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Andrei Popa Date

The Effect of Hamming Distances in a Computational Model of Selection by Consequences

By

Andrei Popa
Master of Arts

Department of Psychology

Jack J McDowell, Ph.D.
Advisor

Eugene K. Emory, Ph.D.
Committee Member

Philip Wolff, Ph.D.
Committee Member

Accepted:

Lisa A. Tedesco, PhD.
Dean of the James T. Laney School of Graduate Studies

Date

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Andrei Popa
B.A., Al. I. Cuza University, 2003

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An Abstract of
a thesis submitted to the Faculty of the Graduate
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McDowell (2004) instantiated the Darwinian principles of selection, recombination, and mutation in a computational model of selection by consequences. The model forces a population of behaviors to evolve under the selection pressure of the environment, by applying low-level Darwinian principles; it has been tested under a variety of conditions and the quantitative outcomes are remarkably similar to those obtained in experiments with live organisms (McDowell et al., 2008). The computational model animates a virtual organism with a repertoire of 100 behaviors, represented by binary strings; this raises the specific issue of Hamming distances, the number of digits in a binary string that must be changed in order to obtain another bit string of equal length (Hamming, 1950). McDowell (2008) hypothesized that in environments that reinforce two alternatives the Hamming distance may be computationally equivalent to a changeover delay (COD). In experiments with live organisms that reinforce two alternatives, an interesting phenomenon is sometimes observed: instead of responding to the alternatives, the organism behaves "as if" switching itself is reinforced. One way to prevent this phenomenon is the use of a changeover delay, a procedure that prevents the organism from acquiring reinforcement if it switches too often (Findley, 1958). The Hamming distances represent, by definition, the difficulty of transforming a binary string. The computational model places the target classes next to each other, and, traditionally, they are separated by a large Hamming cliff, which makes it more difficult for a behavior to switch from one target class to the other. In order to investigate the effects of smaller cliffs between the target classes, they were positioned at different locations along the continuum of integers; in addition, other parameters were systematically varied. Results confirmed McDowell et al.'s Hamming-Distance-As-Changeover-Delay hypothesis and also revealed a robust rule about the effects of Hamming distances within the model. The steady state outcome is, therefore, a product of the reiteration of Darwinian rules, and not an artifact of conveniently choosing an exceptional location for the target classes. This study constitutes another argument for the robustness of the computational model of selection by consequences as a valid account of the behavioral dynamics.

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Abstract

McDowell (2004) instantiated the Darwinian principles of selection, recombination, and mutation in a computational model of selection by consequences. The model forces a population of behaviors to evolve under the selection pressure of the environment, by applying low-level Darwinian principles; it has been tested under a variety of conditions and the quantitative outcomes are remarkably similar to those obtained in experiments with live organisms (McDowell et al., 2008). The computational model animates a virtual organism with a repertoire of 100 behaviors, represented by binary strings; this raises the specific issue of Hamming distances, the number of digits in a binary string that must be changed in order to obtain another bit string of equal length (Hamming, 1950). McDowell (2008) hypothesized that in environments that reinforce two alternatives the Hamming distance may be computationally equivalent to a changeover delay (COD). In experiments with live organisms that reinforce two alternatives, an interesting phenomenon is sometimes observed: instead of responding to the alternatives, the organism behaves "as if" switching itself is reinforced. One way to prevent this phenomenon is the use of a changeover delay, a procedure that prevents the organism from acquiring reinforcement if it switches too often (Findley, 1958). The Hamming distances represent, by definition, the difficulty of transforming a binary string. The computational model places the target classes next to each other, and, traditionally, they are separated by a large Hamming cliff, which makes it more difficult for a behavior to switch from one target class to the other. In order to investigate the effects of smaller cliffs between the target classes, they were positioned at different locations along the continuum of integers; in addition, other parameters were systematically varied. Results confirmed McDowell et al.’s Hamming-Distance-As-Changeover-Delay hypothesis and also revealed a robust rule about the effects of Hamming distances within the model. The steady state outcome is, therefore, a product of the reiteration of Darwinian rules, and not an artifact of conveniently choosing an exceptional location for the target classes. This study constitutes another argument for the robustness of the computational model of selection by consequences as a valid account of the behavioral dynamics.

The Effect of Hamming Distances in a Computational Model of Selection by Consequences

One of the features that seems to be embedded in living organisms is the ability to adjust to a dynamic environment. One way this might be achieved is by selecting and perpetuating those behaviors that proved useful in the past. Behaviors evolve under the pressure exerted by the environment, being shaped by the outcome they produce. Much like species, some behaviors endure and are displayed with regularity, some change, and some perish; and, to a very large extent, it depends on the feedback received from the environment.

This observation opened new horizons for thinkers and researchers, leading them to the next logical set of questions, such as "*What is the nature of the relation between environment and behavior?*", "*Is there an order that can be determined?*", "*Can it be foreseen?*". The potential existence of mathematical equations that describe and predict human behavior have drawn an impressive amount of attention and the first theories did not take long to emerge. In 1943, Clark Hull presented the first mathematical equation of performance, expressed as reaction potential:

$${}_{S}E_{R} = ({}_{S}H_{R} \mathrm{~x~} D \mathrm{~x~} K \mathrm{~x~} V) - I_{R} - {}_{S}I_{R} - {}_{S}O_{R}, \tag{1}$$

where ${}_{S}H_{R}$ is habit strength (the strength of the bond between responses and reinforcements), D is drive, K is incentive motivation, V is stimulus dynamism (saliency of the stimulus), I_{R} is reactive inhibition, ${}_{S}H_{R}$ is conditioned inhibition, and ${}_{S}O_{R}$ is the oscillation of reaction potential. Despite the presence of variables that refer to internal states/qualities, one important aspect of Equation 1 is that performance is viewed as depending on habit strength and stimulus dynamism (among other variables), thus acknowledging the role of the environment on displayed behavior.

Eight years later, Bush and Mosteller (1951) proposed a different equation to describe behavior:

$$\Delta V_A = \alpha_A \beta(\lambda - V_A), \qquad (2)$$

where ΔV_A is the change in the associative strength of the stimulus, λ is a measure of reward-value, β is the rate of learning and α_A is the attention-value (salience) of the stimulus. The main difference between this equation and Equation 1 is a reduction in the number of "internal" variables (e.g. drive), the focus shifting towards the qualities of the stimulus[1].

One common feature of the above mentioned equations is the use of non-specific quantities, which raises important issues. For example, let us assume that Drive is defined as the number of hours of water deprivation: if the equation does not fit the data, the researcher may choose to define Drive as serotonin level or as the difference between body weight in free-feeding conditions and body weight at the time of the experiment. We can see that a variety of factors may be used to operationalize the same hypothetical construct, which makes the theory difficult to falsify, thus violating one basic condition for a valid scientific theory (Popper, 1959).

A few years later, another interesting phenomenon was being observed in experiments with living organisms (e.g. rats, pigeons): apparently random and chaotic at first, the animal's behavior was showing a clear tendency towards a steady-state, indeed reaching equilibrium after a number of trials. What was surprising was the fact that once

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[1] Both theories are very complex, encompassing a large number of equations; the two equations presented here are considered representative for the purpose of this paper.

reached, steady-state behavior was preserved with great precision, and for long periods of time (e.g. a pigeon preserving approximately the same rate of pecking for 10 hours (Ferster and Skinner, 1957). The influence exerted by the environment, previous attempts to capture behavior in mathematical equations, and the quality of steady-state behavior, set the stage for the next mathematical approach to behavior.

The Matching Law

In 1961, while conducting experiments with pigeons in concurrent - schedule environments[2], Richard J. Herrnstein (1961) observed an interesting fact: it appeared that, once equilibrium was reached, the proportion of responses on each alternative was equal to the proportion of reinforcements acquired from that alternative, a relation described by the following equation:

$$\frac{R_1}{R_1 + R_2} = \frac{r_1}{r_1 + r_2}, \tag{3}$$

where R_1 and R_2 refer to the response rates and r_1 and r_2 refer to reinforcement rates. Equation 3 can also be written in a ratio form:

$$\frac{R_1}{R_2} = \frac{r_1}{r_2}. \tag{4}$$

The relation between responses and reinforcements described by Equation 3 was called by Herrnstein *The Matching Law* and it describes free choice, steady-state behavior in a multiple choice environment. The entire family of equations, both for concurrent-schedule environments and for single-alternative environments is shown in Figure 1. It is

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[2] A concurrent schedule typically consists of two schedules of reinforcement, independent of each other, that are associated with two different spatial stimuli (e.g. a rat facing two levers). The organism placed in this situation can choose one of the two alternatives or it may choose to display behaviors totally unrelated to the two alternatives; that is why this environment is referred to as a “free choice environment”.

the first mathematical account of behavior that uses true operational definitions, namely the number of responses and the number of reinforcements, which allows for a scientist to conceive a set of data that may falsify the theory (Bridgman, 1950).

The initial success of the Matching Law generated a large number of experiments that did not manage to shake the theory's foundations, and that led to the discovery of important and interesting facts. In concurrent-schedule environments it was observed that results deviate from perfect conformance to Equation 3 when there are differences between the two alternatives (e.g., one lever is harder to press than the other). This situation is often encountered in laboratory experiments and in order to account for the available data, a new parameter had to be introduced: the bias parameter, *b*. Also, experiments showed another deviation from perfect matching, characterized by a tendency towards indifference. In the case of total indifference, the organism is allocating its responses equally among alternatives, regardless of consequences. Living organisms show a small propensity towards this situation, a propensity called undermatching (Myers & Myers, 1977). Mathematically, undermatching is described by an exponent parameter, *a*. At this time the causes of bias are well known (McDowell, 1989); unfortunately, this is not the case for *a*. With the addition of the new parameters, the ratio form of Equation 3 becomes a power-function equation:

$$\frac{R_1}{R_2} = b\left(\frac{r_1}{r_2}\right)^a , \tag{5}$$

where R_1 and R_2 refer to the response rates and r_1 and r_2 refer to reinforcement rates. When the difference between alternatives is negligible (the two choices are symmetrical), *b* is approximately 1. The exponent is found to vary around the value 0.8 (McDowell, 1989; McDowell & Caron, 2007), depicting a slight tendency towards indifference (undermatching); when $a \geq 1$, we speak of overmatching (or a tendency towards exclusive preference), a situation not often encountered in living organisms. The power-function equation was proposed by Baum (1974) and states that in a free-choice environment, organisms allocate their responses to different alternatives in the same proportion in which reinforcements are allocated among alternatives; however, they do so allowing for bias and with a tendency towards undermatching.

Experimental results supporting the Matching Theory are numerous and their essence is captured in comprehensive reviews of the literature (Baum, 1979; Davison & McCarthy, 1988; McDowell, 1988); in addition, the superiority of Baum's power function has been extensively verified (Baum, 1974; Dallery, Soto, & McDowell, 2005; McDowell et al, 2009). Little room for disagreement exists at the moment in the scientific community and it is widely accepted that the power-function equation describes the relation between responses and reinforcements in a free, multiple-choice environment, providing an excellent mathematical kinematics for instrumental behavior under such conditions. The possibility of mathematically describing behavior at equilibrium constituted a major breakthrough in the field and it allowed for the next major question: *what causes behavior to reach this equilibrium state*?

Different types of mathematical dynamics have been proposed over the years, in an attempt to explain why behaviors and environmental variables are linked the way they are. Such accounts classically use as a starting point a statement of a dynamic theory, from which they obtain a descriptive outcome; the melioration account (Vaughan, 1981; Herrnstein, 1982) and the maximization account (Baum, 1981; Rachlin, Battalio, Kagel,

& Green, 1981) are two prominent examples in this regard. For example, a maximization account may assume that an organism tends to maximize the utility (value) of its behaviors; thus, a certain utility function may be proposed, a function that expresses behavior's *value* in terms of independent variables, like *benefit* and *cost*. Using this utility function a researcher may *predict* what the final outcome will be, assuming that the organism tends to maximize *value*. Although different in theory, most causal accounts of dynamics assume an end-state and use dynamic theories and analytical mathematical models to predict it.

A different account however is selection by consequences, proposed by Skinner (1981). The main feature that differentiates it from the above mentioned dynamic theories is that it does not specify a final outcome for operant behavior. This kind of dynamics entails the implementation of simple, low-level rules that govern the relation between organism and environment, causing some behaviors to be maintained in favor of others. Instrumental behavior thus occurs without being directed to an expected outcome, but emerging without constraints from the simple rules of selection.

Because no end-state is specified in a selection by consequences account, an implementation using analytical mathematical methods is impossible. However, this apparent shortcoming may be overcome by the use of a computational approach, which would require only the specification of simple rules. High-order outcome is not directly linked with the low-level rules and therefore it may not be predicted; only by repeated application of the rules will the final outcome be observed, an aspect that led scientists to call this result an emergent property of the low-level rules (McDowell, 2004).

