13	34	90
	40/40			80	90
	60/60			95	86
	80/80			67	85
7.5	20/20	243	20	47	93
	40/40			83	93
	60/60			97	92
	80/80			73	89
10.0	20/20	249	28	54	95
	40/40			85	94
	60/60			97	92
	80/80			76	89
12.5	20/20	256	36	55	95
	40/40			87	94
	60/60			97	93
	80/80			77	91
15.0	20/20	263	45	58	95
	40/40			87	95
	60/60			97	94
	80/80			77	92
17.5	20/20	265	53	57	95
	40/40			87	95
	60/60			96	93
	80/80			77	91
20.0	20/20	266	60	55	95
	40/40			86	95
	60/60			95	92
	80/80			74	87

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table G.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	78	74	4	403	1
3	Constant a, $c_1 = c_2$	9	31	73	7	406	0
4	Constant a & c	6	55051	1418	10	409	39*
5	Constant a, c & k	3	44824	1486	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	4834	167	8	407	29*
7	Constant k, $a = 1$, $c_1 = c_2$	5	14530	462	11	410	31*
8	Constant k & c, $a = 1$,	2	44561	1582	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table G.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	61	35	4	403	2
3	Constant a, $c_1 = c_2$	9	70	35	7	406	2
4	Constant a & c	6	46276	1165	10	409	40*
5	Constant a, c & k	3	37528	1217	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2432	81	8	407	30*
7	Constant k, $a = 1$, $c_1 = c_2$	5	9431	286	11	410	33*
8	Constant k & c, $a = 1$,	2	36485	1270	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table G.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	1	12	4	403	0
3	Constant a, $c_1 = c_2$	9	63	13	7	406	5*
4	Constant a & c	6	39306	973	10	409	40*
5	Constant a, c & k	3	32330	1032	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1877	49	8	407	38*
7	Constant k, $a = 1$, $c_1 = c_2$	5	7355	209	11	410	35*
8	Constant k & c, $a = 1$,	2	31442	1078	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table G.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	6	7	4	403	1
3	Constant a, $c_1 = c_2$	9	49	7	7	406	7*
4	Constant a & c	6	31279	771	10	409	41*
5	Constant a, c & k	3	25998	827	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1490	36	8	407	42*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4988	140	11	410	36*
8	Constant k & c, $a = 1$,	2	25082	857	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table G.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	3	4	4	403	1
3	Constant a, $c_1 = c_2$	9	36	5	7	406	7*
4	Constant a & c	6	25633	631	10	409	41*
5	Constant a, c & k	3	21473	682	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1196	28	8	407	43*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3733	105	11	410	36*
8	Constant k & c, $a = 1$,	2	20891	713	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table G.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	4	3	4	403	1
3	Constant a, $c_1 = c_2$	9	38	4	7	406	10*
4	Constant a & c	6	21186	521	10	409	41*
5	Constant a, c & k	3	17759	564	13	412	32*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1077	24	8	407	44*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2896	81	11	410	36*
8	Constant k & c, $a = 1$,	2	17294	589	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table G.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	1	3	4	403	0
3	Constant a, $c_1 = c_2$	9	50	3	7	406	14*
4	Constant a & c	6	17737	436	10	409	41*
5	Constant a, c & k	3	14894	473	13	412	32*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1018	23	8	407	45*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2382	66	11	410	36*
8	Constant k & c, $a = 1$,	2	14545	496	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table G.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	1804	1485	1058	799	640	513	418
2	$c_1 = c_2$	12	1800	1484	1050	795	634	510	412
3	Constant a, $c_1 = c_2$	9	1793	1486	1080	836	680	576	523
4	Constant a & c	6	3024	2942	2867	2770	2687	2608	2533
5	Constant a, c & k	3	3040	2957	2889	2796	2716	2637	2564
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2137	1837	1625	1495	1392	1336	1304
7	Constant k, $a = 1$, $c_1 = c_2$	5	2556	2357	2227	2060	1938	1832	1750
8	Constant k & c, $a = 1$	2	3065	2974	2906	2810	2734	2655	2583

Table G.17. Akaike Information Criteria (AIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1105	-1246	-1366	-1471	-1545	-1531	-1487
2	$c_1 = c_2$	8	-1113	-1252	-1374	-1478	-1552	-1538	-1494
3, 4, 5	Constant a & c	2	-1116	-1254	-1344	-1466	-1534	-1516	-1459
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-667	-734	-784	-830	-873	-907	-929

Table G.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	1868	1549	1122	863	705	578	483
2	$c_1 = c_2$	12	1849	1533	1098	843	683	558	460
3	Constant a, $c_1 = c_2$	9	1829	1522	1116	872	716	612	559
4	Constant a & c	6	3048	2966	2891	2795	2711	2632	2558
5	Constant a, c & k	3	3052	2970	2901	2809	2728	2649	2576
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2169	1869	1658	1527	1424	1368	1336
7	Constant k, $a = 1$, $c_1 = c_2$	5	2576	2378	2247	2081	1958	1852	1770
8	Constant k & c, $a = 1$	2	3073	2982	2914	2818	2742	2663	2591

Table G.19. Bayes Information Criteria (BIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1065	-1206	-1326	-1430	-1505	-1491	-1447
2	$c_1 = c_2$	8	-1086	-1225	-1347	-1451	-1526	-1512	-1467
3, 4, 5	Constant a & c	2	-1109	-1247	-1338	-1459	-1527	-1509	-1452
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-667	-734	-784	-830	-873	-907	-929

Table G.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	-0.5	0.5	0.2	0.4	0.1	1
	40/40	-1.3	1.2	0.4	0.6	0.3	2
	60/60	-1.3	1.3	0.6	0.9	0.4	1
	80/80	-1.6	1.7	0.8	1.3	0.5	1
7.5	20/20	-2.5	2.5	0.3	0.9	0.6	6
	40/40	-2.5	2.7	0.6	1.4	0.7	3
	60/60	-4.4	4.3	0.9	2.0	1.1	5
	80/80	-5.6	5.5	1.2	2.6	1.4	5
10.0	20/20	-6.1	6.0	0.4	1.8	1.5	14
	40/40	-8.1	8.1	0.5	2.6	2.1	12
	60/60	-10.6	10.4	0.8	3.3	2.6	12
	80/80	-10.5	10.3	1.5	4.0	2.5	7
12.5	20/20	-8.4	8.3	0.5	2.6	2.1	15
	40/40	-12.5	12.7	0.5	3.7	3.2	15
	60/60	-10.6	10.7	1.5	4.2	2.7	8
	80/80	-13.7	13.5	2.0	5.3	3.3	9
15.0	20/20	-11.7	11.9	0.3	3.4	3.1	18
	40/40	-14.3	14.0	1.2	4.6	3.4	14
	60/60	-16.2	16.2	1.6	5.6	4.1	12
	80/80	-17.7	17.8	2.2	6.7	4.4	10
17.5	20/20	-13.9	14.1	0.5	4.1	3.6	17
	40/40	-17.8	17.8	1.3	5.7	4.4	15
	60/60	-19.2	19.3	1.9	6.8	4.8	12
	80/80	-19.4	19.4	3.0	7.9	4.9	10
20.0	20/20	-15.6	15.8	0.9	4.8	4.0	16
	40/40	-20.9	20.6	1.6	6.7	5.1	15
	60/60	-21.5	21.6	2.4	7.8	5.4	11
	80/80	-22.3	22.2	3.5	9.1	5.5	9

Note. %VAF = Percentage of Variance Accounted For.

Table G.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	1.0	-1.2	4.3	0.045	4.3	-8%	98
	40/40	0.9	-0.8	4.5	0.034	4.5	-4%	99
	60/60	2.8	-2.7	5.3	0.028	5.3	-12%	98
	80/80	1.7	-1.5	5.4	0.023	5.4	-6%	97
7.5	20/20	3.6	-3.6	6.5	0.033	6.5	-14%	99
	40/40	4.1	-4.3	8.3	0.029	8.3	-13%	99
	60/60	2.5	-2.4	8.9	0.025	8.9	-7%	98
	80/80	1.2	-1.2	8.7	0.020	8.7	-4%	98
10.0	20/20	1.5	-1.4	8.4	0.028	8.4	-4%	99
	40/40	3.7	-3.5	10.8	0.024	10.8	-8%	99
	60/60	0.9	-1.1	11.0	0.021	11.0	-3%	99
	80/80	3.9	-3.8	11.9	0.017	11.9	-8%	99
12.5	20/20	2.8	-2.9	10.0	0.023	10.0	-7%	99
	40/40	4.0	-3.3	12.2	0.020	12.2	-5%	99
	60/60	2.7	-2.5	12.5	0.017	12.5	-4%	99
	80/80	2.6	-2.8	13.6	0.014	13.6	-6%	99
15.0	20/20	3.6	-3.7	11.7	0.021	11.7	-8%	99
	40/40	4.1	-4.1	14.2	0.017	14.2	-7%	99
	60/60	2.3	-2.6	14.2	0.014	14.2	-5%	99
	80/80	4.4	-4.3	15.5	0.013	15.5	-7%	99
17.5	20/20	3.6	-3.5	12.7	0.018	12.7	-7%	99
	40/40	3.4	-3.0	14.7	0.015	14.7	-5%	99
	60/60	2.3	-2.2	15.4	0.013	15.4	-3%	99
	80/80	2.7	-2.7	16.0	0.011	16.0	-4%	99
20.0	20/20	7.7	-7.8	14.2	0.016	14.2	-14%	99
	40/40	2.6	-2.6	15.9	0.013	15.9	-4%	99
	60/60	5.4	-5.6	17.4	0.012	17.4	-8%	99
	80/80	6.0	-5.7	18.0	0.010	18.0	-8%	100

Note. %VAF = Percentage of Variance Accounted For.

Appendix H: Experiment 1 Fitting Measures of the Linear-Clone-Bitflip Creature Type

Table H.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	531	10.5	10.6	0.78	99	99
	40/40	531	14.2	14.9	0.77	99	99
	60/60	529	21.0	20.6	0.80	99	100
	80/80	527	25.3	25.2	0.79	99	100
7.5	20/20	540	16.4	16.2	0.81	99	100
	40/40	534	23.5	23.5	0.82	100	100
	60/60	519	28.6	28.1	0.81	100	100
	80/80	499	32.1	31.7	0.80	100	100
10.0	20/20	538	22.0	21.9	0.83	100	100
	40/40	513	28.9	29.2	0.84	100	100
	60/60	490	33.5	33.3	0.83	100	100
	80/80	486	37.2	37.5	0.80	100	99
12.5	20/20	544	27.1	26.7	0.83	100	100
	40/40	504	33.4	33.5	0.84	100	100
	60/60	476	36.9	37.0	0.82	100	99
	80/80	451	39.4	39.7	0.80	100	99
15.0	20/20	532	31.0	31.4	0.84	100	100
	40/40	491	36.6	36.5	0.83	100	100
	60/60	463	39.6	39.8	0.81	100	99
	80/80	439	39.8	39.8	0.77	99	99
17.5	20/20	534	34.7	34.8	0.83	100	100
	40/40	478	39.0	38.8	0.83	100	99
	60/60	448	41.1	40.9	0.79	99	99
	80/80	430	41.0	41.0	0.75	99	98
20.0	20/20	521	37.3	37.3	0.83	100	100
	40/40	466	39.5	39.7	0.81	100	99
	60/60	428	40.3	40.1	0.77	99	98
	80/80	427	41.3	41.0	0.72	99	97

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table H.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	530	10.5	0.78	99	99
	40/40	530	14.7	0.77	99	99
	60/60	528	20.8	0.80	99	100
	80/80	527	25.2	0.79	99	100
7.5	20/20	540	16.3	0.81	99	100
	40/40	534	23.5	0.82	100	100
	60/60	519	28.4	0.81	100	100
	80/80	499	31.9	0.80	100	100
10.0	20/20	538	22.0	0.83	100	100
	40/40	513	29.0	0.84	100	100
	60/60	490	33.4	0.83	100	100
	80/80	486	37.4	0.80	100	99
12.5	20/20	544	26.9	0.83	100	100
	40/40	504	33.4	0.84	100	100
	60/60	476	36.9	0.82	100	99
	80/80	451	39.5	0.80	100	99
15.0	20/20	532	31.2	0.84	100	100
	40/40	491	36.5	0.83	100	100
	60/60	463	39.7	0.81	100	99
	80/80	439	39.8	0.77	99	99
17.5	20/20	534	34.8	0.83	100	100
	40/40	478	38.9	0.83	100	99
	60/60	448	41.0	0.79	99	99
	80/80	430	41.0	0.75	99	98
20.0	20/20	521	37.3	0.83	100	100
	40/40	466	39.6	0.81	100	99
	60/60	428	40.2	0.77	99	98
	80/80	427	41.1	0.72	99	97

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table H.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	528	10.6	0.78	99	99
	40/40	522	14.9		99	99
	60/60	537	20.5		99	99
	80/80	534	25.1		99	100
7.5	20/20	539	16.4	0.81	99	100
	40/40	541	23.3		100	100
	60/60	520	28.4		100	100
	80/80	492	32.0		100	100
10.0	20/20	542	21.8	0.82	100	100
	40/40	526	28.6		100	100
	60/60	493	33.4		100	100
	80/80	461	37.3		100	99
12.5	20/20	551	26.7	0.82	100	100
	40/40	519	33.1		100	100
	60/60	472	37.0		100	99
	80/80	431	39.2		100	99
15.0	20/20	557	30.6	0.81	100	100
	40/40	514	36.4		100	100
	60/60	461	39.7		100	99
	80/80	397	38.7		99	98
17.5	20/20	569	34.5	0.80	100	100
	40/40	509	39.0		100	99
	60/60	445	40.9		99	99
	80/80	377	39.1		99	97
20.0	20/20	580	37.5	0.78	100	99
	40/40	502	40.2		100	99
	60/60	425	40.1		99	98
	80/80	359	38.1		99	96