One specific type of computational approach is the genetic algorithm, a specific sub-set of evolutionary algorithms (Goldberg, 1989; Holland, 1992). Basically, a genetic algorithm is a search technique that implements simple, biologically-inspired rules (e.g. reproduction, mutation, survival of the fittest, etc.) to find solutions to complex problems. Low-level processes are applied repeatedly to a population of solutions until a specified end-state is reached or a specified number of repetitions is achieved. For example, the best solution to the famous *travelling salesman* problem (Applegate, Bixby, Chvátal, & Cook, 2006) can be achieved using a genetic algorithm; the initial data are computed (e.g. number of cities, cost of travelling, etc) and populations of solutions are repeatedly generated and compared with each-other until the best one is found. Another domain that benefits from the use of a genetic algorithm is that of computational creativity (Boden, 1999). This relatively new domain uses computer simulations to replicate human creativity; for example, populations of sounds may be combined, selected, and mutated to give rise to a huge number of possible combinations that may or may not resemble music (Cope, 2005). By contrasting the two examples an important characteristic becomes obvious: although an end-state may be specified (travelling salesman problem), it is not necessarily required (computational creativity), which makes this kind of computational approach an ideal candidate for a computational model of selection by consequences.

In the following sections I will present a specific genetic algorithm that implements Skinner's causal account of instrumental behavior, namely *Selection by Consequences*. The Darwinian rules of selection, recombination, and mutation will be explained, allowing the reader to become familiar with the program's functionality. Evidence that supports the genetic algorithm as a theory of behavior dynamics will also be presented. Afterwards, a specific feature of the program will be addressed, in terms of its characteristics and importance, specifically the Hamming distance.

The Computational Model

Selection by Consequences 2.0 (SC 2.0) is a genetic algorithm designed by McDowell (2004) that implements simple rules of Darwinian evolution (selection, recombination, and mutation). Basically, the model forces a population of behaviors to evolve under the selection pressure of the environment, without specifying a final outcome.

SC 2.0 implements a virtual organism with a total repertoire of 100 behaviors, selected from the integers from 0 to 1023. The behaviors' phenotypes are the integers from 0 to 1023; the genotype of each behavior is the binary correspondent of this integer. For example, the genotype of behavior 678 is 1010100110; each behavior has a genotype of 10 digits. The total number of behaviors is divided into four classes, the class size being established based on the baseline probabilities computed by the user. For example, if we assign a baseline probability of 5% to class 3 and we draw a behavior at random, there is a 5% chance that the behavior will belong to class 3. We may choose to reinforce one class (single-alternative schedule), 2 classes (concurrent schedules) or no class (no reinforcement is available) of behavior. The reinforced classes (referred to as "target classes") correspond to a rat's lever-pressing and the non-reinforced classes (referred to as "extraneous classes") correspond to all other behaviors that a rat may display in a Skinner-box, that do not produce reinforcement (e.g. exploring the cage).

In the beginning of an experiment the program selects a population of 100 behaviors at random; from this population, a first behavior is randomly emitted. Every time-tick a new population is generated in the following general way: parents are selected from the population, they reproduce, mutation occurs, and a new behavior is emitted. Twenty thousand emissions constitute an experiment and they are grouped in 500-generation blocks, each block becoming a data point.

There are two processes that are not affected by the schedules in effect: recombination and mutation. Even though both of them can be implemented in a variety of ways, the discussion will be restricted to the ones used in these experiments.

Recombination

The recombination method used is called “bitwise”. After the two parents are selected, in a manner that will be described later, every bit in the progeny’s string has a 50% chance of being the corresponding bit of one parent and a 50% chance of being the corresponding bit of the other parent. For example, let us suppose that the mother is 340 and the father is 117; their genotypes are 0101010100 and 0001110101 respectively. The bit in the first slot of the child is 0, because it is 0 in both parents. The bit in the second slot has a 50% chance of being 1 (from the mother) and a 50% chance of being 0 (from the father); it is randomly selected based on the 50-50 probability and, in this example, the second slot of the child is 1. The process continues for all ten slots; in our example the resulting child may be 0101010101, with 7 bits being the same in mother and father, 2 bits being from the mother, and 1 bit is from the father; the corresponding integer (phenotype) is 341.

Mutation

The mutation method used is called “bit flip by individual”. We can choose the level of mutation we desire; for all the experiments the mutation rate was set to 10%.

This means that every time “mutation” occurs, every individual in the population has a 10% chance of being affected by it; if affected, one of the 10 bits, at random, is “flipped” from 1 to 0 or vice versa. Using the same example as above, let us assume that the child-behavior 0101010101 (341) is affected by mutation; in this case, 1 bit is “flipped”. The affected bit is randomly selected, each bit of the 10-bits string having a 10% chance[3] of being flipped. In our example the bit affected may be the one in the third slot, which is flipped from 0 to 1; the new, mutated behavior is 011010101 (469). Recombination and mutation ensure the diversity of the population, introducing variation; both processes are illustrated in Figure 2.

After a behavior is emitted (randomly selected from the population of potential behaviors) the program determines whether the behavior is part of the target class; if it is, it determines if reinforcement is available. If the emitted behavior is not part of the target class, or if it is part of the target class but reinforcement is not available, then parents are randomly selected. After they reproduce, mutation affects the new population of behaviors and the whole process is repeated.

Fitness

If the emitted behavior is part of the target class and reinforcement is available (therefore acquired) the process of selection will occur. Selection is based on the fitness of every behavior, which is calculated using a method called *midpoint fitness*. The midpoint of the target class from which the behavior was emitted becomes “fitness zero.” The fitness of each behavior in the population is calculated as the absolute difference

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[3] The selected level of mutation (10% in our example) has nothing to do to the 10 % chance of every bit in the child-behavior of being flipped; this probability is always 10%, given the fact that there are ten bits in every genotype.

between the integer that represents it and "fitness zero". The range of integers from 0 to 1023 is wrapped upon itself, as a circle, 1023 being next to 0. This way, the distance between 1023 and 0 is equal to the distance between 0 and 1. The *fitness value* of a given behavior is the smallest distance, as represented on this circle, between the behavior's phenotype and "fitness zero" (the midpoint of the target class for which the previously reinforced behavior originated); the smaller the fitness value, the fitter the behavior.

For example, if a target class encompasses behaviors between 512 and 552, then its midpoint is 532. If the emitted and reinforced behavior is part of this class, 532 becomes "fitness zero" (best fitness). The fitness value for, let's say, behavior 817 is |532-817| = 285 and for behavior 390 – |532 -390| = 142. The behavior with the smallest fitness value is considered the fittest because it is closest to the target class that was reinforced; in this example, the fitter behavior is 390. The procedure of assigning fitness values is depicted in Figure 3.

Selection

After assigning fitness values, a parental selection function is used to select the parents for the new population of behaviors. The parental selection function assigns greater probabilities of being selected as parents to behaviors with smaller fitness values. In this project the function is linear, but any function that assigns larger probabilities to fitter behaviors can be used (e.g. an exponential). Detailed characteristics of the selection functions will be discussed later.

A summary of the program's functionality is illustrated in Figure 4. In the beginning of the experiment a population of 100 behaviors is randomly selected from the integers between 0 and 1023. One behavior is randomly selected from this population and it constitutes the first emission in the experiment. If the emitted behavior is not part of the target class or is part of the target class but reinforcement does not occur, then parents are selected at random from the existing population. They reproduce and the new population of children is affected by mutation. A new behavior is emitted at random from the mutated population. If reinforcement occurs, then the program calculates the fitness value of each behavior in the population. A parental selection fitness function is used to assign greater probabilities of being selected as parents to fitter behaviors. Therefore, the parents are no longer selected at random, but are selected based on their fitness. They reproduce and the population of children is affected by mutation. From this population a new behavior is randomly emitted. Every emission constitutes a generation; in a typical experiment there are 20,000 emissions, therefore 20,000 generations.

The processes of recombination and mutation tend to spread the behaviors among the four classes. However, if reinforcement is acquired, the parents for the next generation are selected based on fitness, therefore, the probability that parents are selected from that particular target class (or close to it) is relatively large. Therefore, reinforcement, which entails selection based on fitness, is in opposition to recombination and mutation, tending to keep the behavior in the target class that was previously reinforced. After a few thousands generations the opposing forces reach equilibrium, a steady state best described by The Matching Law.

Evidence supporting SC 2.0

The results produced by SC 2.0 are remarkably similar to those displayed by living organisms. When Equation 5 is fitted to the data generated by SC 2.0, the bias parameter (*b*) varies around unity for symmetrical-choice environments and fluctuates with the level of asymmetry introduced by the experimenter. The percentage of variance accounted for is typically about 95%. The exponent (*a*) varies around 0.8, accurately depicting the undermatching phenomena encountered in living organisms (McDowell & Ansari, 2005, McDowell & Caron, 2007, McDowell et al, 2008).

As stated above, there is no direct link between the low-level rules implemented in the program and the final outcome that we observe; moreover, the emergent results have been found to be robust over different experimental conditions, as shown in an experiment conducted by McDowell et al. (2008). The first phase of this experiment modeled a free-choice environment, consisting of symmetrical concurrent schedules. The processes of selection, recombination, and mutation were held constant during this phase. Analysis of the results indicated remarkable similarity to the behavior of living organisms. When Equation 5 was fitted to the data, the exponent, *a*, varied between 0.76 and 0.89, with an average of 0.82, which is an indicator of undermatching. The bias parameter, *b*, varied around an average of 0.99, reflecting the absence of bias in symmetrical choice environments.

The second phase of the experiment modeled an asymmetrical free-choice environment. The difference between the two alternatives was manipulated by altering the parental selection process; more specifically, the severity of the selection process was held constant on one alternative while it varied on the second alternative. The severity of the selection process can be easily manipulated by modifying the mean of the parental selection function; this characteristic will be discussed in detail in the Method section. Different levels in the severity of the parental selection process for the two alternatives were hypothesized to be computationally equivalent to the effects produced by different types (or magnitudes) of reinforcement in experiments with living organisms. For instance, if one alternative provides regular water and the other alternative provides saccharine, a rat shows a preference toward the second alternative. This phenomena is reflected in the value of the bias parameter, *b*, and indicates that the organism is placing a larger proportion of responses (than predicted by perfect matching) on the preferred alternative.

In the computational model, a more severe selection process means that very fit behaviors have a greater chance of becoming parents. The consequence is an increased probability of progeny belonging to the same target class from which the previously reinforced behavior was emitted. If more behaviors in the population belong to this target class, then one would expect the proportion of responses that originate from this class to increase, which would be a similar outcome to that encountered in the example with living organisms mentioned above, namely a larger proportion of responses on one alternative (larger than predicted by perfect matching). This similarity in outcome is the foundation of the hypothesis that severity of the selection process for the two alternatives is computationally equivalent to different types (or magnitudes) of reinforcement delivered by the two alternatives. Because the latter entails differences in preference reflected in the value of *b* one would expect to observe the same differences in the results generated by the model.

The analysis indicated that stronger selection events are indeed favored, as reflected by the bias parameter. When stronger selection events were associated with the first alternative the value of *b* was 2.4; it decreased, approaching 1, as the difference between levels of severity of the selection processes on the two alternatives diminished, reaching 0.7 when the stronger selection event was associated with the second alternative. The average of the exponent, *a*, was 0.83, indicating that the small level of undermatching is preserved even in asymmetrical choice environments.

In the third phase of the experiment the authors varied the mutation rate and the severity of the parental selection process. Although different from the experiments in phase one, severity was kept equal for the two alternatives, thus generating a symmetrical choice environment (equally severe or equally lenient). In other words, the effect of different mutation rates was examined at different levels of severity of the parental selection process. The analysis revealed that for mutation rates between about 5 and 12% the exponent varied around 0.8. For mutation rates lower than 5% the exponent decreased moderately (≈ 0.60) and for mutation rates larger than 12% the exponent decreased dramatically (as low as 0.16). Turning to the effect of the selection process, the results showed that more severe selection processes produce slightly higher exponents. The bias parameter however varied around 1 for all conditions, accurately depicting symmetry between alternatives even for different mutation rates and different levels in the severity of the parental selection process.

For all three phases of the experiment the percentage of variance accounted for was very high, varying around 90% (with a few exceptions for extremely low mutation rates). Analysis of residuals indicated the absence of linear or higher order polynomial trends. The results presented above constitute strong evidence that the computational model produces quantitative outcomes extremely similar to those observed in experiments with living organisms. It does so in a variety of conditions, for different severity levels of the selection process and different mutation rates, both in symmetrical-and asymmetrical-choice environments. These outcomes suggest that McDowell's computational model of selection by consequences may be a valid causal account for instrumental behavior.

Hamming Distance

An important aspect of the program is the fact that behaviors are represented by strings of binary digits. The binary representation has some particular characteristics, one of them being the Hamming distance. A Hamming distance represents the number of digits that must be changed in a string in order to obtain a different string of equal length (Hamming, 1950). For example, to obtain 448 from 447, 7 digits must be changed in the string (0110111111 → 0111000000).