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table H.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF	
					QLOE	ML
5.0	20/20	531	17.5	0.78	89	99
	40/40		16.3		99	99
	60/60		18.5		99	99
	80/80		19.4		93	99
7.5	20/20	534	26.9	0.81	88	100
	40/40		25.3		98	100
	60/60		28.2		99	100
	80/80		30.3		93	99
10.0	20/20	525	34.9	0.82	86	100
	40/40		32.0		98	100
	60/60		36.0		99	100
	80/80		38.4		92	99
12.5	20/20	525	41.5	0.82	84	100
	40/40		38.1		98	99
	60/60		42.5		99	99
	80/80		45.5		91	98
15.0	20/20	530	47.8	0.81	82	100
	40/40		43.9		97	99
	60/60		48.4		99	99
	80/80		52.3		90	97
17.5	20/20	536	53.4	0.80	79	100
	40/40		49.2		96	99
	60/60		54.3		99	99
	80/80		57.8		88	96
20.0	20/20	537	56.2	0.78	77	99
	40/40		51.4		95	99
	60/60		56.9		99	98
	80/80		60.8		87	95

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table H.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	524	17.5	0.79	89	99
	40/40				98	99
	60/60				99	99
	80/80				92	100
7.5	20/20	523	26.7	0.82	87	100
	40/40				97	100
	60/60				99	100
	80/80				92	100
10.0	20/20	513	34.1	0.83	86	100
	40/40				97	100
	60/60				99	100
	80/80				91	99
12.5	20/20	509	40.4	0.82	84	100
	40/40				96	100
	60/60				99	99
	80/80				90	99
15.0	20/20	510	46.4	0.81	81	100
	40/40				95	100
	60/60				99	99
	80/80				88	98
17.5	20/20	510	51.0	0.80	78	100
	40/40				94	99
	60/60				99	99
	80/80				86	97
20.0	20/20	505	53.2	0.78	75	100
	40/40				92	99
	60/60				99	98
	80/80				85	96

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table H.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	465	14.9	97	92
	40/40	443	20.2	97	90
	60/60	440	27.4	98	93
	80/80	420	31.7	98	93
7.5	20/20	468	21.6	98	94
	40/40	454	30.0	99	95
	60/60	420	34.9	99	94
	80/80	388	38.1	98	94
10.0	20/20	467	28.2	99	96
	40/40	435	35.3	99	96
	60/60	393	39.1	99	95
	80/80	357	41.8	98	93
12.5	20/20	458	33.5	99	96
	40/40	415	39.5	99	96
	60/60	365	42.1	98	95
	80/80	324	42.4	98	93
15.0	20/20	444	37.5	99	96
	40/40	392	42.1	99	96
	60/60	340	43.4	98	93
	80/80	290	40.9	97	89
17.5	20/20	428	40.6	99	96
	40/40	369	43.6	99	95
	60/60	313	43.0	98	92
	80/80	266	40.6	96	86
20.0	20/20	409	42.6	99	96
	40/40	343	43.2	98	94
	60/60	286	41.5	97	90
	80/80	243	39.0	95	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table H.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	446	12.9	96	92
	40/40		20.6	97	90
	60/60		28.5	98	93
	80/80		36.8	98	93
7.5	20/20	440	17.8	98	94
	40/40		27.5	99	95
	60/60		39.2	99	94
	80/80		50.7	98	94
10.0	20/20	423	21.2	99	96
	40/40		32.9	99	96
	60/60		46.5	99	95
	80/80		60.4	97	93
12.5	20/20	401	23.5	98	96
	40/40		36.5	99	96
	60/60		51.9	98	95
	80/80		66.6	97	93
15.0	20/20	377	24.5	98	96
	40/40		38.3	99	96
	60/60		54.4	98	93
	80/80		69.9	95	89
17.5	20/20	353	25.0	97	96
	40/40		39.3	98	95
	60/60		55.6	97	92
	80/80		71.5	94	86
20.0	20/20	327	24.4	97	96
	40/40		38.8	98	94
	60/60		54.9	97	90
	80/80		70.1	92	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table H.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	438	23	87	92
	40/40			95	90
	60/60			98	93
	80/80			91	93
7.5	20/20	429	33	87	94
	40/40			97	95
	60/60			98	94
	80/80			91	94
10.0	20/20	410	40	85	96
	40/40			96	96
	60/60			99	95
	80/80			89	93
12.5	20/20	389	45	83	96
	40/40			96	96
	60/60			98	95
	80/80			88	93
15.0	20/20	367	50	80	96
	40/40			94	96
	60/60			98	93
	80/80			86	89
17.5	20/20	344	52	78	96
	40/40			93	95
	60/60			97	92
	80/80			84	86
20.0	20/20	319	52	75	96
	40/40			91	94
	60/60			97	90
	80/80			81	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table H.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	426	92	4	403	5*
3	Constant a, $c_1 = c_2$	9	351	94	7	406	4*
4	Constant a & c	6	16797	498	10	409	34*
5	Constant a, c & k	3	14582	546	13	412	27*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	8319	251	8	407	33*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6323	256	11	410	25*
8	Constant k & c, $a = 1$,	2	17835	691	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table H.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	43	41	4	403	1
3	Constant a, $c_1 = c_2$	9	24	41	7	406	1
4	Constant a & c	6	19300	512	10	409	38*
5	Constant a, c & k	3	16874	572	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	4043	120	8	407	34*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3560	136	11	410	26*
8	Constant k & c, $a = 1$,	2	17688	639	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table H.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	18	20	4	403	1
3	Constant a, $c_1 = c_2$	9	14	20	7	406	1
4	Constant a & c	6	19765	502	10	409	39*
5	Constant a, c & k	3	16902	552	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2985	78	8	407	38*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3113	103	11	410	30*
8	Constant k & c, $a = 1$,	2	17349	607	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table H.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	20	15	4	403	1
3	Constant a, $c_1 = c_2$	9	22	15	7	406	1
4	Constant a & c	6	18780	474	10	409	40*
5	Constant a, c & k	3	15974	519	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2582	66	8	407	39*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3000	95	11	410	32*
8	Constant k & c, $a = 1$,	2	16250	565	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table H.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	9	12	4	403	1
3	Constant a, $c_1 = c_2$	9	21	12	7	406	2
4	Constant a & c	6	17772	446	10	409	40*
5	Constant a, c & k	3	15171	490	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2405	59	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	3011	92	11	410	33*
8	Constant k & c, $a = 1$,	2	15392	533	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table H.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	1	11	4	403	0
3	Constant a, $c_1 = c_2$	9	57	12	7	406	5*
4	Constant a & c	6	16712	419	10	409	40*
5	Constant a, c & k	3	14102	456	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2157	53	8	407	40*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2859	88	11	410	33*
8	Constant k & c, $a = 1$,	2	14099	489	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table H.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	4	10	4	403	0
3	Constant a, $c_1 = c_2$	9	107	12	7	406	9*
4	Constant a & c	6	14944	375	10	409	40*
5	Constant a, c & k	3	12699	410	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2026	50	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	2777	84	11	410	33*
8	Constant k & c, $a = 1$,	2	12623	438	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table H.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	1882	1561	1253	1143	1036	1016	976
2	$c_1 = c_2$	12	1894	1557	1249	1141	1031	1009	969
3	Constant a, $c_1 = c_2$	9	1896	1551	1244	1140	1035	1038	1033
4	Constant a & c	6	2588	2600	2592	2568	2543	2517	2471
5	Constant a, c & k	3	2624	2643	2629	2602	2579	2549	2505
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2305	1998	1819	1747	1701	1661	1632
7	Constant k, $a = 1$, $c_1 = c_2$	5	2311	2046	1930	1899	1886	1864	1849
8	Constant k & c, $a = 1$	2	2721	2689	2667	2637	2613	2577	2531

Table H.17. Akaike Information Criteria (AIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1158	-1279	-1333	-1326	-1320	-1310	-1304
2	$c_1 = c_2$	8	-1158	-1285	-1340	-1334	-1326	-1318	-1311
3, 4, 5	Constant a & c	2	-1168	-1291	-1328	-1330	-1293	-1286	-1267
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-678	-735	-789	-824	-851	-867	-879

Table H.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	1947	1625	1318	1208	1101	1081	1040
2	$c_1 = c_2$	12	1942	1606	1297	1189	1080	1057	1018
3	Constant a, $c_1 = c_2$	9	1932	1587	1281	1176	1071	1074	1069
4	Constant a & c	6	2612	2624	2616	2592	2567	2541	2495
5	Constant a, c & k	3	2636	2656	2641	2615	2591	2561	2517
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2337	2030	1851	1779	1733	1693	1664
7	Constant k, $a = 1$, $c_1 = c_2$	5	2331	2066	1951	1919	1906	1884	1869
8	Constant k & c, $a = 1$	2	2729	2697	2675	2645	2621	2585	2539

Table H.19. Bayes Information Criteria (BIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1118	-1239	-1293	-1286	-1280	-1270	-1264
2	$c_1 = c_2$	8	-1132	-1258	-1313	-1307	-1299	-1291	-1284
3, 4, 5	Constant a & c	2	-1161	-1285	-1321	-1323	-1286	-1279	-1261
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-678	-735	-789	-824	-851	-867	-879

Table H.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	-2.5	2.5	0.7	1.4	0.6	2
	40/40	-6.2	6.0	1.3	2.7	1.4	5
	60/60	-8.8	8.9	1.2	3.4	2.2	8
	80/80	-10.2	10.3	1.4	4.0	2.6	11
7.5	20/20	-11.3	11.3	0.9	3.8	2.8	12
	40/40	-18.5	18.1	1.9	6.3	4.4	14
	60/60	-23.3	23.2	1.8	7.5	5.8	19
	80/80	-22.5	22.9	2.1	7.9	5.8	20
10.0	20/20	-17.9	18.1	1.4	6.0	4.6	16
	40/40	-32.3	32.2	2.1	10.2	8.0	23
	60/60	-37.5	37.8	2.1	11.6	9.5	28
	80/80	-34.0	33.6	3.5	11.8	8.3	26
12.5	20/20	-28.0	29.1	1.1	8.6	7.6	22
	40/40	-42.3	42.5	2.7	13.4	10.7	27
	60/60	-39.8	39.6	4.2	14.0	9.8	23
	80/80	-41.4	41.3	4.6	14.9	10.3	29
15.0	20/20	-35.7	35.8	1.9	10.8	9.0	27
	40/40	-49.9	50.2	3.2	15.8	12.6	30
	60/60	-47.9	47.5	5.0	16.8	11.8	27
	80/80	-40.2	40.3	6.8	16.9	10.1	25
17.5	20/20	-43.0	43.9	1.5	12.7	11.2	30
	40/40	-55.1	56.1	4.0	18.3	14.3	30
	60/60	-49.2	49.1	6.6	18.8	12.2	29
	80/80	-42.2	42.3	8.4	19.0	10.6	26
20.0	20/20	-45.9	46.1	2.5	14.1	11.6	29
	40/40	-56.1	56.3	5.8	19.9	14.1	29
	60/60	-48.0	48.3	8.3	20.5	12.2	26
	80/80	-33.1	32.8	12.2	20.4	8.1	18

Note. %VAF = Percentage of Variance Accounted For.

Table H.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	-0.1	-0.4	8.5	0.030	8.5	-3%	97
	40/40	6.6	-4.6	11.9	0.024	11.9	-6%	98
	60/60	-1.9	1.5	10.5	0.018	10.8	2%	98
	80/80	-3.3	2.8	9.2	0.014	9.8	6%	97
7.5	20/20	-2.9	2.0	13.1	0.021	13.4	2%	99
	40/40	-0.4	0.8	17.5	0.017	17.8	2%	98
	60/60	2.0	-2.0	17.1	0.013	17.1	-3%	98
	80/80	-10.0	10.7	12.3	0.010	15.2	23%	97
10.0	20/20	3.1	-1.4	17.4	0.018	17.4	0%	99
	40/40	-10.3	10.2	20.1	0.012	22.6	13%	98
	60/60	-2.6	1.8	20.6	0.010	20.9	1%	97
	80/80	-9.3	9.4	16.6	0.007	18.9	14%	96
12.5	20/20	-4.4	4.8	19.4	0.014	20.7	7%	99
	40/40	-4.9	4.4	23.9	0.009	24.9	4%	96
	60/60	-7.0	7.0	21.7	0.007	23.4	8%	95
	80/80	-7.6	7.7	19.6	0.006	21.6	10%	92
15.0	20/20	-14.5	15.8	18.0	0.011	22.3	24%	98
	40/40	-12.4	13.2	23.1	0.008	26.6	15%	94
	60/60	-11.3	11.1	22.6	0.006	25.3	12%	92
	80/80	-12.7	12.4	19.7	0.004	22.7	15%	87
17.5	20/20	-7.6	8.3	21.0	0.009	23.3	11%	98
	40/40	-21.6	22.6	22.8	0.006	28.8	26%	93
	60/60	-17.0	17.5	21.5	0.004	25.9	21%	87
	80/80	-18.4	18.5	19.1	0.003	23.7	24%	79
20.0	20/20	-4.6	5.4	23.1	0.008	24.6	7%	97
	40/40	-17.9	17.7	24.4	0.005	28.8	18%	91
	60/60	-18.8	19.0	21.9	0.004	26.7	22%	83
	80/80	-14.2	13.5	20.6	0.002	23.9	16%	65

Note. %VAF = Percentage of Variance Accounted For.