When defining the target classes for the concurrent schedule experiments (McDowell et al, 2008), the authors defined them so they were separated by the maximum Hamming distance (when operating with 10-bit strings, the maximum distance is ten, Russell & Norvig, 2003). This choice was based on the fact that a large Hamming distance between target classes makes it difficult for a behavior to "switch" from one target class to the other by means of recombination and mutation. Also, it was observed that small distances tend to produce frequent switching between classes. This led the authors to hypothesize that the Hamming distance may be computationally equivalent to the role played by a changeover delay (COD) in experiments with living organisms (Findley, 1958).

It is interesting and troubling at the same time that all the computational experiments conducted with concurrent schedules were implemented using a Hamming distance of ten between the two target classes. As it was discovered in other fields (e.g.

telecommunication, cryptography) the Hamming distance may have a significant effect on the behavior of the computational model. In this light, it becomes important to investigate the effect of the Hamming distance on the results produced by SC 2.0.

Hamming Distance and the COD

A concurrent schedule is a specific arrangement for the delivery of reinforcement, which involves two schedules of reinforcement that run simultaneously. In the present project the schedules were random interval schedules (RI); a random interval schedule means that at certain time intervals reinforcement becomes available and the first response after the time interval acquires it. The time intervals are randomly selected form an exponential distribution (hence the name “random interval schedule”) with a mean specified by the user. For example, a random interval schedule with a mean of seven seconds (RI 7) means that the average time between the delivery of a reinforcement and the setup of the next (when the next one becomes available, but not necessarily acquired) is, on average, no less than seven seconds; however, it can be much longer if the organism’s response rate is low. The specific interval however is drawn at random from a distribution. Therefore, the first time interval may be, let’s say, 4 seconds, the second time interval 15 seconds, and so on. The use of the exponential distribution ensures that time intervals are truly randomized and that the average interval is the one specified by the researcher. This way, one may set a very rich schedule (e.g. reinforcement becomes available, on average, every 2 seconds – RI 2) or a very poor schedule (e.g. reinforcement becomes available, on average, every 150 seconds – RI 150). A concurrent random-interval random-interval schedule (concurrent RI RI) means that two RI schedules run, independently of each other, on two physically different alternatives (e.g. two levers).

In experiments with living organisms an important phenomenon was sometimes observed on concurrent schedules: instead of reinforcing responding on the alternatives, the change between alternatives may have been reinforced. In other words, due to some environmental characteristics, the organism was responding as if switching itself was being reinforced, and not the targeted response (e.g. the rat was responding as if reinforcement was delivered for alternatively pressing the two levers, not for consistently pressing one or the other). To prevent this from happening researchers introduced a changeover delay (COD) (Findley, 1958). When a COD is in effect and reinforcement becomes available, the first response does not acquire the reinforcement. Instead, it is acquired at the first response that occurs after the COD elapses. This practice proved to be an efficient method of preventing reinforcement for switching between alternatives.

The effects of CODs on operant behavior were reported as early as the 1960s. The main effect is a strong tendency of behavior towards indifference at small CODs and is mathematically reflected in the small values of the exponent of fits of Equation 5. Indeed, when varying the COD from 0s to 20s, the exponent was found to vary between 0.2 (at COD =0) to 0.9 (COD = 20) (Shull & Pliskoff, 1967; Davison & McCarthy, 1988). Some researchers support the idea that a COD is necessary for matching. Others suggest that matching does occur without the use of COD, if the procedure is very carefully controlled; what parameters should be controlled and how to control for them remains unclear (Baum, 1974, 1979; de Villiers, 1977). Another study that specifically varied the COD values found that if the COD increases, the value of *a* increases as well; for COD = 0, the values of *a* varied between 0.3 and 0.7, in a group of six organisms (Temple, Scown, & Foster, 1995). Although the aforementioned studies do not allow for strong, indisputable conclusions, the results clearly show that the value of *a* drops for small values of the COD, in some cases being extremely close to total indifference (absolute value ≈ 0).

Unpublished data from our laboratory suggest that the Hamming distances have a significant effect on the equilibrium states produced by the computational model, but the nature and extent of this effect remain unclear. At this point, the data that are available suggest that, at least in some cases, the Hamming distance has the effect of a COD (McDowell, 2004). First, the value of the exponent seems to drop with smaller Hamming distances between the target classes, being as low as 0.05 in some cases. A second finding that supports this assumption is the relation between the number of changeovers and the proportion of reinforcement. For living organisms, the larger the proportion of reinforcement obtained from one alternative, the smaller the rate of switching between alternatives (McDowell et al, 2008). Switching between alternatives *increases* as the proportion of reinforcement obtained on one alternative declines towards 0.5, after which it declines, as the proportion of reinforcement obtained on the other alternative increases from 0.5 to 1. In other words, if the reinforcements are obtained almost exclusively on one alternative, the organism switches less often between alternatives. At the other extreme is the case in which reinforcements are equally obtained from both alternatives (proportion = 0.5); in this case we encounter the maximum number of switches between alternatives. The pattern described above is illustrated in the left panel of Figure 5.

Interesting preliminary data show another outcome, illustrated in the right panel of Figure 5. When the only aspect that varies is the Hamming distance that separates the target classes (e.g. distance six instead of ten) the results look completely different from those described above. With smaller Hamming distances between classes, it appears that the number of changeovers *decreases* as the proportion of reinforcement on one alternative declines towards 0.5, after which it increases, as the proportion of reinforcement on the other alternative increases from 0.5 to 1. This is the exact opposite of the pattern described above: if reinforcement is acquired almost exclusively on one alternative, the organism switches most often; if the number of reinforcements is equal for both alternatives, the organism switches least often.

The dramatic change in the exponent, as well as the relation between changeovers and proportion of reinforcement, seem to be consistent with the hypothesis that the Hamming distance between the target classes is computationally equivalent to a changeover delay. The purpose of this project is to elucidate the role and the effect of different Hamming distances on instrumental behavior in a computational model of selection by consequences.

General Method

Traditionally, the computational model uses two specific target classes; Class 1 consists of behaviors from 471 to 511 and Class 2, behaviors from 512 to 552. The two classes, equal in size (41 behaviors in each class), are separated by the largest possible Hamming distance, ten. This means that it is relatively difficult for a behavior, by mutation and reproduction, to switch from one target class to another. The main question that arises is how this particular setting influences the results and what happens if we choose different Hamming distances as boundaries between the two target classes.

As stated before, the behavior of the virtual organism is governed by the simple, low-level rules of selection, recombination, and mutation. When reinforcement is obtained, parents for the next generation of behaviors are selected based on their fitness. Basically, selection is a function of fitness and the probability of being selected as parent. This process is implemented by the use of a probability density function, which assigns higher probabilities of being selected as parents to fitter behaviors. In all experiments conducted for this project the function used was linear; its form is given by the formula:

$$p(x) = -\frac{2}{9\mu^2}x + \frac{2}{3\mu}\,. \tag{6}$$

In the above equation μ is the mean of the function and the fitness value (x) is in the interval $[0, 3\mu]$. The function expresses the probability of a behavior with a given fitness value (x) of becoming a parent. Fitness values represent the difference between the midpoint of the target class from which the previously reinforced behavior occurred and a behavior's phenotype (its integer); as illustrated in Figure 3, behaviors that are closer to the midpoint of the target class have smaller fitness values and higher fitness. After assigning fitness values, a behavior is selected using the cumulative form of Equation 6, that is, its integral:

$$P(x) = -\frac{1}{9\mu^2}x^2 + \frac{2}{3\mu}x \,. \tag{7}$$

The parental selection function depends only on its mean, and by modifying the mean we can alter the strength of the selection process. For example, using Equation 7, the probability of a behavior with a fitness value of 40 being selected as parent is 0.01 for μ = 40, 0.005 for μ = 15, and 0 for μ = 7. As we can see, the probability that one behavior, with a specific fitness value, will become a parent decreases as the mean of the parental function increases; the same behavior has larger and larger chances of becoming a parent as the mean decreases, as illustrated in Figure 6. In other words, the selection process becomes more severe as the mean decreases, allowing only very fit behaviors to be selected as parents; since the parental selection function depends only on its mean, the severity of the selection process can be easily altered by modifying the mean.

After parents are selected they recombine and give rise to the next generation of behaviors. The recombination method used in all experiments is called "bitwise", each bit of the child behavior having a 50 percent chance of coming from one parent or the other, as illustrated in Figure 2. Throughout the present project the level of mutation was kept constant at ten percent, which means that each behavior has a 10% percent chance of being affected by mutation. If affected, one bit, at random, is "flipped" (one becomes zero or zero becomes one), that is why this mutation method is called "bit flip by individual". Both the method and the rate (10%) were kept constant in all experiments. After mutation, a new behavior is emitted and the entire process is reiterated; 210,000 repetitions constituted an experiment and five experiments were run for each experimental condition. Each repetition was fitted and the five sets of parameters were averaged. A data point is thus the average of five values; this refers to exponents' values, values of the bias parameter, and proportion of variance accounted for. Another important aspect that characterizes all experiments is the fact that the two classes were always identical in terms of number of behaviors encompassed in each one and the severity of the selection process associated with them. In other words the virtual organism was always placed in a symmetrical-choice environment.

Mathematical analysis

The data collected were analyzed using the logarithmic transformation of the power function matching equation (Equation 5); the logarithmic transformation results in a straight line, which is easier to fit than a power function and is widely accepted in the field as being the standard method of analysis:

$$\log\left(\frac{R_1}{R_2}\right) = a\log\left(\frac{r_1}{r_2}\right) + \log b\,. \tag{8}$$

In the above equation, a is the slope and *log b* is the y-intercept of the straight line. A slope smaller than one depicts the undermatching phenomenon; values larger than one indicate overmatching. If the straight line intersects the y-axis above zero it means that the organism is biased towards the first alternative. A negative intercept value indicates a preference towards the second alternative. These phenomena can be examined in Figure 7. The actual values were calculated using the Excel functions SLOPE and INTERCEPT; the bias parameter, b, is equal to $10^{\text{INTERCEPT}}$.

Residuals were analyzed for randomness using the Reich method (Reich, 1992), as it was applied by McDowell (2004). The Reich method consists of three tests for the randomness of the residuals. One procedure tests the obtained number of positive residuals for randomness (ideally, half of the values are positive and half are negative), the second procedure tests for consecutive values with the same sign, and the third procedure tests for a lag-1 auto-correlation among residuals. The failure of any of the three tests was taken to indicate a systematic pattern of residuals for that particular experiment. The tests were conducted using an Excel Macro developed by McDowell (2004).

The randomness for any given *group* of experiments was investigated by calculating the binomial probability of concluding that x or more non-random sets of residuals in the entire collection (n) are not random, given the known probability of falsely concluding that a certain set is not random. Since it is enough to fail one test out of three to be considered non-random, and each test has an alpha level of 0.05, the probability of making a Type I error (concluding that a set of residuals is not random when, in fact, it is random) is considered to be the cumulative alpha level, given by Equation 9:

$$1 - (1 - 0.05)\ (1 - 0.05)\ (1 - 0.05) = 0.142625. \tag{9}$$

Under these circumstances, given a collection of experiments with random residuals, one would expect to conclude in approximately 14% of cases that residuals are random, when in fact they are not. We can compare the hypothetical collection described above with the obtained collection by calculating the binomial probability of concluding that x or more sets of residuals are not random in a collection of n sets, all with random residuals, given the fact that there is a 14% chance of falsely concluding that a set of residuals is random. Basically we assume that *x* or more sets of residuals are not random (H_1); if the binomial test is significant (probability ≤ 0.05) we must accept the fact that residuals in our collection are not random. However, if the binomial probability is greater than 0.05 the alternative hypothesis is rejected and we accept that residuals in our collection are, in fact, random (H_0 = true). The binomial probability is calculated using Equation 10, where p = 0.142625:

$$\mathrm{b}(x, n; p) = C_x^n p^x (1-p)^{n-x} \quad (10)$$

Direct correlations between *log* (R_1/R_2) and *log* (r_1/r_2) were used to calculate the proportion of variance accounted for (pVAF) by the power-function equation. An SPSS corelational analysis was used to compare two particular sets of data points; SPSS was also used to generate frequency distributions of the exponent and the bias parameter. The genetic algorithm's utility functions were used to calculate the number of changeovers, defined as the number of times the organisms switches from one alternative to another, averaged per 500-generation blocks.

In the next sections of the project seven experimental series will presented. The absolute effect of the Hamming distances, when using the traditional settings, will be discussed in the first series. The second series investigates and clarifies a certain issue observed in the first series. The third and fourth experimental series explore the effects of different class sizes and different parental selection means, at all nine locations. The fifth and sixth series have the purpose of isolating an effect observed in the previous experiments. From the results of the six experimental series a general rule emerges, and that rule is tested for robustness in the final series of experiments.

Experimental Series 1

The focus of this series of experiments was the absolute effect of the Hamming distance, using the traditional experimental parameters: a class size of 41 behaviors and a parental selection function mean of 40.

Method

In order to study the effect of Hamming distances the two target classes were moved along the continuum of integers from 0 to 1023, placing them in such locations so that the Hamming distance between the two target classes was 9, 8, 7, 6, 5, 4, 3, and 2, as shown in the top panel of Figure 8. All these locations are situated to the left of Hamming distance ten (HD 10). Given the structure of the continuum, which, regarding the position of Hamming distances, is perfectly symmetrical with respect to HD 10, there are no reasons to assume a difference between the two halves: locations to *the left* or to *the right*[4]. However, for control purposes, the eight locations mentioned above were "mirrored" to the right, as shown in the bottom panel of Figure 8; Figure 9 depicts all 17 locations, to *the left* and to the *right*. Five experiments were conducted for each location, giving a total of 85 experiments. Each experiment entailed eleven pairs of concurrent schedules and each pair was in effect for 20,000 generations; therefore, almost 93 million generations were run for the present experimental series. The mean of the parental selection function was kept constant at its traditional value of 40 and its form was linear; the mutation rate was also kept constant, at 10%.

Results and Discussion

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[4] These labels are used throughout the paper to refer to the two halves of continuum. Locations situated between 0 and 512 are referred to as "*left*" and locations situated between 512 and 1023 are referred to as "*right*".

The results are illustrated in Figure 10. When the Hamming distance that separates the two target classes was ten (McDowell, 2004; McDowell et al, 2009) the value of the exponent (*a*) varied around 0.8, the level of undermatching typically encountered in experiments with live organisms (Baum, 1979; McDowell, 1988); similar values emerged in the present experiments when the Hamming distance between the two target classes was nine. However, a significant decrease in the value of *a* was observed when the Hamming distance was reduced to eight: from approximately 0.8 to approximately 0.5, indicating a high level of undermatching. The most interesting phenomenon emerged when the Hamming distance was seven, a phenomenon that is consistent for all the other values of the Hamming distance, as illustrated in the top panel of Figure 10. In all these cases the value of the exponent was very close to zero (varying between 0.07 and 0.15), which indicated an extremely strong tendency towards total indifference. The bottom panel of Figure 10 illustrates the values of the bias parameter (*b*), which varied around unity; not a surprising outcome considering the fact that all the experiments involved symmetrical-choice environments. In addition, results obtained when the two target classes were situated to the *left* were almost identical, both in values and pattern, with those obtained when the target classes were located to the *right*.

Besides the decrease in the exponent’s value down to the point of total indifference, another important phenomenon accompanied the smaller Hamming distances: a striking change in both the pattern and the frequency of the changeovers (switching between the two alternatives). When HD 10 or HD 9 separated the two target classes the pattern typical for live organisms was observed: the number of changeovers increased as the proportion of reinforcement on the first alternative increased from 0 to

0.5, after which it decreased as the proportion of reinforcement on the first alternative increased from 0.5 to 1. This pattern indicates that when reinforcements were acquired almost exclusively from one alternative the number of changeovers was rather small; when reinforcements were obtained equally from both alternatives, the organism switched most often. As illustrated in Figure 11, the number of changeovers in these cases (averaged per 500 generations blocks) varied between 3 and 14. When the two target classes were separated by a Hamming distance of eight the number of changeovers increased from an average of approximately seven to an average of approximately 30; at the same time an almost constant pattern of switching was observed, associated with an exponent value of 0.5. However, the most interesting phenomenon was encountered in the situations in which the Hamming distances between the two target classes were equal to or smaller than seven (situations associated with exponent values close to zero). The frequency of changeovers was approximately ten times higher compared with the first situation (Hamming distance ten). Also, the pattern was in complete opposition to the one observed when HD 10 served as boundary, indicating that when reinforcements were obtained almost exclusively from one alternative the organism switched most often between alternatives.

Experimental series 2

An interesting phenomenon was observed in the previous experimental series when the Hamming distance that separated the two target classes was equal to four. In this case a fracture in the pattern was observed, manifested by a small but noticeable increase in the value of the exponent ($a \approx 0.16$); the identical phenomenon appears at the *right* ($a \approx 0.16$), as depicted in Figure 10. Examining the exact locations it becomes evident that using a class size of 41 behaviors at Hamming distance four, the second target class comprises behaviors from 488 to 528, which includes inside it the Hamming distance ten (between 511 and 512). Similarly, when mirroring the location to the *right* the Hamming distance ten is included *inside* in the first target class, which encompasses behaviors between 495 and 535.

This phenomenon could be better understood if we consider a Skinner box with two levers (concurrent schedules). Also, let's consider that the physical distance between the two levers represent the magnitude of the changeover delay. If the distance is very small, it is very easy for the rat to switch from one alternative to the other; as the distance increases it becomes more difficult for the rat to switch between alternatives. In a Skinner box there is always more than one behavior that may acquire reinforcement from a lever: the rat may press it with one paw, with both front paws, with variable intensity, etc. We may say that all these behaviors constitute a class of behaviors that occasionally result in reinforcement from one alternative, such as, for instance, the second target class in the computational model. In a testing chamber we may represent one response alternative not by one lever, but rather by a collection of buttons next to each other, as depicted in the top panel of Figure 12. The physical distance between the two collections of buttons (the two response alternatives) represents the changeover delay or the Hamming cliff. The first two panels of Figure 12 depict the situations in which the two target classes are separated by a Hamming distance of ten and four respectively. The third panel however, illustrates a very specific situation: that in which the two target classes are separated by a Hamming distance of four and the Hamming distance ten is included inside the second target class. Observing the figure it becomes clear that a potential effect of this setting would be to separate the second target class into two, informal classes. While some behaviors do remain close to the first target class, allowing facile switching between alternatives (mathematically illustrated by exponent values close to zero), an important proportion of behaviors become isolated from the first target class. When the behavior that acquired reinforcement is one that is close to the first alternative it will draw the organism towards indifference, due to the small barrier between the target classes. When the behavior that acquired reinforcement is one that is separated from the other target behaviors (from either target class) by the Hamming distance ten it will draw the organism towards matching. These two opposing phenomena may consequently lead to a compromise: exponent's values that are close enough to zero to indicate a severe level of undermatching and yet large enough to dispute total indifference.

Method

Assuming that this particular setting might be the cause of this phenomenon, the following modification was introduced: a different location was chosen for Hamming distance four. The purpose was to preserve the magnitude of the cliff that separates the target classes, while making sure that Hamming distance ten is not included in any of the classes. One position that meets these two conditions is between 391 and 392. In this case, the first class comprises behaviors between 351 and 391 and the second target class comprises behaviors between 392 and 432.

At the same time, a different location was chosen for Hamming distance five; in this situation the first target class comprises behaviors between 391 and 431 and the second target class comprises behaviors between 432 and 472. But Hamming distance ten is not included in any of the target classes. Therefore, a different location was chosen, between 495 and 496. In this case the second target class encompassed behaviors between 496 and 536, thus including Hamming distance ten. These two new locations were mirrored with respect to Hamming distance ten: the mirrored location for Hamming distance four is between 631 and 632 and the mirrored location for Hamming distance five is between 527 and 528. Five experiments were run for each location, giving a total of 20 experiments; the parental selection function was kept constant (μ =40).

Results and discussion

The results, depicted in Figure 13, confirmed the initial assumption: including HD 10 *inside* either of the target classes produced a slight increase in the exponent's value. When HD 10 was not included in any of the target classes the predicted, smooth pattern was observed: the value of *a* decreased dramatically when the Hamming distance between the two target classes was seven or less, varying between 0.07 and 0.14, mathematically describing total indifference.

This finding raised an interesting problem: is this phenomenon due to the presence of HD 10 in one of the target classes or is it due to the presence of a *larger* HD inside a class than the one that separates the classes? In other words, is the phenomenon caused by the absolute values of the Hamming distances or is it caused by a relation between the Hamming distance that separates the two target classes (referred from now on as HD *between*) and the largest Hamming distance found in one of the classes (referred from now on as HD *within*)?

Experimental series 3

In order to answer this question it was important to systematically investigate the effect of different HDs *within*, their mathematical relation with the different HDs *between*, and the effect of these various relations on the outcomes produced by the computational model. Positioning the two target classes at different locations made possible the manipulation of the Hamming distance that separates the classes. However, just by positioning the target classes at different locations on the continuum of integers, due to the structure of this continuum, the largest Hamming distance found inside a class is still equal for all conditions, namely six.

Method

The only way to address this research question was to manipulate the size of the target class. This allowed for a systematic manipulation of the absolute value of the largest Hamming distance found inside a class. Due to the continuum's structure, by decreasing the number of behaviors encompassed in each target class, the largest HD *within* can be indirectly decreased, as illustrated in Figure 14. When the target classes encompass 41 behaviors, the largest HD *within* is six. If we decrease the number of behaviors in each target class to 25, the largest HD *within* is five. Similarly, the largest HD *within* is four when the class size is reduced to 15 behaviors and three when each class contains only seven behaviors. In addition to the four class sizes mentioned so far (41, 25, 15, and 7), another two values were used, mainly for control purposes; in these two cases the classes included 71 and 151 behaviors respectively. A listing of all class sizes and the corresponding largest Hamming distance found in each class can be examined in Table 1. All six class sizes were tested at all nine Hamming distances between HD 9 and HD 2; this entailed 54 experimental conditions. Five experiments were run for each condition, resulting a total of 270 experiments. For each experiment the severity of the selection process was kept constant ($\mu = 40$)

Results and discussion

The results are depicted in the left panel of Figure 15. The outcomes obtained for the small class sizes are depicted in the top right panel (7, 15, and 25 behaviors). The pattern of exponents was remarkably similar to the one displayed when the classes encompassed 41 behaviors. Moreover, the exponent's values varied arround 0.8 for HD 10, were slightly smaller for HD 9, reached values of aproximatelly 0.5 for HD 8, and varied between 0.01 and 0.23 for all Hamming distances equal to or smaller than seven.

In the case of larger class sizes (71 and 151 behaviors), results followed the same pattern: *a* varied around 0.8 – 0.9 for HD 10 and HD 9, reaching a value close to 0.5 at HD 8. For the Hamming distances between seven and two, the exponent's values decreased, just as happened in the case of the traditional setting (41 behaviors in each target class); however, it did not reach the extreme small values encountered for smaller class sizes, as depicted in the bottom-right panel of Figure 15. This is not surprising when we consider the fact that the absolute number of behaviors that may acquire reinforcement when the class sizes are large is very high; successive generations of behaviors may belong to the same target class just because it is so large that, even if the behavior is not controlled by the environment, it is hard for a behavior to be very different than the previous one just through recombination and mutation. Also, the largest Hamming distance is almost always included in one of the classes. These aspects could overshadow a possible propensity towards total indifference.

It appeared that a systematic decrease in the value of the largest Hamming distance found inside a class yielded similar outcomes, both in pattern and values, as those obtained when its value was kept constant. The emergent results seem to suggest that the relation between HD *between* and HD *within* does not affect the outcomes, thus contradicting the initial hypothesis.

However, the theoretical framework (McDowell, 2004) and empirical data (McDowell et al., 2008) suggest that an important feature of the computational model is the selection process. For example, it was observed that a more severe selection process tends to generate higher exponents, while a weak selection process generates lower exponents.

Experimental series 4

As explained earlier, the parental selection function depends only on its mean; thus, the severity of the selection process is easily manipulated by modifying the function's mean. In general, smaller means are associated with higher exponents and larger means with lower exponents (McDowell et al., 2008); results obtained so far are in agreement with previous findings, as illustrated in Figure 16. In investigating different experimental conditions an interesting relation was observed: the number of behaviors that can be selected as parents is equal to three times the value of the mean, as illustrated in Figure 17. For example, when the mean is equal to 40, behaviors with fitness values greater than 120 have no chance of becoming parents and all behaviors with fitness values smaller than 120 can, in theory, be selected as parents. Therefore, regardless of the position on the continuum and of the number of behaviors in each target class, when using the traditional mean of 40 the number of behaviors that can be selected as parents is always equal to approximately 120.

In other words, by decreasing the class size and keeping the mean constant, the number of behaviors that can acquire reinforcement decreases, while the number of behaviors that can become parents remains constant. A lot of behaviors are considered “fit”, while very few behaviors are, in fact, reinforced.

Even more interesting is the fact that, in the traditional setting, the number of behaviors that can be selected as parents is approximately three times larger than the number of behaviors that constitute a target class (41 behaviors). This particular relation, between the number of behaviors that can acquire reinforcement (class size) and the number of behaviors that can be selected as parents (which depends on the mean of the parental selection function), might have contaminated the results examined in the previous experimental series. More precisely, the size of the target class was decreased, thus systematically excluding larger Hamming distances from the target classes. However, at the same time, the parental selection function mean was kept constant ($\mu = 40$), which means that the absolute number of behaviors that can become parents remained constant when the class size decreased. In other words, the number of behaviors that can acquire reinforcement becomes smaller but the number of behaviors that are considered fit remains constant, which indirectly creates weaker and weaker selection processes. Since the severity of the selection process directly influences the outcomes (McDowell, 2004; McDowell et al., 2009) it becomes obvious that this phenomenon must be isolated and studied systematically before strong conclusions can be reached.