Appendix I: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Uniform Creature Type

Table I.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	519	13.1	13.8	0.74	92	96
	40/40	460	17.6	17.6	0.73	96	98
	60/60	369	16.1	17.4	0.73	96	98
	80/80	319	16.6	17.9	0.74	97	98
7.5	20/20	488	16.7	17.6	0.76	97	98
	40/40	381	16.5	16.9	0.73	98	99
	60/60	293	14.4	15.5	0.75	98	99
	80/80	243	13.0	13.6	0.75	98	99
10.0	20/20	481	22.2	22.5	0.78	99	99
	40/40	338	17.2	17.2	0.75	98	99
	60/60	257	14.8	15.1	0.77	99	99
	80/80	216	12.4	12.8	0.74	99	99
12.5	20/20	436	22.7	22.9	0.79	99	99
	40/40	298	16.8	16.9	0.77	99	99
	60/60	228	13.4	13.4	0.76	99	99
	80/80	193	11.5	11.5	0.73	99	99
15.0	20/20	402	22.5	22.2	0.78	99	99
	40/40	274	15.7	16.0	0.76	99	100
	60/60	206	12.3	12.1	0.75	99	99
	80/80	175	10.2	10.3	0.72	99	99
17.5	20/20	379	22.9	23.3	0.78	99	100
	40/40	254	16.1	16.0	0.77	99	99
	60/60	192	11.3	11.4	0.74	99	99
	80/80	164	9.5	9.6	0.71	99	99
20.0	20/20	356	22.9	23.7	0.78	99	100
	40/40	236	14.3	14.5	0.74	99	99
	60/60	179	10.3	10.2	0.72	99	99
	80/80	154	9.0	9.1	0.71	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table I.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	518	13.6	0.74	92	96
	40/40	460	17.6	0.73	96	98
	60/60	366	17.2	0.74	96	97
	80/80	317	17.6	0.75	97	98
7.5	20/20	485	17.1	0.76	96	98
	40/40	382	16.9	0.73	98	99
	60/60	293	15.4	0.76	98	98
	80/80	242	13.4	0.75	98	99
10.0	20/20	481	22.4	0.78	99	99
	40/40	338	17.2	0.75	98	99
	60/60	257	15.0	0.77	99	99
	80/80	215	12.7	0.74	99	99
12.5	20/20	436	22.8	0.79	99	99
	40/40	298	16.8	0.77	99	99
	60/60	228	13.4	0.76	99	99
	80/80	193	11.5	0.73	99	99
15.0	20/20	402	22.3	0.78	99	99
	40/40	274	15.9	0.76	99	100
	60/60	206	12.2	0.76	99	99
	80/80	175	10.2	0.72	99	99
17.5	20/20	379	23.2	0.78	99	100
	40/40	254	16.0	0.77	99	99
	60/60	192	11.4	0.74	99	99
	80/80	163	9.5	0.71	99	99
20.0	20/20	356	23.5	0.79	99	100
	40/40	236	14.4	0.74	99	99
	60/60	179	10.3	0.72	99	99
	80/80	154	9.1	0.71	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table I.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	518	13.6	0.74	92	96
	40/40	453	17.8		96	98
	60/60	366	17.2		96	97
	80/80	322	17.5		97	98
7.5	20/20	491	16.9	0.75	97	98
	40/40	375	17.1		98	99
	60/60	295	15.3		98	98
	80/80	242	13.4		98	99
10.0	20/20	496	22.1	0.76	99	99
	40/40	334	17.4		98	99
	60/60	260	14.8		99	99
	80/80	212	12.8		99	99
12.5	20/20	453	22.3	0.76	99	99
	40/40	301	16.8		99	99
	60/60	228	13.4		99	99
	80/80	187	11.7		99	99
15.0	20/20	418	21.9	0.75	99	99
	40/40	275	15.8		99	100
	60/60	207	12.2		99	99
	80/80	170	10.4		99	99
17.5	20/20	400	22.8	0.75	99	99
	40/40	262	15.9		99	99
	60/60	190	11.4		99	99
	80/80	157	9.7		99	99
20.0	20/20	385	23.1	0.74	99	99
	40/40	239	14.4		99	99
	60/60	176	10.4		99	99
	80/80	150	9.2		99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table I.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	430	20.7	0.74	45	95
	40/40		19.1		91	98
	60/60		20.4		94	98
	80/80		21.8		81	97
7.5	20/20	362	20.7	0.74	50	98
	40/40		18.7		93	98
	60/60		20.3		96	99
	80/80		22.6		81	98
10.0	20/20	334	22.6	0.75	60	99
	40/40		20.8		93	99
	60/60		22.9		97	99
	80/80		24.8		83	98
12.5	20/20	293	20.9	0.75	60	99
	40/40		19.0		94	99
	60/60		21.4		97	99
	80/80		23.1		83	98
15.0	20/20	268	19.5	0.75	61	99
	40/40		17.8		95	99
	60/60		20.2		98	99
	80/80		21.4		82	98
17.5	20/20	244	18.5	0.75	62	99
	40/40		16.9		94	99
	60/60		18.7		98	99
	80/80		20.0		83	98
20.0	20/20	228	17.0	0.73	64	99
	40/40		15.6		94	99
	60/60		17.4		97	99
	80/80		18.4		84	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table I.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	423	20.0	0.74	46	95
	40/40				90	98
	60/60				94	97
	80/80				78	98
7.5	20/20	352	19.7	0.75	50	98
	40/40				91	99
	60/60				96	98
	80/80				77	99
10.0	20/20	320	21.2	0.76	59	99
	40/40				91	99
	60/60				97	99
	80/80				81	99
12.5	20/20	281	19.6	0.76	59	99
	40/40				92	99
	60/60				98	99
	80/80				81	99
15.0	20/20	255	18.2	0.75	59	99
	40/40				92	100
	60/60				98	99
	80/80				81	99
17.5	20/20	235	17.5	0.75	61	99
	40/40				92	99
	60/60				98	99
	80/80				82	99
20.0	20/20	219	16.0	0.74	62	99
	40/40				92	99
	60/60				98	99
	80/80				83	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table I.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	435	20.7	87	86
	40/40	361	25.3	92	86
	60/60	291	24.0	92	86
	80/80	248	22.6	94	87
7.5	20/20	400	24.4	93	89
	40/40	299	23.4	93	87
	60/60	235	20.1	95	88
	80/80	196	17.9	95	88
10.0	20/20	382	28.7	97	91
	40/40	267	23.3	95	88
	60/60	211	19.8	96	91
	80/80	172	16.2	96	87
12.5	20/20	351	29.4	97	92
	40/40	238	21.6	96	90
	60/60	185	17.2	96	89
	80/80	153	14.5	95	86
15.0	20/20	317	28.3	97	92
	40/40	216	20.3	97	89
	60/60	168	15.6	97	89
	80/80	139	13.1	95	84
17.5	20/20	297	28.6	98	92
	40/40	202	19.7	97	91
	60/60	155	14.6	96	88
	80/80	129	12.1	94	83
20.0	20/20	279	28.8	98	92
	40/40	184	17.8	96	87
	60/60	143	13.1	95	85
	80/80	122	11.4	94	82

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table I.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	355	11.0	83	86
	40/40		24.2	92	86
	60/60		38.7	90	86
	80/80		52.1	90	87
7.5	20/20	299	10.1	87	89
	40/40		23.5	93	87
	60/60		37.1	92	88
	80/80		49.2	88	88
10.0	20/20	268	10.1	89	91
	40/40		23.4	95	88
	60/60		36.6	94	91
	80/80		48.7	89	87
12.5	20/20	238	9.2	89	92
	40/40		21.4	96	90
	60/60		33.3	94	89
	80/80		44.1	87	86
15.0	20/20	213	8.4	88	92
	40/40		19.4	97	89
	60/60		29.8	94	89
	80/80		39.4	86	84
17.5	20/20	195	8.0	88	92
	40/40		17.6	97	91
	60/60		27.4	93	88
	80/80		36.0	85	83
20.0	20/20	178	7.2	86	92
	40/40		16.1	96	87
	60/60		24.6	92	85
	80/80		32.1	86	82

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table I.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	322	26	41	86
	40/40			85	86
	60/60			90	86
	80/80			74	87
7.5	20/20	268	25	46	89
	40/40			86	87
	60/60			93	88
	80/80			74	88
10.0	20/20	241	26	56	91
	40/40			88	88
	60/60			95	91
	80/80			77	87
12.5	20/20	212	24	56	92
	40/40			89	90
	60/60			95	89
	80/80			77	86
15.0	20/20	193	22	57	92
	40/40			90	89
	60/60			95	89
	80/80			77	84
17.5	20/20	178	21	58	92
	40/40			90	91
	60/60			95	88
	80/80			77	83
20.0	20/20	164	19	59	92
	40/40			89	87
	60/60			93	85
	80/80			77	82

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table I.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	1111	193	4	403	6*
3	Constant a, $c_1 = c_2$	9	671	192	7	406	3*
4	Constant a & c	6	33529	999	10	409	34*
5	Constant a, c & k	3	26147	1003	13	412	26*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	8136	340	8	407	24*
7	Constant k, $a = 1$, $c_1 = c_2$	5	8956	419	11	410	21*
8	Constant k & c, $a = 1$,	2	28955	1159	14	413	25*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table I.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	622	80	4	403	8*
3	Constant a, $c_1 = c_2$	9	362	79	7	406	5*
4	Constant a & c	6	28369	766	10	409	37*
5	Constant a, c & k	3	22678	787	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	5217	175	8	407	30*
7	Constant k, $a = 1$, $c_1 = c_2$	5	8034	288	11	410	28*
8	Constant k & c, $a = 1$,	2	24172	891	14	413	27*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table I.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	62	40	4	403	2
3	Constant a, $c_1 = c_2$	9	45	39	7	406	1
4	Constant a & c	6	24932	648	10	409	38*
5	Constant a, c & k	3	20244	677	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3165	101	8	407	31*
7	Constant k, $a = 1$, $c_1 = c_2$	5	7256	233	11	410	31*
8	Constant k & c, $a = 1$,	2	20965	749	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table I.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	7	28	4	403	0
3	Constant a, $c_1 = c_2$	9	26	28	7	406	1
4	Constant a & c	6	19877	513	10	409	39*
5	Constant a, c & k	3	16318	542	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2237	71	8	407	31*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6021	189	11	410	32*
8	Constant k & c, $a = 1$,	2	16782	596	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table I.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	49	14	4	403	3*
3	Constant a, $c_1 = c_2$	9	40	14	7	406	3*
4	Constant a & c	6	15449	391	10	409	39*
5	Constant a, c & k	3	12761	416	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2136	56	8	407	38*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5263	155	11	410	34*
8	Constant k & c, $a = 1$,	2	13278	464	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table I.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	22	10	4	403	2
3	Constant a, $c_1 = c_2$	9	51	10	7	406	5*
4	Constant a & c	6	13367	336	10	409	40*
5	Constant a, c & k	3	10922	354	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1772	44	8	407	40*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4726	136	11	410	35*
8	Constant k & c, $a = 1$,	2	11272	391	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table I.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	63	9	4	403	7*
3	Constant a, $c_1 = c_2$	9	81	10	7	406	8*
4	Constant a & c	6	10883	275	10	409	40*
5	Constant a, c & k	3	8903	289	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1704	42	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4479	129	11	410	35*
8	Constant k & c, $a = 1$,	2	9402	327	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table I.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2184	1806	1542	1402	1110	957	914
2	$c_1 = c_2$	12	2201	1832	1541	1395	1116	959	935
3	Constant a, $c_1 = c_2$	9	2196	1826	1537	1395	1116	980	963
4	Constant a & c	6	2878	2768	2698	2601	2488	2425	2341
5	Constant a, c & k	3	2877	2776	2713	2621	2511	2444	2360
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2432	2156	1926	1783	1679	1584	1562
7	Constant k, $a = 1$, $c_1 = c_2$	5	2516	2359	2272	2184	2101	2048	2024
8	Constant k & c, $a = 1$	2	2936	2827	2754	2659	2555	2484	2410

Table I.17. Akaike Information Criteria (AIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-989	-1099	-1192	-1213	-1299	-1334	-1380
2	$c_1 = c_2$	8	-985	-1092	-1197	-1221	-1304	-1340	-1379
3, 4, 5	Constant a & c	2	-996	-1101	-1195	-1215	-1289	-1306	-1324
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-668	-686	-694	-709	-715	-729	-737

Table I.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2249	1871	1607	1467	1174	1022	978
2	$c_1 = c_2$	12	2249	1880	1589	1444	1165	1007	984
3	Constant a, $c_1 = c_2$	9	2232	1863	1573	1431	1153	1016	999
4	Constant a & c	6	2902	2792	2722	2625	2512	2449	2365
5	Constant a, c & k	3	2889	2788	2725	2633	2523	2456	2372
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2464	2188	1958	1815	1711	1616	1594
7	Constant k, $a = 1$, $c_1 = c_2$	5	2536	2379	2292	2204	2122	2068	2045
8	Constant k & c, $a = 1$	2	2944	2835	2762	2667	2563	2492	2418

Table I.19. Bayes Information Criteria (BIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-949	-1059	-1152	-1173	-1259	-1294	-1340
2	$c_1 = c_2$	8	-958	-1065	-1170	-1194	-1278	-1313	-1352
3, 4, 5	Constant a & c	2	-990	-1095	-1188	-1208	-1283	-1299	-1317
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-668	-686	-694	-709	-715	-729	-737

Table I.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	0.1	-0.1	0.0	0.0	0.0	1
	40/40	0.0	0.0	0.0	0.0	0.0	0
	60/60	0.0	-0.1	0.1	0.0	0.0	1
	80/80	0.0	0.0	0.1	0.1	0.0	1
7.5	20/20	0.0	-0.1	0.1	0.1	0.0	1
	40/40	0.1	-0.1	0.1	0.1	0.0	0
	60/60	0.0	0.0	0.1	0.1	0.0	1
	80/80	0.0	0.0	0.1	0.2	0.0	1
10.0	20/20	-0.3	0.3	0.1	0.2	0.1	2
	40/40	-0.1	0.1	0.1	0.2	0.0	0
	60/60	-0.3	0.3	0.1	0.2	0.1	1
	80/80	-0.3	0.3	0.2	0.3	0.1	1
12.5	20/20	-0.6	0.5	0.1	0.3	0.1	3
	40/40	-0.5	0.4	0.2	0.3	0.1	2
	60/60	-0.7	0.6	0.2	0.3	0.2	2
	80/80	-0.8	0.8	0.2	0.4	0.2	2
15.0	20/20	-0.9	0.9	0.2	0.4	0.2	4
	40/40	-1.0	1.0	0.2	0.4	0.2	3
	60/60	-1.0	1.0	0.2	0.5	0.3	3
	80/80	-0.7	0.6	0.4	0.5	0.1	1
17.5	20/20	-1.5	1.4	0.2	0.6	0.3	5
	40/40	-1.8	1.8	0.2	0.6	0.5	6
	60/60	-1.2	1.1	0.4	0.6	0.3	2
	80/80	-1.2	1.2	0.4	0.7	0.3	1
20.0	20/20	-1.8	1.7	0.3	0.7	0.4	5
	40/40	-2.2	2.1	0.3	0.8	0.5	5
	60/60	-1.6	1.6	0.4	0.8	0.4	2
	80/80	-1.7	1.6	0.6	1.0	0.4	2

Note. %VAF = Percentage of Variance Accounted For.