Method

In order to control for the special relation between the class size and the mean of the parental selection function, three categories of means were selected. The first and most important one was a category called *proportional*; its purpose was to preserve the relation for each experimental condition. For each class size a mean was selected so that the number of behaviors in the target class was three times smaller than the number of behaviors that could be selected as parents. For example, for a class size of 25 behaviors, the mean that satisfies the condition is 25; for 15 behaviors the mean is 15, and its value is eight when the target classes includes seven behaviors.

In addition, given the relation between the size of the target class and the mean's value, it was important to determine if the emergent results were due to the values of the mean relative to the size of the target class (as predicted) or to the absolute values of the mean. Therefore, two other values were used for every class size and at all nine locations. A very small value of the mean ($\mu = 8$) was used to control for the general effect of a very severe selection process; a very large value ($\mu = 150$) was used to control for a very weak selection process. This experimental series was characterized by 135 new experimental conditions, thus requiring 675 additional experiments (≈ 148 million generations).

Results and discussion

In the usual setting the proportional mean is equal to the traditional mean; each target class encompasses 41 behaviors and the parental selection function mean is 40. As shown in Experimental Series 1, *a* varied around 0.8 for HD 10 and HD 9; at HD 8 the exponent was approximately 0.5, after which its value decreased significantly, reaching values close to zero for all other locations (HD 7 to HD 2). These results were very similar when the class size was reduced to 25, 15, and 7 behaviors and the parental selection function mean was kept constant ($\mu = 40$) in Experimental Series 3. The outcomes were remarkably different however when a *proportional* mean was used, as depicted in Figure 18. When the class size was 25 ($\mu = 25$), the exponent varied around

0.8 for HD 10, HD 9, and HD 8; it was approximately 0.35 at HD 7, and it was close to zero for all other locations. When the class size was 15 ($\mu = 15$), *a* was close to 0.8 for HD 10, HD 9, HD 8, and HD 7; its value declined to 0.28 for HD 6, and was very close to zero for all other locations. The identical trend was found when the class size was 7 ($\mu = 7$), with one important difference: *a* varied around 0.8 for HD 10, HD 9, HD 8, HD 7, and HD 6, after which it declined considerably, as depicted in Figure 18.

An important aspect needs to be restated: the size of the target class was decreased so that the largest Hamming distance inside a class decreases as well. The reason was to investigate the relation between the Hamming distance that separates the two target classes (HD *between*) and the largest Hamming distance that is found inside a target class (HD *within*). In the traditional situation (41 behaviors in each target class) the largest Hamming distance inside a class is HD 6, regardless of their position on the continuum of integers from 0 to 1023. When the size of the target classes is decreased to 25, the largest Hamming distance inside a class is HD 5; the largest one is HD 4 for 15 behaviors and HD 3 for 7 behaviors in each target class.

When examining the relation between HD *between* classes and HD *within* classes, it can be observed that the difference between the two, at HD 10, is four, when the class size comprises 41 behaviors; five, when the class size comprises 25 behaviors, six, for 15 behaviors, and seven for 7 behaviors. In other words, as the size of the target class decreases, the difference between HD *between* and HD *within* increases. In this light, when we closely examine the results presented above, we observe that basically the exponent varied around 0.8 only when the difference between *HD between* and *HD within* was equal to or larger than three; exponents' values are depicted in Table 2. As depicted in Figure 19, when the difference was equal to or larger than three, the exponent's values clustered around 0.8; when the difference was smaller than two, *a* varied between 0.07 and 0.35, its values clustering around 0.1 (average = 0.13, SD = 0.07). In other words, it becomes apparent that in order to obtain good matching the distance between the Hamming distance that separates the target classes and the largest Hamming distance found within a class must be equal to or larger than three. This condition is remarkably similar to the proper use of a changeover delay in experiments with live organisms: the magnitude of the COD must exceed a certain value (threshold) in order to obtain good matching; below this threshold[5] the organism is pulled towards indifference. The findings presented so far seem to be robust; however, there are three important issues that need to be addressed before strong conclusions can be formulated. First, results should be identical to the *left* and to the *right* of Hamming distance ten. Second, it must be determined if a weak selection process is sufficient to produce very low exponents; more precisely, it must be determined if a systematic increase in the parental selection function mean is associated with a systemic decrease in the exponents' values. This would explain why keeping the severity of the selection process constant while decreasing the class size (Experimental Series 3) resulted in low exponents' values. Third, it becomes apparent that only two conditions must be met in order to obtain good matching: the difference between HD *between* and HD *within* must be equal to or larger than three and the mean of the parental selection function must be approximately equal to the number of behaviors encompassed in each target class. Therefore, a different

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[5] The threshold does not have a certain absolute value; it s magnitude depends on a variety of factors, like species, schedules of reinforcements that are in use, the type of COD, etc..

experimental condition must be investigated, one that was not studied so far and which satisfies the aforementioned conditions.

Experimental series 5

In order to study the effect of Hamming distance (HD) on the results produced by the computational model, the two target classes in Experimental Series 1 were placed along the continuum of integers from 0 to 1023 so that the Hamming distance between the two target classes was 10, 9, 8, 7, 6, 5, 4 ,3, and 2. This way, there were 9 locations that were investigated: the traditional location (between 511 and 512) and 8 other locations; they were all situated to the left of HD 10 (HD 10 = Hamming Distance 10), between 0 and 511. In order to verify that the results are robust, these 8 specific locations were mirrored with respect to HD 10; all locations are depicted in Figure 8. In the first experimental series, all conditions were tested and results obtained at the *left* were almost identical with those obtained at the *right*. However, two new variables were added afterwards, the size of the target class and the parental selection function mean.

Method

Given that the structure of the continuum is perfectly symmetric with respect to HD 10 and the first experimental series yielded almost identical outcomes at the *left* and the *right* of HD 10, it was considered unnecessary to replicate each experimental condition (192 experimental conditions, each requiring 5 experiments). Instead, 61 experimental conditions were randomly selected and tested at the *right* of HD 10; the outcomes were then compared with their homologues at the *left*. Five experiments were run for each condition, giving a total of 305 experiments (≈.67 million generations).

Results and discussion

The parameter of interest was the exponent, since it is the most affected and most informative of the obtained values. The correlation between the two sets of data was very strong and positive ($r^2 = 0.99$, $p < 0.01$). An illustration of the results can be examined in the two panels of Figure 20. From these data we can conclude that there were no significant differences between the *left* and *right* situations, thus we do not need to mirror all 192 experimental conditions; results were robust with respect to the location used: at the *left* or the *right* of the largest possible Hamming distance, ten.

Experimental series 6

The fourth series of experiments suggested that in order to obtain results similar to those observed in experiments with live organisms two conditions must be met: the difference between HD *between* and the largest HD *within* must be equal to or larger than three; in addition, the parental selection function mean must be relatively proportional with the number of behaviors in each target class (e.g. target class = 15 behaviors, mean ≈ 15).

An important question is why this pattern was not observed in the 3rd experimental series, when the mean of the parental selection function was kept constant and the size of the target class was systematically decreased. As shown before, smaller means yield larger exponent values, while larger means are associated with smaller values. Therefore, the argument is that even for situations in which the difference between *HD between* and *HD within* was equal to, or larger than three, the mean was large enough to keep the exponent at low values. The data accumulated thus far seem to suggest that this is the case; however, in the current form, it does not provide enough evidence for strong conclusions.

Method

In order to verify that this phenomenon is indeed caused by large values of the parental selection function mean (weak selection process) more experiments were needed, with more values of the mean, at the same HD location. If the argument described above is indeed correct, we should observe a gradual decline in the exponent's value, as the mean increases (a large mean describes a weak selection process); in addition, the effect should appear regardless of the size of the target classes and the locations used. Therefore, a class size of 25 behaviors was placed at HD 10, HD 9, and HD 8. For this class size, at all three locations, 14 different values for the parental selection function mean were used: 8, 25, 40, 50, 70, 90, 110, 130, 150, 190, 230, 250, 275, and 300. Five experiments were run for each of the 42 locations, requiring a total of 210 experiments (≈ 46 million generations).

Results and discussion

For all three locations the same pattern was observed and is illustrated in Figure 21. The exponent declined from values close to 0.85 to values close to zero. Another noteworthy aspect is that *a* declined faster as the difference between *HD between* and *HD within* became smaller. A closer look at the actual values of *a* indicates that the exponent's value was noticeably below 0.8 when the mean of the parental selection function was about two or three times larger than the number of behaviors in each target class. In other words, the exponent's values decreased gradually as the mean increased; the decline was more rapid as the difference between *HD between* and *HD within* became smaller. These findings provide support for the idea that in the third experimental series the lack of noticeable results was due to the fact that the parental selection function mean was kept constant, while the number of behaviors in each class was decreased considerably.

Experimental series 7

In Experimental Series 4 it was shown that in order to obtain results similar to those observed in experiments with live organisms the absolute value of the Hamming distance that separates the two target classes is not crucial. The only two conditions that must be satisfied are: the difference between HD *between* and HD *within* must be equal to or larger than three and the parental selection function mean must be approximately equal to the number of behaviors encompassed by each target class. This phenomenon seems to be robust; however, in order to accept it as a general rule, it must be encountered in all experimental settings that satisfy these two conditions.

Method

Testing this rule required a setting in which the difference between *HD between* and *HD within* is equal to three and the mean of the parental selection function is proportional to the size of the target class. Evidently, this experimental condition must be different than those in which the phenomenon was previously observed. Until now, exponents with values close to 0.8 were encountered in all the locations from HD 10 to HD 6 (7 behaviors, mean 8, $a = 0.72$). Therefore, potential locations of interest are HD 5 and HD 4. These two are the only locations that can be examined; HD 3 would require that the Hamming distance inside a class is zero, which is impossible because the Hamming distance, by definition, cannot be zero. In the first condition, when the classes are separated by HD 5, the largest Hamming distance inside a class must not be larger than two. Therefore, given the way in which the Hamming cliffs are distributed throughout the continuum, the number of behaviors in each target class must be reduced to three. In the second condition, when the classes are separated by HD 4, the largest Hamming distance inside a class must not be larger than one. Therefore, the number of behaviors in each target class must be reduced to two. The parental selection function mean must be proportional to the number of behaviors in each target class; therefore, the values used were three and two respectively. A noteworthy fact is that these parameters have never been used before: they were considered much too extreme to produce acceptable results. The two conditions (class size = 3 behaviors and class size = 2 behaviors) were tested at all nine locations: HD =10 through HD = 2. Five experiments were run for each of the 18 locations.

Results and discussion

Results are depicted in Figure 22 and Table 3. For the first condition (class size = 3), when the difference between *HD between* and *HD within* was three (at HD 5) the exponent was close to 0.8 ($a \approx 0.79$), as expected. At HD 4, when the difference was two, the exponent's value ($a \approx 0.53$) was extremely similar to the other conditions in which the difference was two. At HD 3 and HD 2 the exponent varied around 0.2. For all the locations from HD 6 through HD 10, a was situated around 0.8. As shown in Table 3, the bias parameter varied around unity, which is typical for symmetrical choice environments.

For the second condition (class size = 2), when the difference between *HD between* and *HD within* was three (at HD 4) the exponent was close to 0.8, as expected ($a \approx 0.86$). At HD 3, when the difference was two, the exponent's value ($a \approx 0.61$) was extremely similar to the other conditions in which the difference was two. At HD 2 the value of *a* approached 0.2. For all locations from HD 5 to HD 10 *a* varied around 0.8. The bias parameter varied around unity, which is typical for symmetrical choice environments. Furthermore, when examining the number and pattern of the changeovers in relation to the proportion of reinforcement on the first alternative we encountered the exact same phenomena as in previous experiments: the frequency of COs increased dramatically when the difference between HD *within* and HD *between* was smaller than 3, as illustrated in Figure 23. In addition, the pattern indicated that when reinforcement was obtained almost exclusively from one alternative the organism switched most often.

Results presented so far constitute a solid argument for the idea that the exponent varies around 0.8 only when the difference between the Hamming distance that serves as boundary and the largest Hamming distance inside a class is equal to, or larger than three, and the parental selection function mean is approximately equal to the number of behaviors encompassed by each target class. A frequency distribution of all *a* values obtained in such settings is shown in the top panel of Figure 24. The middle panel illustrates the distribution of exponents when the difference between HD *between* and HD *within* is smaller than three. Also, a frequency distribution of the bias parameters' values is depicted in the bottom panel of Figure 24.