Table I.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	-0.6	0.5	0.6	0.067	0.7	21%	93
	40/40	-0.1	0.0	0.7	0.063	0.7	0%	97
	60/60	0.3	-0.3	0.6	0.053	0.6	-13%	95
	80/80	0.2	-0.1	0.6	0.047	0.6	-2%	96
7.5	20/20	0.7	-0.8	1.4	0.057	1.4	-17%	98
	40/40	1.0	-1.2	1.5	0.056	1.5	-22%	96
	60/60	1.3	-1.5	1.5	0.051	1.5	-26%	98
	80/80	0.8	-1.0	1.5	0.045	1.5	-20%	98
10.0	20/20	1.4	-1.5	2.2	0.054	2.2	-19%	98
	40/40	1.8	-1.7	2.2	0.051	2.2	-18%	98
	60/60	2.1	-2.1	2.4	0.050	2.4	-23%	98
	80/80	1.5	-1.7	2.4	0.044	2.4	-19%	97
12.5	20/20	0.2	-0.3	2.6	0.048	2.6	-4%	98
	40/40	3.1	-3.5	3.6	0.049	3.6	-27%	97
	60/60	1.8	-1.8	3.3	0.046	3.3	-14%	98
	80/80	0.8	-0.7	3.0	0.040	3.0	-5%	97
15.0	20/20	1.3	-1.3	3.6	0.044	3.6	-9%	98
	40/40	3.0	-3.1	4.0	0.043	4.0	-20%	99
	60/60	0.7	-0.7	3.5	0.040	3.5	-4%	97
	80/80	2.5	-2.7	4.0	0.036	4.0	-18%	98
17.5	20/20	1.9	-1.9	4.3	0.039	4.3	-11%	98
	40/40	2.9	-2.9	4.8	0.040	4.8	-15%	99
	60/60	3.9	-4.4	5.6	0.040	5.6	-22%	98
	80/80	4.6	-4.7	5.8	0.038	5.8	-20%	97
20.0	20/20	2.6	-3.0	5.3	0.038	5.3	-16%	98
	40/40	2.4	-2.4	6.0	0.040	6.0	-10%	97
	60/60	1.9	-1.9	5.8	0.037	5.8	-9%	98
	80/80	5.5	-5.3	6.8	0.036	6.8	-19%	97

Note. %VAF = Percentage of Variance Accounted For.

Appendix J: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Linear Creature Type

Table J.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	522	13.0	13.5	0.74	96	97
	40/40	458	17.4	18.7	0.76	97	98
	60/60	394	18.5	19.0	0.74	97	98
	80/80	357	19.1	19.7	0.72	98	99
7.5	20/20	498	17.6	18.0	0.77	97	98
	40/40	420	20.8	21.6	0.77	98	99
	60/60	318	17.6	17.7	0.76	99	99
	80/80	263	15.9	15.9	0.76	99	99
10.0	20/20	475	21.3	21.1	0.78	99	99
	40/40	363	20.6	21.3	0.78	99	99
	60/60	279	16.7	16.7	0.76	99	99
	80/80	225	13.5	13.8	0.74	99	99
12.5	20/20	461	24.7	25.3	0.80	99	100
	40/40	329	20.3	20.9	0.78	99	99
	60/60	249	16.0	16.0	0.76	99	99
	80/80	201	12.4	12.5	0.73	99	99
15.0	20/20	432	25.4	25.8	0.79	99	100
	40/40	293	18.2	18.4	0.77	99	100
	60/60	221	14.5	14.6	0.77	99	99
	80/80	182	11.3	11.2	0.72	99	100
17.5	20/20	408	26.4	26.9	0.79	99	100
	40/40	269	17.4	17.1	0.76	99	100
	60/60	204	12.8	12.9	0.74	99	99
	80/80	165	9.8	9.8	0.71	99	100
20.0	20/20	383	25.5	25.8	0.78	100	100
	40/40	251	16.4	16.5	0.75	99	100
	60/60	187	11.1	11.2	0.72	99	100
	80/80	154	9.1	9.1	0.70	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table J.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	521	13.2	0.74	96	97
	40/40	455	18.6	0.77	96	98
	60/60	394	18.8	0.74	97	98
	80/80	356	19.5	0.72	98	99
7.5	20/20	497	17.9	0.77	97	98
	40/40	419	21.4	0.77	98	99
	60/60	318	17.6	0.76	99	99
	80/80	263	15.9	0.76	99	99
10.0	20/20	475	21.2	0.78	99	99
	40/40	363	21.1	0.78	99	99
	60/60	279	16.7	0.76	99	99
	80/80	225	13.8	0.74	99	99
12.5	20/20	461	25.1	0.80	99	100
	40/40	329	20.7	0.78	99	99
	60/60	249	16.0	0.76	99	99
	80/80	201	12.4	0.73	99	99
15.0	20/20	432	25.6	0.79	99	100
	40/40	293	18.3	0.77	99	100
	60/60	221	14.6	0.77	99	99
	80/80	182	11.2	0.72	99	100
17.5	20/20	408	26.7	0.79	99	100
	40/40	269	17.3	0.76	99	100
	60/60	204	12.8	0.74	99	99
	80/80	165	9.8	0.71	99	100
20.0	20/20	353	21.7	0.78	99	100
	40/40	249	16.2	0.75	99	100
	60/60	185	11.0	0.72	99	100
	80/80	149	8.2	0.70	99	100

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table J.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	520	13.2	0.74	96	97
	40/40	468	18.0		96	98
	60/60	392	18.8		97	98
	80/80	346	19.7		98	99
7.5	20/20	501	17.7	0.76	97	98
	40/40	422	21.3		98	99
	60/60	316	17.7		99	99
	80/80	261	16.0		99	99
10.0	20/20	485	20.8	0.76	99	99
	40/40	373	20.8		99	99
	60/60	276	16.8		99	99
	80/80	219	13.9		99	99
12.5	20/20	484	24.6	0.77	99	99
	40/40	337	20.5		99	99
	60/60	247	16.0		99	99
	80/80	193	12.7		99	99
15.0	20/20	454	25.2	0.76	99	99
	40/40	296	18.2		99	100
	60/60	223	14.5		99	99
	80/80	174	11.4		99	99
17.5	20/20	445	26.4	0.75	99	99
	40/40	275	17.2		99	99
	60/60	202	12.9		99	99
	80/80	159	10.0		99	99
20.0	20/20	419	25.6	0.73	99	99
	40/40	258	16.4		99	100
	60/60	183	11.2		99	100
	80/80	149	9.2		99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table J.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	453	22.6	0.74	55	97
	40/40		19.3		92	97
	60/60		22.8		96	98
	80/80		24.4		82	98
7.5	20/20	402	24.6	0.75	57	98
	40/40		21.8		95	99
	60/60		25.5		97	99
	80/80		28.1		82	98
10.0	20/20	348	24.8	0.76	62	99
	40/40		21.9		93	99
	60/60		25.3		98	99
	80/80		27.3		83	98
12.5	20/20	328	25.9	0.76	62	99
	40/40		22.8		95	99
	60/60		26.4		98	99
	80/80		28.7		83	98
15.0	20/20	292	23.3	0.75	62	99
	40/40		21.1		94	99
	60/60		23.6		98	99
	80/80		26.1		82	98
17.5	20/20	262	21.0	0.74	62	99
	40/40		19.5		93	99
	60/60		21.2		98	99
	80/80		22.9		82	98
20.0	20/20	240	18.9	0.73	61	99
	40/40		17.2		93	99
	60/60		18.9		98	100
	80/80		20.5		83	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table J.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	434	21.3	0.75	55	97
	40/40				88	98
	60/60				96	98
	80/80				79	99
7.5	20/20	380	23.2	0.76	55	98
	40/40				91	99
	60/60				97	99
	80/80				79	99
10.0	20/20	329	23.0	0.76	60	99
	40/40				90	99
	60/60				98	99
	80/80				81	99
12.5	20/20	310	24.2	0.76	60	99
	40/40				91	99
	60/60				98	99
	80/80				81	99
15.0	20/20	276	21.9	0.76	60	99
	40/40				92	100
	60/60				98	99
	80/80				81	99
17.5	20/20	250	19.8	0.75	60	99
	40/40				91	99
	60/60				98	99
	80/80				81	99
20.0	20/20	230	17.8	0.73	59	99
	40/40				91	100
	60/60				98	100
	80/80				81	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table J.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF	
				QLOE	ML
5.0	20/20	425	18.8	92	87
	40/40	371	25.8	93	89
	60/60	303	25.4	93	87
	80/80	262	25.0	94	84
7.5	20/20	414	25.3	94	91
	40/40	329	27.8	97	90
	60/60	252	23.2	96	90
	80/80	209	20.5	96	89
10.0	20/20	383	27.9	97	92
	40/40	289	26.6	97	91
	60/60	219	21.3	97	89
	80/80	176	17.3	95	87
12.5	20/20	370	31.9	98	93
	40/40	262	26.1	97	92
	60/60	196	19.8	97	89
	80/80	157	15.7	95	86
15.0	20/20	341	32.0	98	93
	40/40	228	22.4	97	90
	60/60	177	18.1	97	90
	80/80	142	14.1	95	85
17.5	20/20	318	32.3	98	93
	40/40	210	21.4	97	90
	60/60	159	15.8	96	87
	80/80	130	12.3	94	82
20.0	20/20	291	30.8	98	92
	40/40	193	19.8	97	88
	60/60	146	14.0	94	84
	80/80	121	11.3	93	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table J.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	358	10.6	89	87
	40/40		23.4	93	89
	60/60		37.9	91	87
	80/80		51.1	90	84
7.5	20/20	321	11.9	90	91
	40/40		26.2	97	90
	60/60		41.8	93	90
	80/80		55.6	90	89
10.0	20/20	276	10.5	91	92
	40/40		23.4	97	91
	60/60		37.9	94	89
	80/80		50.5	88	87
12.5	20/20	254	10.7	91	93
	40/40		23.9	97	92
	60/60		38.0	94	89
	80/80		50.0	87	86
15.0	20/20	225	9.5	89	93
	40/40		21.5	97	90
	60/60		33.4	94	90
	80/80		44.0	86	85
17.5	20/20	201	8.3	87	93
	40/40		18.8	97	90
	60/60		29.4	93	87
	80/80		38.5	84	82
20.0	20/20	183	7.5	86	92
	40/40		16.9	96	88
	60/60		26.2	91	84
	80/80		34.4	83	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table J.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	330	28	52	87
	40/40			86	89
	60/60			91	87
	80/80			75	84
7.5	20/20	287	29	51	91
	40/40			90	90
	60/60			94	90
	80/80			77	89
10.0	20/20	246	28	58	92
	40/40			88	91
	60/60			96	89
	80/80			77	87
12.5	20/20	228	28	58	93
	40/40			89	92
	60/60			96	89
	80/80			77	86
15.0	20/20	203	25	57	93
	40/40			90	90
	60/60			96	90
	80/80			77	85
17.5	20/20	183	23	58	93
	40/40			88	90
	60/60			95	87
	80/80			75	82
20.0	20/20	167	21	57	92
	40/40			88	88
	60/60			93	84
	80/80			75	81

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table J.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	763	143	4	403	5*
3	Constant a, $c_1 = c_2$	9	457	142	7	406	3*
4	Constant a & c	6	35023	990	10	409	35*
5	Constant a, c & k	3	29025	1048	13	412	28*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	8602	303	8	407	28*
7	Constant k, $a = 1$, $c_1 = c_2$	5	8912	372	11	410	24*
8	Constant k & c, $a = 1$,	2	30767	1175	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table J.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	190	73	4	403	3*
3	Constant a, $c_1 = c_2$	9	98	72	7	406	1
4	Constant a & c	6	28657	771	10	409	37*
5	Constant a, c & k	3	24412	840	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	4362	156	8	407	28*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6961	257	11	410	27*
8	Constant k & c, $a = 1$,	2	25681	940	14	413	27*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table J.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	79	36	4	403	2
3	Constant a, $c_1 = c_2$	9	53	36	7	406	1
4	Constant a & c	6	25700	663	10	409	39*
5	Constant a, c & k	3	21348	708	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2985	94	8	407	32*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6424	207	11	410	31*
8	Constant k & c, $a = 1$,	2	21744	772	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table J.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	104	19	4	403	5*
3	Constant a, $c_1 = c_2$	9	94	20	7	406	5*
4	Constant a & c	6	23118	583	10	409	40*
5	Constant a, c & k	3	19252	625	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2324	64	8	407	36*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6456	191	11	410	34*
8	Constant k & c, $a = 1$,	2	19590	682	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table J.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	20	13	4	403	2
3	Constant a, $c_1 = c_2$	9	39	13	7	406	3*
4	Constant a & c	6	18065	454	10	409	40*
5	Constant a, c & k	3	15068	488	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2033	52	8	407	39*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5821	169	11	410	35*
8	Constant k & c, $a = 1$,	2	15492	537	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table J.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	37	11	4	403	4*
3	Constant a, $c_1 = c_2$	9	87	12	7	406	8*
4	Constant a & c	6	15837	397	10	409	40*
5	Constant a, c & k	3	12923	418	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1817	46	8	407	40*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5623	161	11	410	35*
8	Constant k & c, $a = 1$,	2	13254	459	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table J.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	108	8	4	403	13*
3	Constant a, $c_1 = c_2$	9	73	8	7	406	9*
4	Constant a & c	6	12510	313	10	409	40*
5	Constant a, c & k	3	10208	329	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1738	41	8	407	42*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4826	136	11	410	35*
8	Constant k & c, $a = 1$,	2	10587	366	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table J.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2061	1793	1501	1231	1074	985	832
2	$c_1 = c_2$	12	2075	1795	1502	1245	1073	991	882
3	Constant a, $c_1 = c_2$	9	2070	1788	1498	1252	1082	1028	886
4	Constant a & c	6	2874	2770	2708	2654	2550	2495	2395
5	Constant a, c & k	3	2895	2803	2732	2680	2577	2512	2413
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2384	2108	1895	1736	1654	1598	1553
7	Constant k, $a = 1$, $c_1 = c_2$	5	2466	2312	2222	2190	2137	2118	2049
8	Constant k & c, $a = 1$	2	2942	2849	2767	2715	2616	2551	2456

Table J.17. Akaike Information Criteria (AIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1026	-1138	-1207	-1261	-1335	-1380	-1470
2	$c_1 = c_2$	8	-1025	-1142	-1213	-1268	-1340	-1385	-1474
3, 4, 5	Constant a & c	2	-1034	-1151	-1211	-1245	-1309	-1321	-1397
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-672	-691	-705	-711	-727	-737	-750

Table J.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2125	1857	1566	1295	1139	1049	896
2	$c_1 = c_2$	12	2124	1844	1551	1294	1121	1040	931
3	Constant a, $c_1 = c_2$	9	2107	1825	1534	1288	1118	1065	922
4	Constant a & c	6	2898	2794	2732	2679	2574	2519	2419
5	Constant a, c & k	3	2907	2815	2744	2693	2589	2525	2425
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2416	2140	1927	1769	1687	1630	1585
7	Constant k, $a = 1$, $c_1 = c_2$	5	2487	2332	2243	2210	2157	2138	2069
8	Constant k & c, $a = 1$	2	2950	2857	2775	2723	2624	2559	2464

Table J.19. Bayes Information Criteria (BIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-986	-1097	-1167	-1221	-1295	-1340	-1430
2	$c_1 = c_2$	8	-998	-1116	-1187	-1242	-1313	-1358	-1448
3, 4, 5	Constant a & c	2	-1027	-1145	-1204	-1238	-1302	-1315	-1390
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-672	-691	-705	-711	-727	-737	-750

Table J.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	-0.1	0.1	0.0	0.0	0.0	1
	40/40	0.0	0.0	0.1	0.1	0.0	1
	60/60	0.0	0.0	0.1	0.1	0.0	0
	80/80	0.0	0.0	0.1	0.1	0.0	0
7.5	20/20	-0.1	0.1	0.1	0.1	0.0	0
	40/40	-0.2	0.1	0.1	0.1	0.0	2
	60/60	-0.2	0.2	0.1	0.1	0.0	1
	80/80	-0.2	0.2	0.1	0.2	0.1	1
10.0	20/20	-0.4	0.4	0.1	0.2	0.1	2
	40/40	-0.4	0.4	0.1	0.2	0.1	2
	60/60	-0.5	0.5	0.2	0.3	0.1	2
	80/80	-0.4	0.3	0.2	0.3	0.1	1
12.5	20/20	-1.0	0.9	0.2	0.4	0.2	5
	40/40	-0.9	0.8	0.2	0.4	0.2	4
	60/60	-1.0	1.0	0.2	0.4	0.3	4
	80/80	-0.8	0.8	0.3	0.5	0.2	2
15.0	20/20	-1.3	1.3	0.2	0.5	0.3	5
	40/40	-1.8	1.7	0.2	0.6	0.4	6
	60/60	-1.5	1.5	0.3	0.6	0.4	4
	80/80	-1.2	1.3	0.4	0.7	0.3	2
17.5	20/20	-2.4	2.3	0.2	0.8	0.6	9
	40/40	-1.9	2.0	0.3	0.8	0.5	5
	60/60	-1.9	2.0	0.3	0.8	0.5	4
	80/80	-1.3	1.3	0.6	0.9	0.3	1
20.0	20/20	-2.8	2.8	0.3	1.0	0.7	7
	40/40	-2.7	2.6	0.4	1.0	0.6	6
	60/60	-1.9	1.8	0.6	1.0	0.4	2
	80/80	-2.0	1.9	0.7	1.2	0.5	2

Note. %VAF = Percentage of Variance Accounted For.

Table J.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	-0.1	0.0	0.6	0.052	0.6	-6%	98
	40/40	0.6	-0.5	0.8	0.055	0.8	-14%	97
	60/60	0.5	-0.4	0.7	0.050	0.7	-11%	96
	80/80	1.2	-1.2	1.0	0.045	1.0	-29%	97
7.5	20/20	-0.6	0.5	1.2	0.049	1.3	8%	98
	40/40	1.1	-1.2	1.6	0.049	1.6	-22%	98
	60/60	-0.1	0.0	1.3	0.043	1.3	-1%	97
	80/80	1.5	-1.4	1.9	0.047	1.9	-16%	97
10.0	20/20	1.3	-1.2	2.1	0.043	2.1	-14%	98
	40/40	1.2	-1.1	2.2	0.044	2.2	-12%	98
	60/60	1.9	-1.8	2.6	0.045	2.6	-16%	97
	80/80	1.6	-1.4	2.5	0.039	2.5	-13%	97
12.5	20/20	2.5	-2.4	3.4	0.043	3.4	-17%	98
	40/40	2.1	-2.0	3.3	0.042	3.3	-14%	98
	60/60	2.2	-2.1	3.3	0.039	3.3	-14%	98
	80/80	2.0	-1.8	3.5	0.037	3.5	-11%	97
15.0	20/20	3.5	-3.5	4.4	0.039	4.4	-20%	99
	40/40	3.3	-3.7	4.9	0.040	4.9	-21%	98
	60/60	2.5	-2.6	4.6	0.038	4.6	-15%	98
	80/80	2.7	-2.7	5.1	0.038	5.1	-13%	96
17.5	20/20	2.9	-2.5	5.1	0.038	5.1	-11%	98
	40/40	2.5	-2.9	5.4	0.036	5.4	-16%	97
	60/60	3.1	-2.9	5.3	0.035	5.3	-13%	98
	80/80	2.8	-2.6	5.4	0.032	5.4	-12%	97
20.0	20/20	2.7	-2.5	6.1	0.036	6.1	-9%	97
	40/40	3.0	-2.9	6.3	0.035	6.3	-12%	97
	60/60	3.8	-3.8	6.5	0.033	6.5	-15%	98
	80/80	3.1	-3.2	7.1	0.032	7.1	-12%	96

Note. %VAF = Percentage of Variance Accounted For.

Appendix K: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Exponential Creature Type

Table K.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	544	13.3	13.7	0.74	99	99
	40/40	510	18.8	19.5	0.74	99	99
	60/60	461	21.4	22.1	0.72	99	99
	80/80	419	23.2	23.6	0.72	99	99
7.5	20/20	538	18.0	18.4	0.75	100	100
	40/40	459	21.5	21.9	0.75	99	99
	60/60	394	22.5	22.3	0.73	99	99
	80/80	324	19.0	19.1	0.71	99	99
10.0	20/20	521	22.2	22.4	0.76	99	100
	40/40	427	23.4	23.5	0.74	99	99
	60/60	331	19.7	19.5	0.73	99	99
	80/80	273	16.8	16.7	0.70	99	99
12.5	20/20	509	24.8	24.9	0.76	100	100
	40/40	378	21.9	22.0	0.74	99	100
	60/60	291	18.6	18.5	0.73	99	99
	80/80	233	14.3	14.4	0.70	99	99
15.0	20/20	477	26.4	26.4	0.77	100	100
	40/40	343	20.7	20.7	0.73	99	100
	60/60	260	16.0	15.9	0.70	99	99
	80/80	209	12.9	12.9	0.68	99	99
17.5	20/20	459	26.8	26.8	0.75	100	100
	40/40	319	20.2	20.2	0.72	99	99
	60/60	236	14.7	14.6	0.70	99	99
	80/80	190	11.6	11.6	0.67	99	100
20.0	20/20	434	27.0	26.9	0.75	100	100
	40/40	290	18.4	18.3	0.72	99	100
	60/60	219	13.5	13.5	0.68	99	99
	80/80	174	10.4	10.4	0.66	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table K.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	544	13.5	0.74	99	99
	40/40	509	19.3	0.74	99	99
	60/60	460	21.8	0.73	99	99
	80/80	418	23.4	0.72	99	99
7.5	20/20	538	18.2	0.75	100	100
	40/40	459	21.7	0.75	99	99
	60/60	394	22.4	0.73	99	99
	80/80	324	19.1	0.71	99	99
10.0	20/20	522	22.3	0.76	99	100
	40/40	427	23.5	0.74	99	99
	60/60	331	19.7	0.73	99	99
	80/80	273	16.7	0.70	99	99
12.5	20/20	509	24.8	0.76	100	100
	40/40	378	21.9	0.74	99	100
	60/60	291	18.5	0.73	99	99
	80/80	233	14.3	0.70	99	99
15.0	20/20	477	26.4	0.77	100	100
	40/40	343	20.7	0.73	99	100
	60/60	260	15.9	0.70	99	99
	80/80	209	12.9	0.68	99	99
17.5	20/20	459	26.8	0.75	100	100
	40/40	319	20.2	0.72	99	99
	60/60	236	14.7	0.70	99	99
	80/80	190	11.6	0.67	99	100
20.0	20/20	434	27.0	0.75	100	100
	40/40	290	18.4	0.72	99	100
	60/60	219	13.5	0.68	99	99
	80/80	174	10.4	0.66	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table K.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	549	13.4	0.73	99	99
	40/40	514	19.2		98	99
	60/60	457	21.8		99	99
	80/80	411	23.4		99	99
7.5	20/20	549	18.0	0.73	100	100
	40/40	469	21.6		99	99
	60/60	393	22.4		99	99
	80/80	311	19.1		99	99
10.0	20/20	548	21.9	0.73	99	99
	40/40	437	23.4		99	99
	60/60	328	19.7		99	99
	80/80	260	16.7		99	99
12.5	20/20	534	24.7	0.73	100	100
	40/40	386	21.9		99	100
	60/60	292	18.5		99	99
	80/80	221	14.4		99	99
15.0	20/20	524	26.3	0.72	100	99
	40/40	352	20.7		99	100
	60/60	254	15.9		99	99
	80/80	199	12.9		99	99
17.5	20/20	503	27.0	0.71	99	99
	40/40	330	20.3		99	99
	60/60	232	14.6		99	99
	80/80	180	11.6		99	99
20.0	20/20	486	27.5	0.70	99	99
	40/40	300	18.4		99	100
	60/60	214	13.5		99	99
	80/80	166	10.4		99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table K.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF	
					QLOE	ML
5.0	20/20	515	24.6	0.73	68	99
	40/40		22.2		95	99
	60/60		24.9		98	99
	80/80		27.2		85	98
7.5	20/20	477	29.1	0.73	64	100
	40/40		26.2		94	99
	60/60		30.0		98	99
	80/80		32.6		82	98
10.0	20/20	437	30.3	0.73	61	99
	40/40		27.5		94	99
	60/60		31.2		98	99
	80/80		34.0		81	98
12.5	20/20	396	30.1	0.72	59	100
	40/40		27.3		93	99
	60/60		30.7		98	99
	80/80		33.1		80	98
15.0	20/20	351	27.2	0.71	57	99
	40/40		24.8		92	99
	60/60		27.7		97	99
	80/80		29.9		79	98
17.5	20/20	323	25.5	0.70	55	99
	40/40		23.5		91	99
	60/60		25.8		97	99
	80/80		27.9		79	98
20.0	20/20	291	23.1	0.69	52	99
	40/40		21.3		90	99
	60/60		23.2		97	99
	80/80		24.9		78	98

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table K.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	496	23.5	0.73	67	99
	40/40				93	99
	60/60				98	99
	80/80				82	99
7.5	20/20	449	27.3	0.74	62	100
	40/40				91	99
	60/60				98	99
	80/80				80	99
10.0	20/20	407	28.2	0.73	58	99
	40/40				90	99
	60/60				98	99
	80/80				79	99
12.5	20/20	369	27.8	0.73	57	100
	40/40				90	100
	60/60				98	99
	80/80				78	99
15.0	20/20	327	25.0	0.72	55	99
	40/40				88	100
	60/60				98	99
	80/80				78	99
17.5	20/20	301	23.5	0.71	52	99
	40/40				88	99
	60/60				98	99
	80/80				77	99
20.0	20/20	274	21.4	0.70	50	99
	40/40				87	100
	60/60				98	99
	80/80				76	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table K.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	443	19.2	96	87
	40/40	389	26.0	95	86
	60/60	335	28.2	96	85
	80/80	289	28.2	96	83
7.5	20/20	424	24.9	97	88
	40/40	345	27.9	97	88
	60/60	284	27.7	96	86
	80/80	229	23.4	94	83
10.0	20/20	407	29.3	97	90
	40/40	313	29.3	97	88
	60/60	241	24.5	95	85
	80/80	194	20.4	94	81
12.5	20/20	379	31.2	97	89
	40/40	277	27.0	96	87
	60/60	212	22.2	95	85
	80/80	168	17.4	93	80
15.0	20/20	357	32.7	97	90
	40/40	247	25.0	96	86
	60/60	186	19.2	94	81
	80/80	151	15.6	92	77
17.5	20/20	331	32.5	97	89
	40/40	228	24.0	95	85
	60/60	169	17.5	93	80
	80/80	138	14.2	90	75
20.0	20/20	307	31.7	97	88
	40/40	207	22.0	95	84
	60/60	156	16.2	92	77
	80/80	127	12.8	88	72