General discussion

An important aspect that characterizes McDowell's computational model (2004) is that it uses binary strings to represent behaviors' genotypes; this raises the important issue of the Hamming distance (Hamming, 1950), which is the number of bits that must be changed in a string in order to obtain a different string of equal length. McDowell and colleagues (2008) hypothesized that in concurrent-schedule environments the Hamming distance that separates the two target classes may be the computational equivalent of the changeover delay used in experiments with live organisms (Findley, 1958). The continuum of integers from zero to 1023 does not allow us to directly manipulate the Hamming distance; however, we can do so by placing the target classes at different locations on the continuum.

When the Hamming distance that separated the two target classes was ten or nine, the exponent varied around 0.8, indicating the typical level of undermatching displayed by live organisms (Myers & Myers, 1977; McDowell, 1989; McDowell & Caron, 2006). At HD 8 *a* decreased significantly (≈ 0.5) and reached values close to zero for all other locations (HD 7 through HD 2), mathematically describing a very strong tendency towards total indifference (Baum, 1979; Davison & McCarthy, 1988; McDowell, 1988). These findings are consistent with results obtained with live organisms, results that indicate that below a certain COD value the organism is drawn towards indifference, mathematically described by exponent values close to zero (Shull & Pliskoff, 1967; Davison & McCarthy, 1988; Temple, Scown, & Foster, 1995).

Another important phenomenon observed when the Hamming distance that separates the two target classes was equal to or smaller than seven, was the remarkable change in the pattern and frequency of changeovers. For Hamming distances ten and nine the pattern was typical, indicating that when reinforcements were acquired almost exclusively from one alternative the number of changeovers was rather small; when reinforcements were obtained equally from both alternatives, the organism switched most often. The complete opposite pattern was observed for Hamming distances equal to or smaller than seven, indicating that when reinforcements were obtained almost exclusively from one alternative the organism switched most often between alternatives. Also, in these situations, the number of changeovers was approximately ten times higher than for Hamming distances ten and nine (Figure 11). In other words, when the two target classes were separated by Hamming distance ten or nine the results depicted the typical level of undermatching and the classic pattern in changeovers. When the Hamming distance was equal to or smaller than seven, the exponent depicted a strong tendency towards total indifference and the number of changeovers was extremely high.

The second experimental series suggested that the relation between the Hamming distance that separates the target classes (HD *between*) and the largest Hamming distance found inside a class (HD *within*) may also affect the outcomes. Results obtained in the third and fourth experimental series showed not only that the relation between HD *between* and HD *within* is important, thus emphasizing the relative value of the Hamming distance, but also that it plays a decisive role in obtaining results similar to those observed in live organisms. Moreover, it was shown that desirable outcomes are obtained when the difference between the two Hamming cliffs (HD *between* minus HD *within*) was equal to or larger than three and the mean of the parental selection function was approximately equal to the number of behaviors included in each target class. The rule mentioned above was tested using two extreme experimental conditions: a class size of three behaviors with a mean of three and a class size of two behaviors with a mean of two. Despite the very extreme parameters, results were remarkably similar with those encountered in previous situations both in pattern and value, as depicted in Figure 22, providing strong support for the findings previously mentioned.

The occurrence of this phenomenon in all experimental conditions, corroborated with results that indicate perfect symmetry between the two halves of the continuum (Figure 20) and with the fact that, for any given experimental series, the probability of non-random residuals is extremely close or equal to zero (Table 4), constitute evidence that the phenomenon may be accepted as a general rule. In order to obtain results similar to those observed in experiments with live organisms, the difference between the Hamming distance that separates the target classes and the largest Hamming distance found inside a class must be equal to or larger than three and the parental selection function mean must be approximately equal to the number of behaviors included in each target class. A noteworthy aspect is that the rule strongly emphasizes the relative values of all parameters involved (the Hamming cliffs, the size of the target classes, and the severity of the selection process) and not their absolute values. The initial question is thus answered: HD 10, by itself, is neither necessary nor sufficient: good results may be obtained in many conditions with a variety of parameters.

Not only is HD 10 not important by itself, but the fact that a certain difference (three) is necessary for obtaining results similar with those displayed by live organisms, corroborated with the fact that similar results are obtained even when the difference is very large (e.g. in the most extreme case, class size = 2, the largest difference is nine) are consistent with the large body of data involving experiments with live organisms in which changeover delays were used (Shull & Pliskoff, 1967; Temple, Scown, & Foster, 1995).

Limitations and future directions

Understanding the role and effect of Hamming distances constitutes an important step; however, even if we know what the effects are and how they can be manipulated, this still does not refute the fact that their existence imposes certain restrictions on the model. For example, it would be hard to test the organism in a free-choice environment with more than two alternatives. Also, the use of a proper, completely flexible changeover delay remains problematic. An elegant solution that would bypass these issues would be the implementation of the reflected binary code, also known as Gray code (Gray, 1947; Russell & Norvig, 2003), as suggested by McDowell (2008). The Gray code is a binary numeral system in which two successive values differ in only one bit, thus making the Hamming distance irrelevant (since it is equal to one throughout the continuum).

Conclusion

The extreme low values of the exponent that describe situations in which the difference between the Hamming distance that separates the target classes and the largest Hamming distance inside a class is lower than three, the pattern and absolute number of changeovers that accompany these situations, and the fact that the phenomenon can be replicated even with extreme parameters, together provide strong support for the conclusion that the Hamming distance is indeed the computational equivalent of the changeover delay used in experiments involving live organisms. Furthermore, this vast body of data shows that the results produced by the computational model are not caused by conveniently positioning the two target classes so they are separated by the largest Hamming distance (ten), but they emerge from the rules that govern the computational model: the Darwinian laws of selection, recombination, and mutation. These findings are consistent with and build on previous research (McDowell, 2004; McDowell and Caron, 2007; McDowell et al., 2008), providing further support for the robustness of McDowell's computational model of selection by consequences as a valid account of the dynamics of instrumental behavior.

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Table 1.

The list of class sizes used in the current project and largest Hamming distance found inside each class.

Class size	Largest HD *within*
151 Behaviors	HD 8
71 Behaviors	HD 7
41 Behaviors	HD 6
25 Behaviors	HD 5
15 Behaviors	HD 4
7 Behaviors	HD 3
3 Behaviors	HD 2
2 Behaviors	HD 1

Table 2.

When using a proportional mean, the exponent varies around 0.8 as indicated by shading, only when the difference between HD between and HD within is larger than or equal to three.

Class size	HD *between*	Largest HD *within*	HD *between* - HD *within*	a
41	HD 10	6	4	0.87
41	HD 9	6	3	0.79
41	HD 8	6	2	0.50
41	HD 7	6	1	0.14
41	HD 6	7	-1	0.09
41	HD 5	7	-2	0.09
41	HD 4	10	-6	0.16
41	HD 3	10	-7	0.07
41	HD 2	10	-8	0.07
25	HD 10	5	5	0.79
25	HD 9	5	4	0.81
25	HD 8	5	3	0.75
25	HD 7	5	2	0.35
25	HD 6	5	1	0.09
25	HD 5	7	-2	0.11
25	HD 4	6	-2	0.07
25	HD 3	6	-3	0.09
25	HD 2	6	-4	0.09
15	HD 10	4	6	0.78
15	HD 9	4	5	0.80
15	HD 8	4	4	0.81

15	HD 7	4	3	0.71
15	HD 6	4	2	0.28
15	HD 5	4	1	0.10
15	HD 4	6	-2	0.13
15	HD 3	6	-3	0.18
15	HD 2	6	-4	0.23
7	HD 10	3	7	0.82
7	HD 9	3	6	0.77
7	HD 8	3	5	0.74
7	HD 7	3	4	0.80
7	HD 6	3	3	0.72
7	HD 5	3	2	0.33
7	HD 4	3	1	0.10
7	HD 3	6	-3	0.15
7	HD 2	6	-4	0.35

Table 3.

Results obtained when the class size is reduced to three and two behaviors; the parental selection function mean is three and two respectively (proportional). The grey cells represent the situation in which the difference between HD between and HD within equals 3, at HD 5 and HD 4 respectively.

3 behaviors				2 behaviors			
HD	a	b	pVAF	HD	a	b	pVAF
10	0.91	1.01	0.85	10	0.81	1.01	0.90
9	0.82	0.97	0.88	9	0.96	0.93	0.83
8	0.82	1.08	0.90	8	0.89	0.96	0.92
7	0.81	0.92	0.92	7	0.89	1.04	0.87
6	0.81	1.05	0.81	6	0.90	0.91	0.82
5	0.81	0.99	0.82	5	0.87	0.94	0.78
4	0.58	0.95	0.73	4	0.86	1.04	0.76
3	0.18	0.95	0.34	3	0.61	1.11	0.68
2	0.21	1.08	0.46	2	0.27	0.96	0.44

Table 4

Results of the Reich test as an analysis of residuals.

Reich test for the analysis of residuals

H_0: x or more sets of residuals are random

H_1: x or more sets of residuals are not random

Experimental Series	Total (n)	Fail (x)	Signifficant ($\alpha = 0.05$)	p
1	85	3	No	1.00
2	20	0	N/A	N/A
3	275	17	No	1.00
4	675	19	No	1.00
5	305	33	No	1.00
6	140	6	No	1.00
7	90	3	No	1.00

Figure Captions

Figure1. The left column depicts the equations that form the Matching Theory; they are all derived from the first equation, discovered by Herrnstein (1961). This family of equations constitutes the Classic Theory of Matching. The right column of the table depicts the new form of the equation, after introducing the two new parameters: *b* (bias) and *a* (undermatching). These equations form what is called the Modern Theory of Matching (McDowell, 2005). At this point, for single-alternative environments researchers use the classic theory equation (Eq. 2); for concurrent-schedules environments researchers use the modern version of the equation (Eq. 5). A detailed analysis of the classic and modern theories was conducted by McDowell (1986, 2005). [Figure reprinted with permission of author (McDowell, 2005, p. 112).]

Figure 2. Recombination and Mutation. The two parents are 340 and 117. The bitwise recombination method entails that each slot in the child's string has a 50% chance of being the bit of one parent and a 50% chance of being the bit of the other parent. In our example 7 bits are the same in both parents, so they will be the same in the child. Based on a 50-50 chance, the program selects the remaining three bits at random; in our example bit 2 and bit 5 come from the left-side parent and bit 10 from the right-side parent; the resulting behavior is 341 (the changed bits are in bold). This progeny is also affected by mutation: each bit has a 10% chance of being flipped and, in our example, the bit affected by this process is the third bit in the string (in bold) – it is flipped from 0 to 1, the resulting behavior being 469. Recombination and Mutation ensure variability in the population.

Figure 3. Fitness values. The fitness of each behavior is defined as the absolute distance between the behavior's phenotype and the phenotype of the midpoint of the target class from which the previously reinforced behavior originated. This way of calculating fitness values is referred to as *midpoint fitness*. The figure illustrates an example in which the reinforced behavior originated in a target class that extends from phenotype 512 to phenotype 552. The midpoint of this class is 532. Three behaviors are considered in this example, namely 95, 390, and 817, and the fitness value of each of them is illustrated in the figure. The smallest fitness value represents the fittest behavior because, as we can see, it is closest to the midpoint of the target class.

Figure 4. The figure illustrates the functionality of McDowell's Computational Model of Selection by Consequences (version 2.0). In the beginning of the experiment a population of 100 behaviors is randomly selected from the integers between 0 and 1023. One behavior is randomly selected from this population and it constitutes the first emission in the experiment. If the emitted behavior is not part of the target class or is part of the target class but reinforcement is not available, then parents are selected at random from the existing population. They reproduce and the new population of children is affected by mutation. A new behavior is emitted at random from the mutated population. If reinforcement occurs, then the program calculates the fitness value of each behavior in the population. A parental selection fitness function is used to assign greater probabilities of being selected as parents to fitter behaviors. Therefore, the parents are no longer selected at random, but are selected based on their fitness. They reproduce and the population of children is affected by mutation. From this population a new behavior is randomly emitted. The procedure typically continues for 20,000 emissions. The basic

Darwinian rules of selection, recombination, and mutation are depicted in boxes with grey backgrounds.

Figure 5. The relation between Changeovers and the proportion of reinforcement on the first alternative of a concurrent schedule (data generated by McDowell's computational model). In the left panel are results obtained when the two target classes were separated by a Hamming distance of 10. In this case we observe the pattern typical of live organisms: the number of changeovers increased as the proportion of reinforcement on the first alternative increased from 0 to 0.5, after which it decreased as the proportion of reinforcement on the first alternative increased from 0.5 to 1. This pattern indicates that when the reinforcements were acquired almost exclusively from one alternative the number of changeovers was smaller; when reinforcements were obtained equally from both alternatives, the number of changeovers increased. [Figure reprinted with permission of author (McDowell et al, 2008).] The exact opposite pattern is depicted in the right panel, when the Hamming distance that separates the two target classes was 6. The only parameter that varied in the two experiments is the Hamming distance. Also, note the very large difference in the rates of changeovers between the two conditions, regardless of the proportion of reinforcement on the first alternative; when the Hamming distance that separates the target classes was ten, the maximum number of changeovers per 500 generations varied around 7. When the Hamming distance was six, the maximum number of changeovers per 500 generations varied around 90.