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table K.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	381	11.6	94	87
	40/40		24.5	95	86
	60/60		38.7	95	85
	80/80		53.1	93	83
7.5	20/20	337	12.3	93	88
	40/40		26.1	97	88
	60/60		41.7	94	86
	80/80		56.5	89	83
10.0	20/20	300	12.0	92	90
	40/40		26.2	96	88
	60/60		41.6	93	85
	80/80		55.6	86	81
12.5	20/20	267	11.3	90	89
	40/40		24.5	96	87
	60/60		39.1	93	85
	80/80		51.9	83	80
15.0	20/20	236	9.8	87	90
	40/40		21.9	96	86
	60/60		34.8	91	81
	80/80		46.1	81	77
17.5	20/20	214	9.1	85	89
	40/40		20.3	95	85
	60/60		32.0	90	80
	80/80		42.0	79	75
20.0	20/20	193	8.1	83	88
	40/40		18.2	94	84
	60/60		28.7	89	77
	80/80		37.5	76	72

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table K.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	356	30	64	87
	40/40			90	86
	60/60			95	85
	80/80			79	83
7.5	20/20	311	33	60	88
	40/40			89	88
	60/60			95	86
	80/80			75	83
10.0	20/20	274	32	56	90
	40/40			88	88
	60/60			95	85
	80/80			74	81
12.5	20/20	243	30	54	89
	40/40			86	87
	60/60			95	85
	80/80			72	80
15.0	20/20	214	27	52	90
	40/40			85	86
	60/60			93	81
	80/80			70	77
17.5	20/20	195	25	49	89
	40/40			84	85
	60/60			92	80
	80/80			68	75
20.0	20/20	178	23	46	88
	40/40			82	84
	60/60			90	77
	80/80			65	72

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table K.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	348	55	4	403	6*
3	Constant a, $c_1 = c_2$	9	185	54	7	406	3*
4	Constant a & c	6	33979	881	10	409	39*
5	Constant a, c & k	3	28183	939	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	8353	215	8	407	39*
7	Constant k, $a = 1$, $c_1 = c_2$	5	8601	281	11	410	31*
8	Constant k & c, $a = 1$,	2	30722	1091	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table K.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	108	23	4	403	5*
3	Constant a, $c_1 = c_2$	9	98	23	7	406	4*
4	Constant a & c	6	31729	797	10	409	40*
5	Constant a, c & k	3	26846	868	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	5560	131	8	407	42*
7	Constant k, $a = 1$, $c_1 = c_2$	5	7725	229	11	410	34*
8	Constant k & c, $a = 1$,	2	28025	971	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table K.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	31	21	4	403	1
3	Constant a, $c_1 = c_2$	9	89	22	7	406	4*
4	Constant a & c	6	27769	699	10	409	40*
5	Constant a, c & k	3	23552	763	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	4109	101	8	407	41*
7	Constant k, $a = 1$, $c_1 = c_2$	5	7353	218	11	410	34*
8	Constant k & c, $a = 1$,	2	24495	850	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table K.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	6	14	4	403	0
3	Constant a, $c_1 = c_2$	9	55	14	7	406	4*
4	Constant a & c	6	23211	581	10	409	40*
5	Constant a, c & k	3	19387	625	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3472	82	8	407	43*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6819	196	11	410	35*
8	Constant k & c, $a = 1$,	2	20366	704	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table K.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	3	10	4	403	0
3	Constant a, $c_1 = c_2$	9	95	11	7	406	8*
4	Constant a & c	6	20197	503	10	409	40*
5	Constant a, c & k	3	16877	542	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3042	69	8	407	44*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6763	191	11	410	35*
8	Constant k & c, $a = 1$,	2	17679	609	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table K.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	1	8	4	403	0
3	Constant a, $c_1 = c_2$	9	75	9	7	406	8*
4	Constant a & c	6	16330	407	10	409	40*
5	Constant a, c & k	3	13561	436	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2717	61	8	407	44*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5919	166	11	410	36*
8	Constant k & c, $a = 1$,	2	14400	496	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table K.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	2	7	4	403	0
3	Constant a, $c_1 = c_2$	9	88	8	7	406	10*
4	Constant a & c	6	13854	346	10	409	40*
5	Constant a, c & k	3	11340	365	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2448	55	8	407	44*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5355	151	11	410	36*
8	Constant k & c, $a = 1$,	2	12074	416	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table K.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	1657	1301	1277	1100	964	873	828
2	$c_1 = c_2$	12	1676	1313	1275	1094	958	865	821
3	Constant a, $c_1 = c_2$	9	1668	1319	1294	1115	1016	923	896
4	Constant a & c	6	2826	2784	2730	2653	2593	2505	2437
5	Constant a, c & k	3	2850	2817	2763	2680	2621	2530	2456
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2241	2035	1927	1838	1771	1718	1674
7	Constant k, $a = 1$, $c_1 = c_2$	5	2350	2264	2243	2200	2189	2132	2090
8	Constant k & c, $a = 1$	2	2911	2863	2807	2728	2668	2583	2510

Table K.17. Akaike Information Criteria (AIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1216	-1334	-1341	-1400	-1458	-1490	-1524
2	$c_1 = c_2$	8	-1216	-1336	-1349	-1407	-1466	-1498	-1532
3, 4, 5	Constant a & c	2	-1223	-1333	-1326	-1385	-1385	-1430	-1447
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-670	-693	-710	-726	-740	-752	-765

Table K.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	1721	1366	1342	1165	1029	938	893
2	$c_1 = c_2$	12	1724	1362	1324	1143	1006	914	870
3	Constant a, $c_1 = c_2$	9	1704	1355	1330	1151	1052	959	933
4	Constant a & c	6	2850	2809	2754	2677	2617	2529	2461
5	Constant a, c & k	3	2862	2829	2775	2692	2633	2542	2468
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2273	2067	1960	1870	1803	1750	1707
7	Constant k, $a = 1$, $c_1 = c_2$	5	2370	2284	2263	2220	2209	2152	2110
8	Constant k & c, $a = 1$	2	2919	2871	2815	2736	2676	2591	2518

Table K.19. Bayes Information Criteria (BIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-1176	-1294	-1301	-1360	-1418	-1450	-1484
2	$c_1 = c_2$	8	-1189	-1309	-1322	-1380	-1439	-1471	-1505
3, 4, 5	Constant a & c	2	-1217	-1327	-1319	-1378	-1378	-1423	-1440
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-670	-693	-710	-726	-740	-752	-765

Table K.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	-0.2	0.2	0.1	0.1	0.1	2
	40/40	-0.1	0.1	0.1	0.1	0.0	1
	60/60	-0.3	0.3	0.1	0.2	0.1	1
	80/80	-0.5	0.4	0.1	0.2	0.1	3
7.5	20/20	-0.7	0.7	0.1	0.3	0.2	3
	40/40	-0.8	0.8	0.1	0.3	0.2	4
	60/60	-0.6	0.6	0.2	0.4	0.2	2
	80/80	-0.6	0.6	0.3	0.4	0.1	1
10.0	20/20	-1.3	1.3	0.2	0.5	0.3	5
	40/40	-1.2	1.2	0.3	0.5	0.3	4
	60/60	-1.1	1.2	0.3	0.6	0.3	3
	80/80	-1.0	1.1	0.4	0.7	0.3	2
12.5	20/20	-1.8	1.8	0.3	0.8	0.4	5
	40/40	-1.8	1.8	0.3	0.8	0.4	4
	60/60	-2.2	2.3	0.3	0.9	0.6	5
	80/80	-1.5	1.5	0.6	1.0	0.4	2
15.0	20/20	-3.0	3.0	0.3	1.1	0.7	8
	40/40	-2.8	2.8	0.4	1.1	0.7	5
	60/60	-2.4	2.5	0.6	1.2	0.6	3
	80/80	-2.1	2.1	0.8	1.3	0.5	2
17.5	20/20	-3.7	3.7	0.4	1.4	0.9	7
	40/40	-3.2	3.3	0.5	1.4	0.9	5
	60/60	-3.6	3.6	0.6	1.5	0.9	4
	80/80	-2.1	2.2	1.1	1.6	0.6	1
20.0	20/20	-4.3	4.3	0.6	1.7	1.1	6
	40/40	-3.5	3.6	0.8	1.7	0.9	3
	60/60	-3.6	3.6	0.9	1.8	0.9	3
	80/80	-2.1	1.9	1.5	2.0	0.4	1

Note. %VAF = Percentage of Variance Accounted For.

Table K.21. Quadratic-exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	0.5	-0.6	1.2	0.039	1.2	-14%	95
	40/40	0.7	-0.7	1.0	0.032	1.0	-18%	96
	60/60	1.0	-0.9	1.2	0.035	1.2	-18%	96
	80/80	0.5	-0.5	1.3	0.033	1.3	-11%	94
7.5	20/20	0.6	-0.6	1.8	0.031	1.8	-9%	97
	40/40	0.8	-0.9	1.9	0.032	1.9	-13%	97
	60/60	0.5	-0.5	1.8	0.028	1.8	-8%	97
	80/80	0.5	-0.5	2.0	0.027	2.0	-6%	96
10.0	20/20	0.6	-0.7	3.0	0.032	3.0	-6%	97
	40/40	1.2	-1.0	2.6	0.028	2.6	-7%	96
	60/60	0.9	-0.6	2.8	0.028	2.8	-4%	97
	80/80	0.5	-0.6	3.0	0.026	3.0	-5%	96
12.5	20/20	3.0	-2.8	4.2	0.029	4.2	-16%	96
	40/40	2.7	-2.4	4.1	0.029	4.1	-13%	96
	60/60	1.5	-1.3	4.0	0.027	4.0	-7%	96
	80/80	2.3	-2.3	4.5	0.025	4.5	-13%	95
15.0	20/20	2.1	-2.0	4.9	0.026	4.9	-10%	97
	40/40	1.1	-1.0	5.0	0.027	5.0	-4%	96
	60/60	1.6	-1.8	5.3	0.026	5.3	-9%	95
	80/80	1.5	-1.3	5.2	0.024	5.2	-5%	95
17.5	20/20	1.1	-1.1	5.8	0.025	5.8	-4%	96
	40/40	3.5	-3.3	6.1	0.024	6.1	-12%	96
	60/60	2.4	-2.4	6.4	0.025	6.4	-9%	96
	80/80	1.9	-1.8	6.5	0.023	6.5	-6%	95
20.0	20/20	3.5	-3.7	7.6	0.026	7.6	-13%	95
	40/40	3.4	-3.3	7.3	0.024	7.3	-11%	96
	60/60	1.6	-1.3	7.1	0.024	7.1	-4%	95
	80/80	3.6	-3.7	7.8	0.022	7.8	-12%	95

Note. %VAF = Percentage of Variance Accounted For.

Appendix L: Experiment 1 Fitting Measures of the Linear-Clone-Pheno-Gaussian Creature Type

Table L.1. Model 1 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c_1	c_2	a	%VAF QLOE	%VAF ML
5.0	20/20	504	10.0	11.0	0.72	93	95
	40/40	497	15.3	16.6	0.68	94	95
	60/60	410	16.0	17.5	0.71	96	97
	80/80	360	17.3	17.9	0.73	96	97
7.5	20/20	486	13.9	14.3	0.74	96	97
	40/40	394	14.3	14.9	0.72	94	97
	60/60	332	15.0	15.6	0.73	97	98
	80/80	281	15.0	15.1	0.75	98	99
10.0	20/20	458	15.2	15.8	0.74	96	98
	40/40	349	15.2	15.9	0.76	97	98
	60/60	278	13.9	14.5	0.76	98	99
	80/80	244	13.1	13.4	0.74	98	99
12.5	20/20	426	16.8	17.6	0.77	97	98
	40/40	321	14.9	15.5	0.76	99	99
	60/60	261	14.4	14.7	0.76	98	99
	80/80	223	12.8	12.8	0.74	99	99
15.0	20/20	411	18.5	18.6	0.77	99	99
	40/40	296	15.4	15.9	0.78	99	99
	60/60	237	12.9	13.1	0.75	99	99
	80/80	201	11.3	11.4	0.73	99	99
17.5	20/20	397	19.6	20.6	0.78	99	100
	40/40	278	15.0	15.3	0.77	99	99
	60/60	221	12.4	12.5	0.75	99	99
	80/80	189	11.2	11.3	0.74	99	99
20.0	20/20	384	21.2	21.6	0.78	99	100
	40/40	263	14.8	15.0	0.77	99	99
	60/60	208	12.5	12.6	0.76	99	99
	80/80	174	10.5	10.6	0.75	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table L.2. Model 2 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	500	10.9	0.73	92	95
	40/40	489	16.2	0.70	94	94
	60/60	404	17.1	0.72	95	97
	80/80	359	17.7	0.73	96	97
7.5	20/20	486	14.2	0.75	96	97
	40/40	393	14.6	0.72	94	97
	60/60	331	15.4	0.73	97	98
	80/80	281	15.1	0.75	98	99
10.0	20/20	456	15.6	0.75	96	97
	40/40	348	15.6	0.76	97	98
	60/60	278	14.4	0.77	98	99
	80/80	244	13.3	0.74	98	99
12.5	20/20	425	17.4	0.77	97	98
	40/40	320	15.3	0.76	99	99
	60/60	261	14.6	0.76	98	99
	80/80	223	12.8	0.74	99	99
15.0	20/20	411	18.5	0.77	99	99
	40/40	296	15.7	0.78	99	99
	60/60	237	13.0	0.75	99	99
	80/80	201	11.3	0.73	99	99
17.5	20/20	396	20.3	0.78	99	99
	40/40	278	15.1	0.77	99	99
	60/60	221	12.4	0.75	99	99
	80/80	189	11.2	0.74	99	99
20.0	20/20	384	21.4	0.78	99	100
	40/40	263	14.9	0.77	99	99
	60/60	208	12.6	0.76	99	99
	80/80	174	10.6	0.75	99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table L.3. Model 3 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	504	10.7	0.72	92	95
	40/40	474	16.4		94	94
	60/60	406	17.0		95	97
	80/80	365	17.6		96	97
7.5	20/20	490	14.1	0.74	96	97
	40/40	387	14.9		94	97
	60/60	330	15.5		97	98
	80/80	285	14.9		98	99
10.0	20/20	453	15.7	0.75	96	97
	40/40	351	15.5		97	98
	60/60	283	14.2		98	99
	80/80	241	13.4		98	99
12.5	20/20	432	17.1	0.76	97	98
	40/40	320	15.3		99	99
	60/60	263	14.5		98	99
	80/80	218	13.0		99	99
15.0	20/20	419	18.3	0.75	99	99
	40/40	304	15.4		99	99
	60/60	235	13.0		99	99
	80/80	195	11.5		99	99
17.5	20/20	409	20.0	0.76	99	99
	40/40	281	15.0		99	99
	60/60	219	12.5		99	99
	80/80	185	11.3		99	99
20.0	20/20	395	21.2	0.76	99	100
	40/40	264	14.9		99	99
	60/60	208	12.6		99	99
	80/80	171	10.7		99	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table L.4. Model 4 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	457	18.2	0.71	48	95
	40/40		16.1		92	95
	60/60		17.8		93	97
	80/80		19.8		81	96
7.5	20/20	383	18.1	0.73	59	97
	40/40		16.3		90	97
	60/60		18.3		95	98
	80/80		20.4		83	97
10.0	20/20	342	18.7	0.75	55	97
	40/40		16.6		94	98
	60/60		18.9		96	98
	80/80		20.8		82	98
12.5	20/20	316	18.8	0.75	59	98
	40/40		16.9		96	99
	60/60		19.2		97	99
	80/80		21.3		82	98
15.0	20/20	290	18.6	0.75	60	99
	40/40		16.7		94	99
	60/60		18.8		97	99
	80/80		20.6		83	98
17.5	20/20	275	18.6	0.75	64	99
	40/40		16.9		95	99
	60/60		19.0		98	99
	80/80		20.5		84	98
20.0	20/20	260	18.9	0.76	69	100
	40/40		17.4		95	99
	60/60		19.2		98	99
	80/80		20.8		85	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table L.5. Model 5 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	a	%VAF QLOE	%VAF ML
5.0	20/20	443	17.4	0.72	49	95
	40/40				88	94
	60/60				93	97
	80/80				77	97
7.5	20/20	370	17.2	0.73	58	97
	40/40				88	97
	60/60				95	98
	80/80				80	99
10.0	20/20	330	17.7	0.75	54	97
	40/40				91	98
	60/60				96	99
	80/80				79	99
12.5	20/20	303	17.8	0.76	57	98
	40/40				93	99
	60/60				97	99
	80/80				80	99
15.0	20/20	279	17.7	0.75	59	99
	40/40				92	99
	60/60				98	99
	80/80				81	99
17.5	20/20	264	17.7	0.76	63	99
	40/40				93	99
	60/60				98	99
	80/80				83	99
20.0	20/20	250	17.8	0.76	67	100
	40/40				93	99
	60/60				98	99
	80/80				84	99

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table L.6. Model 6 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	425	16.9	87	84
	40/40	365	22.4	87	76
	60/60	306	22.5	90	82
	80/80	273	23.2	93	83
7.5	20/20	400	20.5	93	87
	40/40	316	21.8	88	85
	60/60	260	20.8	93	85
	80/80	225	20.1	95	88
10.0	20/20	368	21.8	92	87
	40/40	284	21.1	94	89
	60/60	228	18.8	95	90
	80/80	194	17.4	95	87
12.5	20/20	353	24.1	94	91
	40/40	259	20.5	96	89
	60/60	211	18.7	96	89
	80/80	178	16.7	96	87
15.0	20/20	335	25.2	96	91
	40/40	244	20.6	97	91
	60/60	192	17.3	96	88
	80/80	160	14.8	95	86
17.5	20/20	319	26.3	97	91
	40/40	224	19.4	97	90
	60/60	178	16.0	96	88
	80/80	151	14.2	96	86
20.0	20/20	304	27.1	98	92
	40/40	212	19.1	97	90
	60/60	171	16.1	97	90
	80/80	143	13.6	96	88

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law

Table L.7. Model 7 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	359	9.4	83	84
	40/40		21.3	87	76
	60/60		33.9	89	82
	80/80		44.5	89	83
7.5	20/20	313	9.2	88	87
	40/40		21.2	88	85
	60/60		33.6	91	85
	80/80		44.7	90	88
10.0	20/20	283	9.4	86	87
	40/40		21.0	94	89
	60/60		33.2	93	90
	80/80		44.5	89	87
12.5	20/20	260	9.3	88	91
	40/40		20.8	96	89
	60/60		32.5	94	89
	80/80		43.5	89	87
15.0	20/20	240	9.0	89	91
	40/40		19.6	97	91
	60/60		31.1	93	88
	80/80		41.4	87	86
17.5	20/20	223	8.7	89	91
	40/40		18.9	97	90
	60/60		29.5	94	88
	80/80		39.0	89	86
20.0	20/20	210	8.6	90	92
	40/40		18.5	97	90
	60/60		28.4	95	90
	80/80		37.3	90	88

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table L.8. Model 8 Fit Parameter Values and Percentages of Variance Accounted For

Mutation Rate	Reinforcer Magnitude	k	c	%VAF QLOE	%VAF ML
5.0	20/20	332	23	44	84
	40/40			82	76
	60/60			88	82
	80/80			73	83
7.5	20/20	285	23	55	87
	40/40			82	85
	60/60			91	85
	80/80			77	88
10.0	20/20	256	23	49	87
	40/40			88	89
	60/60			94	90
	80/80			75	87
12.5	20/20	235	22	54	91
	40/40			90	89
	60/60			95	89
	80/80			77	87
15.0	20/20	217	22	56	91
	40/40			90	91
	60/60			95	88
	80/80			77	86
17.5	20/20	202	21	60	91
	40/40			91	90
	60/60			95	88
	80/80			79	86
20.0	20/20	194	22	65	92
	40/40			91	90
	60/60			96	90
	80/80			81	88

Note. %VAF = Percentage of Variance Accounted For, QLOE = Quantitative Law of Effect, and ML = Matching Law. The ML fit for this model is identical to Model 6.

Table L.9. Extra Sum of Squares Difference Tests at Mutation Rate 5.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	2786	230	4	403	12*
3	Constant a, $c_1 = c_2$	9	1587	228	7	406	7*
4	Constant a & c	6	31412	967	10	409	32*
5	Constant a, c & k	3	25459	1001	13	412	25*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	10728	411	8	407	26*
7	Constant k, $a = 1$, $c_1 = c_2$	5	10557	482	11	410	22*
8	Constant k & c, $a = 1$,	2	29078	1183	14	413	25*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table L.10. Extra Sum of Squares Difference Tests at Mutation Rate 7.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	326	126	4	403	3*
3	Constant a, $c_1 = c_2$	9	214	125	7	406	2
4	Constant a & c	6	26393	766	10	409	34*
5	Constant a, c & k	3	21523	799	13	412	27*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	6453	248	8	407	26*
7	Constant k, $a = 1$, $c_1 = c_2$	5	8266	342	11	410	24*
8	Constant k & c, $a = 1$,	2	23699	923	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table L.11. Extra Sum of Squares Difference Tests at Mutation Rate 10.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	390	84	4	403	5*
3	Constant a, $c_1 = c_2$	9	239	84	7	406	3*
4	Constant a & c	6	22236	623	10	409	36*
5	Constant a, c & k	3	18200	653	13	412	28*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	4781	173	8	407	28*
7	Constant k, $a = 1$, $c_1 = c_2$	5	6854	263	11	410	26*
8	Constant k & c, $a = 1$,	2	19715	747	14	413	26*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table L.12. Extra Sum of Squares Difference Tests at Mutation Rate 12.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	296	57	4	403	5*
3	Constant a, $c_1 = c_2$	9	155	56	7	406	3*
4	Constant a & c	6	19446	529	10	409	37*
5	Constant a, c & k	3	16227	565	13	412	29*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	3292	118	8	407	28*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5934	212	11	410	28*
8	Constant k & c, $a = 1$,	2	17205	636	14	413	27*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table L.13. Extra Sum of Squares Difference Tests at Mutation Rate 15.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	36	27	4	403	1
3	Constant a, $c_1 = c_2$	9	27	27	7	406	1
4	Constant a & c	6	17794	462	10	409	39*
5	Constant a, c & k	3	14715	491	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2671	79	8	407	34*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5439	172	11	410	32*
8	Constant k & c, $a = 1$,	2	15329	546	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table L.14. Extra Sum of Squares Difference Tests at Mutation Rate 17.5%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	186	19	4	403	10*
3	Constant a, $c_1 = c_2$	9	123	19	7	406	6*
4	Constant a & c	6	15564	397	10	409	39*
5	Constant a, c & k	3	12838	422	13	412	30*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	2217	61	8	407	37*
7	Constant k, $a = 1$, $c_1 = c_2$	5	5250	158	11	410	33*
8	Constant k & c, $a = 1$,	2	13425	472	14	413	28*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table L.15. Extra Sum of Squares Difference Tests at Mutation Rate 20.0%

Comparison Model	Assumptions	Parameters	Num	Den	df Num	df Den	F
Modern Quantitative Law of Effect							
2	$c_1 = c_2$	12	38	13	4	403	3*
3	Constant a, $c_1 = c_2$	9	35	13	7	406	3*
4	Constant a & c	6	13793	349	10	409	39*
5	Constant a, c & k	3	11316	369	13	412	31*
Classic Quantitative Law of Effect							
6	$a = 1$, $c_1 = c_2$	8	1883	49	8	407	38*
7	Constant k, $a = 1$, $c_1 = c_2$	5	4709	138	11	410	34*
8	Constant k & c, $a = 1$,	2	11603	405	14	413	29*

Note. N = 416; * $p < 0.05$ that model 1 is different from this model

Table L.16. Akaike Information Criteria (AIC) for Quantitative Law of Effect Fits

Model	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2227	2018	1843	1678	1390	1203	1060
2	$c_1 = c_2$	12	2272	2021	1855	1692	1387	1237	1065
3	Constant a, $c_1 = c_2$	9	2266	2017	1850	1684	1383	1237	1066
4	Constant a & c	6	2865	2768	2682	2613	2557	2495	2441
5	Constant a, c & k	3	2876	2782	2698	2638	2579	2517	2461
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2510	2300	2152	1992	1826	1714	1627
7	Constant k, $a = 1$, $c_1 = c_2$	5	2574	2431	2322	2233	2146	2109	2055
8	Constant k & c, $a = 1$	2	2944	2841	2753	2686	2623	2562	2499

Table L.17. Akaike Information Criteria (AIC) for Matching Law Fits

Model(s)	Assumptions	Parameters	Mutation Rate 5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-954	-1014	-1050	-1135	-1228	-1296	-1297
2	$c_1 = c_2$	8	-943	-1019	-1053	-1139	-1232	-1291	-1302
3, 4, 5	Constant a & c	2	-952	-1029	-1061	-1143	-1225	-1284	-1306
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-653	-670	-678	-689	-699	-705	-713

Table L.18. Bayes Information Criteria (BIC) for Quantitative Law of Effect Fits

			Mutation Rate						
Model	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	16	2291	2083	1908	1743	1454	1267	1124
2	$c_1 = c_2$	12	2321	2070	1903	1741	1435	1286	1113
3	Constant a, $c_1 = c_2$	9	2302	2053	1886	1721	1419	1273	1103
4	Constant a & c	6	2889	2792	2706	2638	2581	2519	2465
5	Constant a, c & k	3	2888	2794	2710	2650	2592	2529	2473
Classic Quantitative Law of Effect									
6	$a = 1$, $c_1 = c_2$	8	2543	2333	2184	2024	1858	1747	1659
7	Constant k, $a = 1$, $c_1 = c_2$	5	2594	2451	2342	2253	2167	2130	2075
8	Constant k & c, $a = 1$	2	2952	2849	2761	2694	2631	2570	2507

Table L.19. Bayes Information Criteria (BIC) for Matching Law Fits

			Mutation Rate						
Model(s)	Assumptions	Parameters	5.0	7.5	10.0	12.5	15.0	17.5	20.0
Modern Quantitative Law of Effect									
1	None	12	-914	-974	-1010	-1095	-1188	-1256	-1256
2	$c_1 = c_2$	8	-917	-992	-1026	-1113	-1205	-1264	-1276
3, 4, 5	Constant a & c	2	-946	-1022	-1054	-1137	-1218	-1278	-1299
Classic Quantitative Law of Effect									
6, 7, 8	$a = 1$, $c_1 = c_2$	0	-653	-670	-678	-689	-699	-705	-713

Table L.20. Quadratic Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	C_{Max}	C_{Δ}	%VAF
5.0	20/20	0.0	0.0	0.0	0.0	0.0	4
	40/40	0.0	-0.1	0.0	0.0	0.0	2
	60/60	0.1	-0.1	0.0	0.0	0.0	2
	80/80	0.0	0.0	0.0	0.1	0.0	0
7.5	20/20	0.0	0.0	0.0	0.0	0.0	1
	40/40	0.1	-0.1	0.1	0.0	0.0	2
	60/60	0.0	-0.1	0.1	0.0	0.0	1
	80/80	-0.1	0.1	0.1	0.1	0.0	0
10.0	20/20	0.1	-0.1	0.1	0.1	0.0	1
	40/40	0.0	0.0	0.1	0.1	0.0	1
	60/60	-0.2	0.1	0.1	0.1	0.0	2
	80/80	-0.1	0.1	0.1	0.1	0.0	0
12.5	20/20	-0.1	0.1	0.1	0.1	0.0	1
	40/40	-0.2	0.2	0.1	0.1	0.0	1
	60/60	-0.3	0.3	0.1	0.2	0.1	1
	80/80	-0.2	0.2	0.2	0.2	0.0	1
15.0	20/20	-0.2	0.2	0.1	0.2	0.1	1
	40/40	-0.4	0.3	0.1	0.2	0.1	2
	60/60	-0.3	0.3	0.2	0.2	0.1	1
	80/80	-0.3	0.3	0.2	0.3	0.1	1
17.5	20/20	-0.4	0.3	0.2	0.3	0.1	2
	40/40	-0.7	0.6	0.2	0.3	0.1	3
	60/60	-0.7	0.6	0.2	0.3	0.1	3
	80/80	-0.7	0.7	0.2	0.4	0.2	2
20.0	20/20	-1.3	1.3	0.1	0.4	0.3	7
	40/40	-1.0	1.0	0.2	0.4	0.2	3
	60/60	-1.0	1.0	0.2	0.5	0.2	3
	80/80	-0.9	0.8	0.4	0.5	0.2	2

Note. %VAF = Percentage of Variance Accounted For.