Figure 6. The figure depicts the relation between the mean of the linear parental selection function and the probability density associated with a behavior having a given fitness of becoming a parent. For smaller means the process of selection is more severe than for

larger means. The intersection between a line and the *x*-axis represents the largest possible fitness value that has a chance of becoming a parent; all values greater than this have zero chance of being selected. For example, when the mean is 7, behaviors with fitness values greater than 21 have no chance of being selected as parents. The figure also captures an important feature of the selection process: behaviors with smaller fitness values have a greater chance of becoming parents.

Figure 7. The figure illustrates how Equations 3, 4, and 8 (the last two being versions of Equation 3) are applied to data obtained from concurrent schedules. Equation 3 is fitted in the top panel (the original form), Equation 4 is fitted in the middle panel (the ratio form), and Equation 5 (the logarithmic transformation of Equation 4) is fitted in the bottom panel. In the last case *a* is the slope of the line and depicts the phenomena of under- and overmatching: a slope greater than 1 depicts overmatching and a slope smaller than 1 depicts undermatching; in this example the slope is 0.81, depicting the level of undermatching typically encountered in experiments with live organisms. In the same panel *log b* is the *y*-intercept, therefore *b* is $10^{\text{INTERCEPT}}$. A deviation of *b* from unity reflects an asymmetry between alternatives; a value larger than one (positive intercept) indicates a preference towards the 1st alternative and a value smaller than one (negative intercept) indicates a preference towards the 2nd alternative; in this example b = 0.83, indicating a preference towards the second alternative.

Figure 8. The top panel illustrates the position of Hamming distances to the left of the largest possible Hamming distance – ten (between 511 and 512). Each column in the chart represents the boundary between two target classes. The integers and their

corresponding binary representations are depicted for all 9 distances. The bottom panel illustrates the position of Hamming distances to the right of the largest possible Hamming distance. These were obtained by mirroring the positions in the left, with respect to the Hamming distance of ten.

Figure 9. The figure illustrates the position of all 17 Hamming distances, in the order in which they appear in the range of integers from 0 to 1023; it also depicts the perfect symmetry with regard to the largest Hamming distance (ten – between 511 and 512).

Figure 10. Values of the exponent and bias parameter when using the traditional setting: 41 behaviors in each target class and a parental selection function mean of 40. The top panel of the figure depicts the values of *a* when different Hamming distances served as boundaries between the target classes. For the traditional setting all locations were mirrored with respect to HD 10. The bottom panel illustrates the values of the bias parameter, *b*; it varied around unity, an expected outcome since all experiments involved symmetrical-choice environments.

Figure 11. The change in pattern and number of changeovers, as the Hamming distance that separates the two target classes decreased. The trendlines are quadratic polynomials, as used by McDowell (2004). The aspects of interest are the change in the pattern of changeovers and the very large increase in the absolute number of changeovers (as averaged per 500 generations blocks). The figure omits the conditions in which the Hamming distance between the classes had values between seven and two (six, five, four, and three); they were very similar, in values and pattern, with the conditions in which the Hamming distance that separates the classes was equal to seven and two, respectively.

Figure 12. The top panel illustrates the situation in which two target classes, each encompassing a number of behaviors, were separated by Hamming distance ten. In an experiment with living organisms the different behaviors that constitute a target class may be regarded as different modes of pressing a lever, while the physical distance between the two levers represents the changeover delay; as the changeover delay decreases it becomes easier (and more likely)for the organism to switch between alternatives. The second panel illustrates the situation in which the Hamming distance that separates the two target classes is four, represented here by a smaller physical distance between the two alternatives. The third panel depicts a special situation, in which the two target classes are separated by hamming distance four and the second target class includes Hamming distance ten.

Figure 13. The effect of including HD 10 in one of the target classes. When small Hamming distances separate the two target classes and HD 10 is included in one of the classes we observe a small but noticeable increase in the value of the exponent. Keeping the Hamming distance between the classes equal to four, but positioning the classes at another location, so that neither of them encompasses HD 10, the phenomenon does not appear (top panel). When the target classes were separated by Hamming distance five, HD 10 was not included in any of the classes and the value of *a* was the expected one (very close to zero). The two target classes were positioned so that the target classes at a different location, so that HD 10 was included in one of the classes: the result is depicted in the bottom panel. This process was repeated for the mirrored locations as well (to the right), yielding the same outcome.

Figure 14. As the size of the target class decreases, the largest Hamming distance included in a class decreases as well. The example refers to the second target class, when the two target classes are separated by Hamming distance eight.

Figure 15. Values of the exponent at different class sizes. The left panel illustrates the results obtained for all six class sizes, at all nine Hamming distances. The top right panel illustrates only the values associated with class sizes smaller than 41. The bottom right panel shows the exponents' values associated with class sizes of 41, 71, and 151 behaviors. In all three panels the *x*-axis represents the value of the Hamming distance that separates the two target classes (HD *between*).

Figure 16. Comparison between exponents' values when using different means for the parental selection function. Results are congruent with previous research (McDowell et al., 2008): stronger selection processes yield higher exponents' values.

Figure 17. The relation between fitness value and the severity of the parental selection process. The four panels illustrate that the largest fitness value (least fit behavior) that can be selected as parent is equal to approximately three times the value of the mean. For example, when the mean is 15 (bottom-left panel), the largest fitness value that can be selected is approximately 45.

Figure 18. Comparison between values of *a* when using the traditional mean of 40 with values of *a* when using a proportional mean, for all class sizes and at all Hamming distances. The upper left panel illustrates only the traditional setting; let it be noted that when using a mean of 40 the values of the exponent vary around 0.8 only for HD 10 and HD 9, regardless of the number of behaviors in the target class. When using a proportional mean the values of the exponent vary around 0.8 for HD 10, HD 9, and HD

8 (bottom left panel). The top right panel shows that when the target class encompasses 15 behaviors the exponent varies around 0.8 for HD 10, HD 9, HD 8 and HD 7. The bottom right panel illustrates results obtained when the class size is reduced to seven behaviors: the exponent's values remain close to 0.8 for HD 10 through HD 6 (inclusive).

Figure 19. The distribution of exponents when using a proportional mean at class size 41, 25, 15, and 7 (combined). The left panel illustrates the frequency of exponents obtained when the difference between the Hamming distance that separates the two target classes and the larger Hamming distance inside a class is equal to or larger than three. The right panel illustrates the frequency of exponents obtained when the difference between the Hamming distance that separates the two target classes and the larger Hamming distance inside a class is smaller than 2.

Figure 20. Values of the exponent when the target classes are situated to the left and to the right with respect to HD 10. Sixty-one random locations situated to the left of HD 10 were mirrored to the right of HD 10. The top panel of the figure depicts the correlation between the two data sets. The bottom panel depicts the same relation but in a different visual way.

Figure 21. The gradual decline in the exponent's value as the mean increases. The decrease is more rapid as the difference between HD *between* and HD *within* decreases. The class size of 25 behaviors includes a HD 5, therefore the abovementioned difference is 5, for HD 10, 4, for HD 9, and three, for HD 8.

Figure 22. Values of the exponent, *a*, when the two target classes encompass 41, three and two behaviors; the parental selection function mean is proportional, namely 41, three, and two. The noteworthy aspect is that even with such extreme parameters, when the

difference between HD *between* and HD *within* is equal to three (at HD 9, HD 5, and HD 4 respectively) the exponent is close to 0.8. It decreases noticeably when the difference is two (ranging between 0.5 and 0.6) and reaches values close to zero when the difference is smaller than two. Also, regardless of how much the difference increases, the exponent still varies around 0.8.

Figure 23. The relation between changeovers and the proportion of reinforcement on the first alternative of a concurrent schedule, when the target classes comprise three behaviors (left panel) and two behaviors (right panel). In both cases a proportional mean was used ($\mu = 3$ and 2). In both cases we observe the same phenomenon illustrated in Figure 5. When the difference between HD *between* and HD *within* is larger than three we observe the pattern typical of live organisms: the number of changeovers increases as the proportion of reinforcement on the first alternative increases from 0 to 0.5, after which it decreases as the proportion of reinforcement on the first alternative increases from 0.5 to 1. This pattern indicates that when the reinforcements are acquired almost exclusively from one alternative the number of changeovers is smaller; when reinforcements are obtained equally from both alternatives, the number of changeovers increases. The exact opposite pattern is observed when the difference between HD *between* and HD *within* is one. This change in pattern and number of COs is associated with a substantial decrease in the exponent's value, emphasizing once more the relation between HD *between* and HD *within* and not the absolute values of the Hamming distances.

Figure 24. Frequency distributions of the exponent and the bias parameter. The top panel illustrates the frequency distribution of *a* when the difference between the Hamming

distance that separates the target classes and the largest Hamming distance inside a class is equal to or larger than three. The middle panel depicts the frequency distribution of *a* when the aforementioned difference is smaller than three. The bottom panel presents the frequency distribution of the bias parameter, *b*.

Figure 1

Classic	*Modern*
(1) $\frac{R_1}{R_1+R_2}=\frac{r_1}{r_1+r_2}$	(5) $\frac{R_1}{R_2}=b\left(\frac{r_1}{r_2}\right)^{a}$
(2) $R=\frac{kr}{r+r_e}$	(6) $R=\frac{kr^a}{r^a+\frac{r_e^{\,a}}{b}}$
(3) $R_1=\frac{kr_1}{r_1+r_2+r_e}$	(7) $R_1=k\left[\frac{1}{b_{1e}}\left(\frac{r_e}{r_1}\right)^{a_{1e}}+\frac{1}{b_{12}}\left(\frac{r_2}{r_1}\right)^{a_{12}}+1\right]^{-1}$
(4) $R_2=\frac{kr_2}{r_1+r_2+r_e}$	(8) $R_2=k\left[\frac{1}{b_{2e}}\left(\frac{r_e}{r_2}\right)^{a_{2e}}+b_{12}\left(\frac{r_1}{r_2}\right)^{a_{12}}+1\right]^{-1}$
	(9) $\frac{R_1}{R_2}=\frac{1}{b_{2e}}\left(\frac{r_e}{r_2}\right)^{a_{2e}}b_{1e}\left(\frac{r_1}{r_e}\right)^{a_{1e}}$