Table L.21. Quadratic-Exponential Fit to Changeover Behaviors

Mutation Rate	Reinforcer Magnitude	a	b	c	d	C_{Max}	$C_{\Delta\%}$	%VAF
5.0	20/20	1.2	-1.4	0.8	0.072	0.8	-55%	94
	40/40	0.6	-0.6	0.4	0.052	0.4	-42%	96
	60/60	0.5	-0.6	0.5	0.056	0.5	-34%	96
	80/80	0.4	-0.5	0.5	0.047	0.5	-30%	96
7.5	20/20	-0.2	0.1	0.6	0.054	0.6	0%	96
	40/40	0.3	-0.3	0.7	0.055	0.7	-12%	96
	60/60	0.6	-0.7	0.9	0.052	0.9	-22%	98
	80/80	0.0	0.0	0.8	0.048	0.8	-4%	96
10.0	20/20	0.5	-0.5	0.9	0.049	0.9	-12%	97
	40/40	0.6	-0.7	1.1	0.049	1.1	-18%	98
	60/60	0.6	-0.6	1.2	0.049	1.2	-10%	98
	80/80	0.5	-0.4	1.4	0.048	1.4	-5%	97
12.5	20/20	2.0	-1.7	2.1	0.058	2.1	-17%	98
	40/40	1.6	-1.8	2.2	0.054	2.2	-23%	98
	60/60	0.9	-0.8	2.0	0.050	2.0	-8%	97
	80/80	1.6	-1.7	2.4	0.047	2.4	-19%	97
15.0	20/20	0.7	-0.9	2.2	0.047	2.2	-12%	98
	40/40	2.1	-2.2	2.5	0.047	2.5	-22%	98
	60/60	1.7	-1.6	2.6	0.046	2.6	-14%	98
	80/80	1.3	-1.5	2.6	0.040	2.6	-17%	97
17.5	20/20	1.8	-2.3	3.2	0.046	3.2	-21%	98
	40/40	2.7	-3.0	3.5	0.046	3.5	-23%	99
	60/60	1.3	-1.6	3.0	0.042	3.0	-15%	98
	80/80	2.1	-1.9	3.2	0.039	3.2	-12%	98
20.0	20/20	1.3	-1.4	3.4	0.042	3.4	-12%	98
	40/40	1.9	-1.8	3.5	0.042	3.5	-12%	99
	60/60	2.2	-2.5	4.2	0.042	4.2	-17%	98
	80/80	1.4	-1.5	3.7	0.037	3.7	-10%	98

Note. %VAF = Percentage of Variance Accounted For.

Appendix M: Experiment 2 Bivariate Matching Fitting Measures

Table M.1. Bivariate Matching Fits to the Behavior of the Exponential-Bitwise-Bitflip Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5				
1.0				
2.5				
5.0	0.84	0.55	1.01	100
7.5	0.87	0.55	1.01	100
10.0	0.87	0.53	0.99	100
12.5	0.85	0.52	1.00	100
15.0	0.82	0.49	0.99	100
17.5	0.78	0.47	0.99	100
20.0	0.74	0.45	1.01	99
25.0	0.65	0.40	1.00	99
30.0	0.57	0.37	1.00	99
35.0	0.51	0.34	1.00	98
40.0	0.46	0.31	1.00	98
45.0	0.40	0.29	1.00	97
50.0	0.36	0.27	1.00	97

Note. %VAF = Percentage of Variance Accounted For. 0.5, 1.0, and 2.5% mutation rates were unable to be run using this algorithm.

Table M.2. Bivariate Matching Fits to the Behavior of the Exponential-Clone-Bitflip Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.57	0.31	0.95	97
1.0	0.67	0.27	0.98	100
2.5	0.76	0.35	0.98	100
5.0	0.80	0.39	1.00	100
7.5	0.80	0.43	0.99	100
10.0	0.79	0.44	0.98	100
12.5	0.75	0.44	1.01	100
15.0	0.72	0.43	1.00	100
17.5	0.69	0.41	1.00	99
20.0	0.65	0.40	1.00	99
25.0	0.57	0.37	1.00	99
30.0	0.51	0.34	1.00	99
35.0	0.45	0.31	1.01	98
40.0	0.41	0.29	1.00	98
45.0	0.37	0.26	1.01	98
50.0	0.34	0.25	1.00	98

Note. %VAF = Percentage of Variance Accounted For.

Table M.3. Bivariate Matching Fits to the Behavior of the Exponential-Clone-Pheno-Uniform Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.54	0.36	0.96	96
1.0	0.64	0.42	0.97	99
2.5	0.71	0.33	1.00	100
5.0	0.77	0.35	0.96	99
7.5	0.75	0.30	1.00	100
10.0	0.73	0.28	1.01	100
12.5	0.73	0.29	1.00	100
15.0	0.71	0.27	1.00	100
17.5	0.70	0.26	0.99	100
20.0	0.69	0.25	1.00	100
25.0	0.68	0.24	1.00	100
30.0	0.67	0.21	1.00	100
35.0	0.66	0.19	1.00	100
40.0	0.65	0.18	1.00	100
45.0	0.63	0.17	0.99	100
50.0	0.61	0.16	1.00	100

Note. %VAF = Percentage of Variance Accounted For.

Table M.4. Bivariate Matching Fits to the Behavior of the Exponential-Clone-Pheno-Linear Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.55	0.39	1.06	98
1.0	0.61	0.41	1.06	99
2.5	0.72	0.31	1.00	100
5.0	0.75	0.32	1.03	100
7.5	0.74	0.30	1.02	100
10.0	0.73	0.29	1.00	100
12.5	0.71	0.27	0.99	100
15.0	0.70	0.28	1.00	100
17.5	0.70	0.27	1.00	100
20.0	0.68	0.25	1.01	100
25.0	0.67	0.23	1.00	100
30.0	0.66	0.21	1.01	100
35.0	0.65	0.20	1.00	100
40.0	0.63	0.18	1.00	100
45.0	0.62	0.17	1.00	100
50.0	0.60	0.16	1.00	100

Note. %VAF = Percentage of Variance Accounted For.

Table M.5. Bivariate Matching Fits to the Behavior of the Exponential-Clone-Pheno-Exponential Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.56	0.29	0.98	97
1.0	0.63	0.34	1.03	99
2.5	0.71	0.33	1.00	100
5.0	0.71	0.30	1.01	100
7.5	0.70	0.31	1.00	100
10.0	0.69	0.31	1.01	100
12.5	0.69	0.29	1.00	100
15.0	0.68	0.28	1.00	100
17.5	0.67	0.26	1.01	100
20.0	0.68	0.26	1.00	100
25.0	0.66	0.23	1.00	100
30.0	0.64	0.21	1.00	100
35.0	0.62	0.20	1.00	100
40.0	0.61	0.19	1.00	100
45.0	0.58	0.17	1.00	100
50.0	0.57	0.16	1.00	100

Note. %VAF = Percentage of Variance Accounted For.

Table M.6. Bivariate Matching Fits to the Behavior of the Exponential-Clone-Pheno-Gaussian Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.51	0.41	1.04	94
1.0	0.60	0.38	1.14	97
2.5	0.68	0.32	1.00	99
5.0	0.74	0.29	0.95	100
7.5	0.74	0.32	0.98	100
10.0	0.73	0.30	0.99	100
12.5	0.73	0.31	1.00	100
15.0	0.72	0.26	1.00	100
17.5	0.71	0.28	1.01	100
20.0	0.71	0.28	1.01	100
25.0	0.70	0.24	1.00	100
30.0	0.68	0.23	1.01	100
35.0	0.67	0.22	1.00	100
40.0	0.67	0.20	1.00	100
45.0	0.66	0.20	1.00	100
50.0	0.65	0.19	1.00	100

Note. %VAF = Percentage of Variance Accounted For.

Table M.7. Bivariate Matching Fits to the Behavior of the Linear-Bitwise-Bitflip Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5				
1.0				
2.5				
5.0	0.81	0.69	1.01	100
7.5	0.83	0.68	1.01	100
10.0	0.81	0.62	1.01	100
12.5	0.79	0.59	1.01	100
15.0	0.75	0.58	0.98	99
17.5	0.72	0.54	0.99	99
20.0	0.67	0.52	1.01	99
25.0	0.58	0.47	1.00	98
30.0	0.50	0.42	1.00	97
35.0	0.44	0.37	1.00	97
40.0	0.38	0.34	1.00	97
45.0	0.34	0.31	1.00	97
50.0	0.30	0.28	1.00	96

Note. %VAF = Percentage of Variance Accounted For. 0.5, 1.0, and 2.5% mutation rates were unable to be run using this algorithm.

Table M.8. Bivariate Matching Fits to the Behavior of the Linear-Clone-Bitflip Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.59	0.41	0.95	99
1.0	0.65	0.46	0.96	100
2.5	0.75	0.57	1.00	99
5.0	0.73	0.53	0.99	100
7.5	0.74	0.56	0.99	99
10.0	0.72	0.55	1.00	99
12.5	0.67	0.52	1.00	100
15.0	0.63	0.50	1.01	99
17.5	0.60	0.48	1.00	99
20.0	0.55	0.46	1.00	98
25.0	0.48	0.41	1.00	98
30.0	0.42	0.37	1.00	98
35.0	0.37	0.34	1.00	97
40.0	0.33	0.31	1.00	97
45.0	0.29	0.28	1.00	96
50.0	0.26	0.26	1.00	96

Note. %VAF = Percentage of Variance Accounted For.

Table M.9. Bivariate Matching Fits to the Behavior of the Linear-Clone-Pheno-Uniform Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.59	0.58	1.09	96
1.0	0.64	0.61	0.99	99
2.5	0.68	0.52	1.00	99
5.0	0.70	0.41	1.03	100
7.5	0.69	0.37	0.97	100
10.0	0.70	0.34	0.99	100
12.5	0.68	0.32	1.00	100
15.0	0.67	0.30	1.00	100
17.5	0.66	0.28	1.00	100
20.0	0.67	0.27	0.98	100
25.0	0.65	0.25	1.01	100
30.0	0.64	0.22	0.99	100
35.0	0.63	0.21	1.00	100
40.0	0.62	0.18	1.00	100
45.0	0.61	0.17	1.01	100
50.0	0.59	0.16	0.99	100

Note. %VAF = Percentage of Variance Accounted For.

Table M.10. Bivariate Matching Fits to the Behavior of the Linear-Clone-Pheno-Linear Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.53	0.72	1.06	99
1.0	0.65	0.66	1.07	98
2.5	0.70	0.51	1.00	100
5.0	0.70	0.41	1.02	100
7.5	0.70	0.38	1.01	100
10.0	0.68	0.35	0.99	100
12.5	0.68	0.33	1.00	100
15.0	0.67	0.30	0.99	100
17.5	0.67	0.29	1.01	100
20.0	0.66	0.27	1.00	100
25.0	0.65	0.25	1.00	100
30.0	0.64	0.23	1.00	100
35.0	0.63	0.21	1.00	100
40.0	0.62	0.19	1.00	100
45.0	0.60	0.18	1.00	100
50.0	0.58	0.16	1.00	100

Note. %VAF = Percentage of Variance Accounted For.

Table M.11. Bivariate Matching Fits to the Behavior of the Linear-Clone-Pheno-Exponential Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.55	0.57	1.04	98
1.0	0.64	0.51	1.04	99
2.5	0.65	0.48	1.00	100
5.0	0.66	0.41	1.00	100
7.5	0.65	0.39	1.00	100
10.0	0.64	0.35	0.99	100
12.5	0.64	0.33	1.01	100
15.0	0.64	0.31	1.00	100
17.5	0.64	0.29	1.00	100
20.0	0.64	0.27	1.00	100
25.0	0.63	0.25	1.00	100
30.0	0.62	0.22	1.01	100
35.0	0.60	0.21	1.00	100
40.0	0.59	0.19	1.00	100
45.0	0.57	0.18	1.00	100
50.0	0.54	0.16	1.00	100

Note. %VAF = Percentage of Variance Accounted For.

Table M.12. Bivariate Matching Fits to the Behavior of the Linear-Clone-Pheno-Gaussian Creature Type

Mutation Rate	a_r	a_m	b	%VAF
0.5	0.57	0.83	0.99	94
1.0	0.55	0.60	1.07	97
2.5	0.65	0.57	1.00	99
5.0	0.69	0.44	1.02	100
7.5	0.71	0.42	1.02	100
10.0	0.72	0.38	1.04	99
12.5	0.70	0.35	1.01	100
15.0	0.68	0.34	1.01	100
17.5	0.68	0.31	0.98	100
20.0	0.68	0.31	0.99	100
25.0	0.67	0.27	1.00	100
30.0	0.65	0.25	1.01	100
35.0	0.65	0.24	1.00	100
40.0	0.64	0.22	1.00	100
45.0	0.64	0.21	1.00	100
50.0	0.63	0.19	1.01	100

Note. %VAF = Percentage of Variance Accounted For