Figure 2

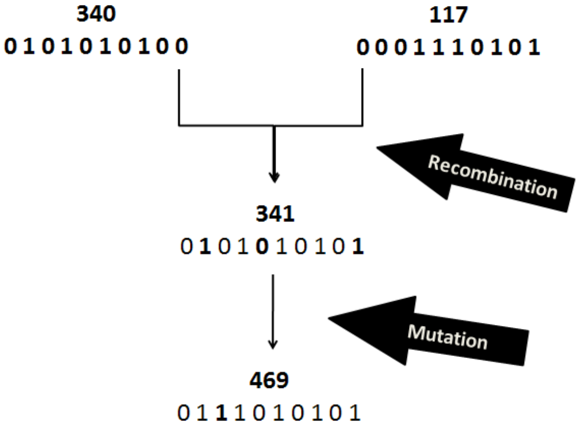


Figure 3

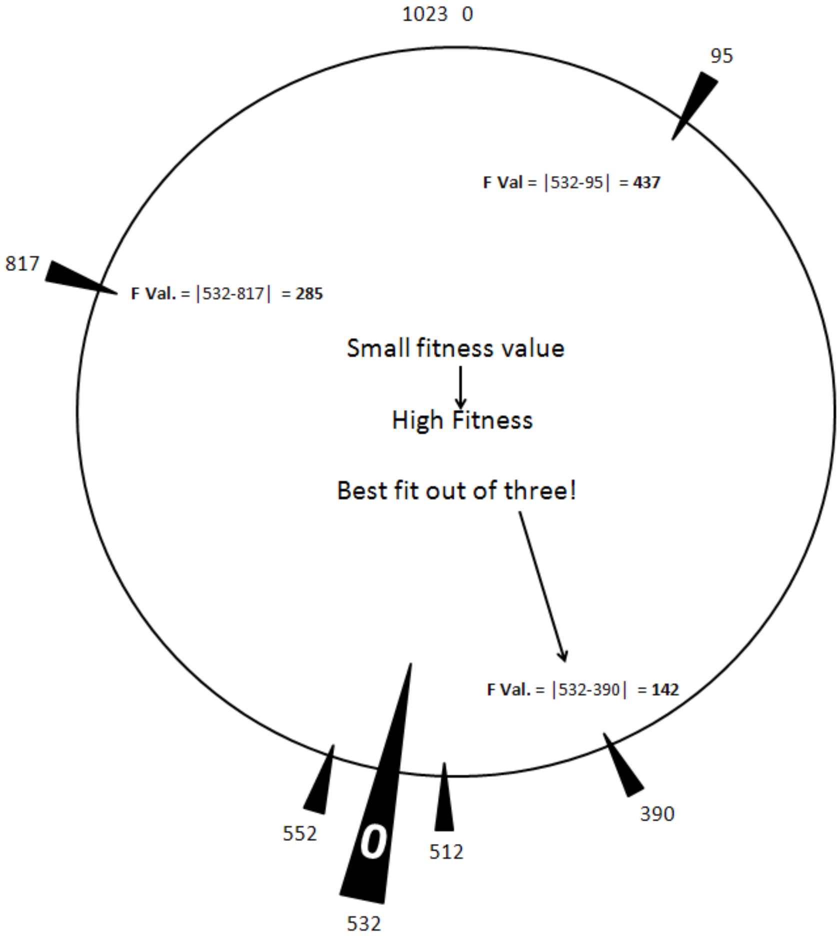


Figure 4

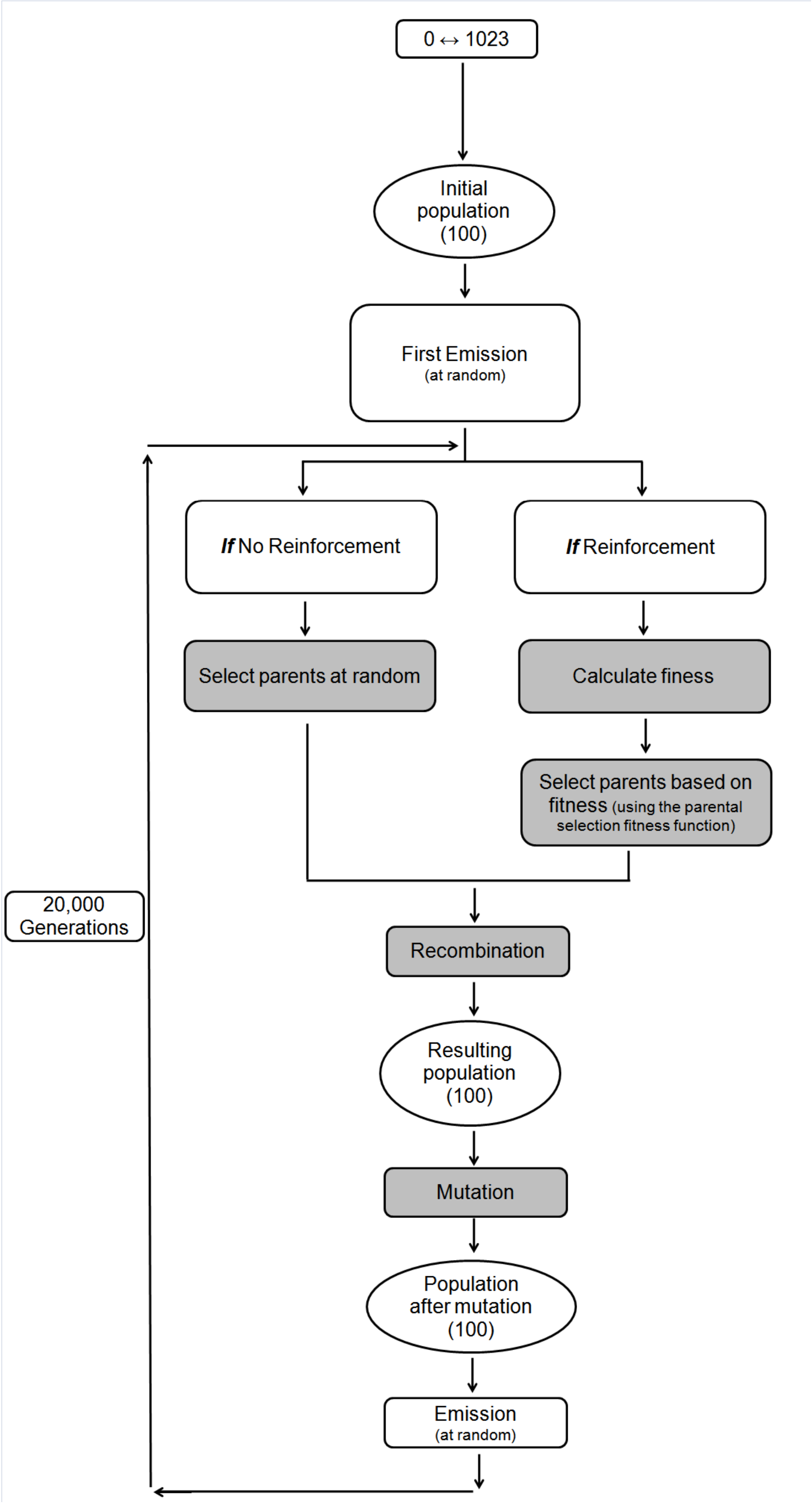

0 ↔ 1023
Initial population (100)
First Emission (at random)
If No Reinforcement
If Reinforcement
Select parents at random
Calculate finess
Select parents based on fitness (using the parental selection fitness function)
Recombination
Resulting population (100)
Mutation
Population after mutation (100)
Emission (at random)
20,000 Generations

Figure 5

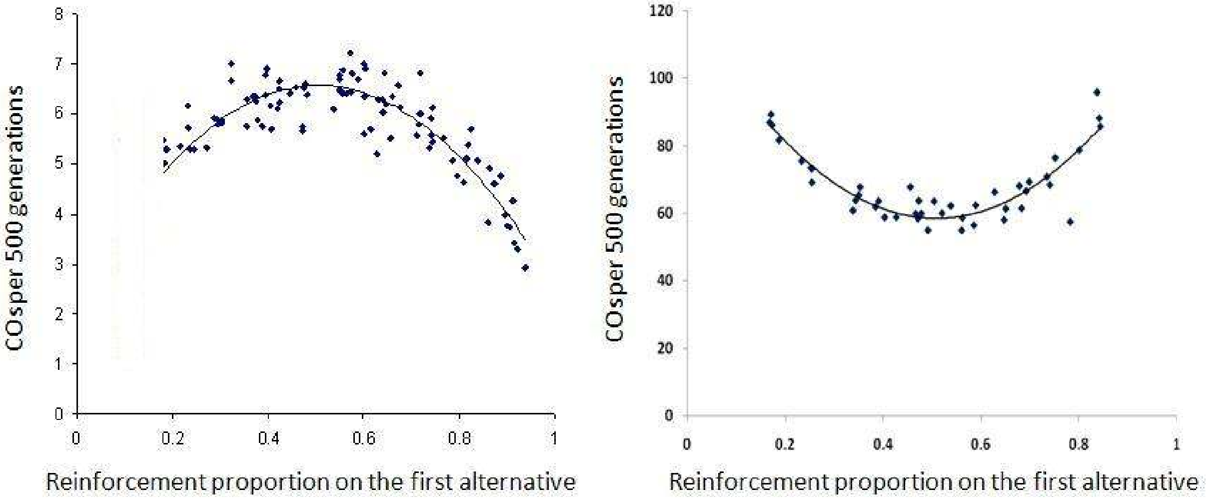


Figure 6

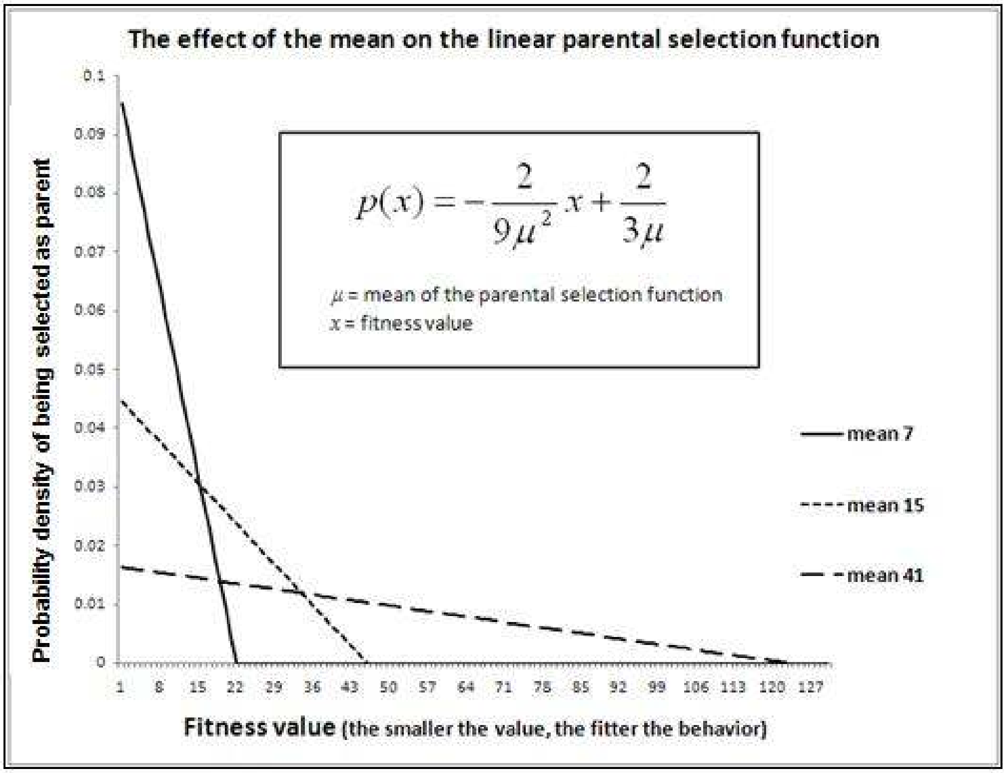


Figure 7

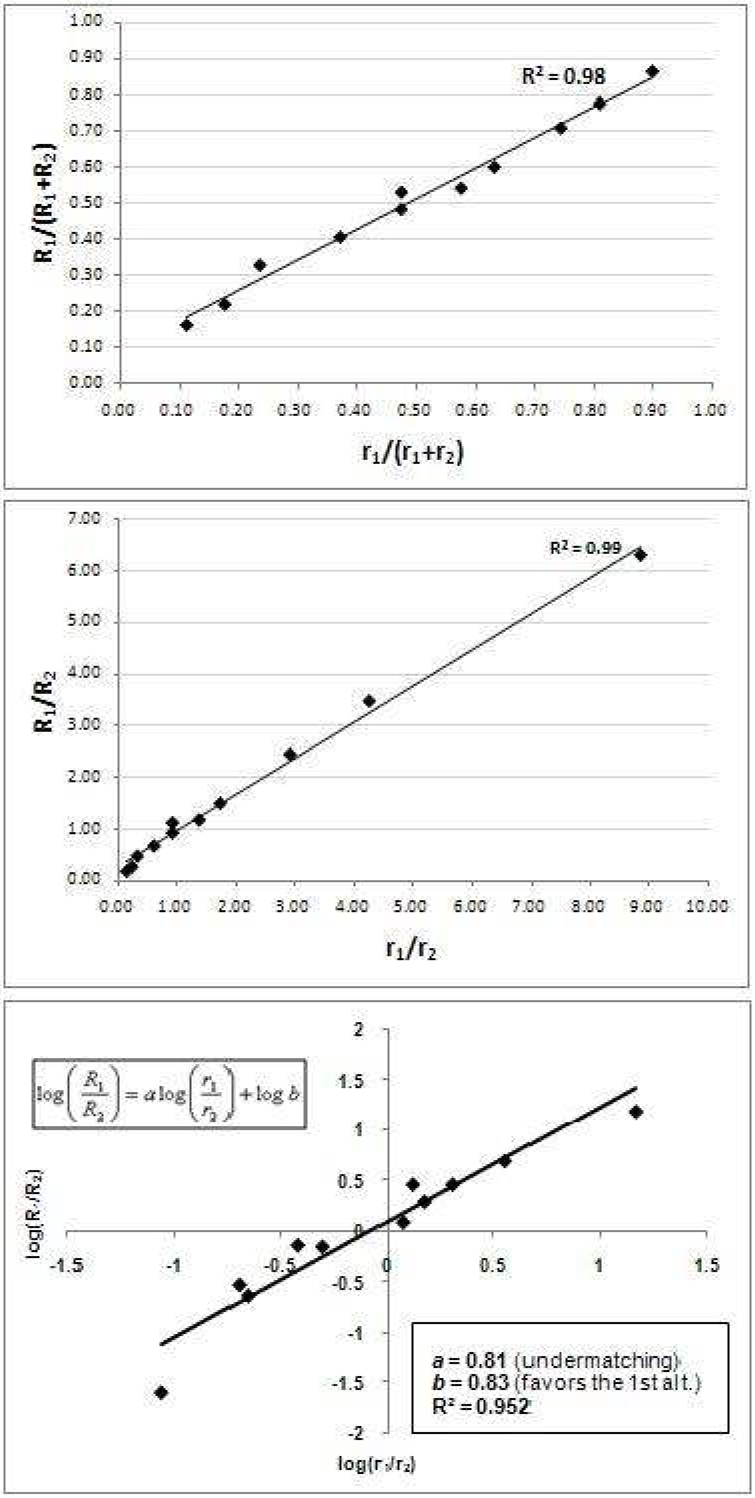
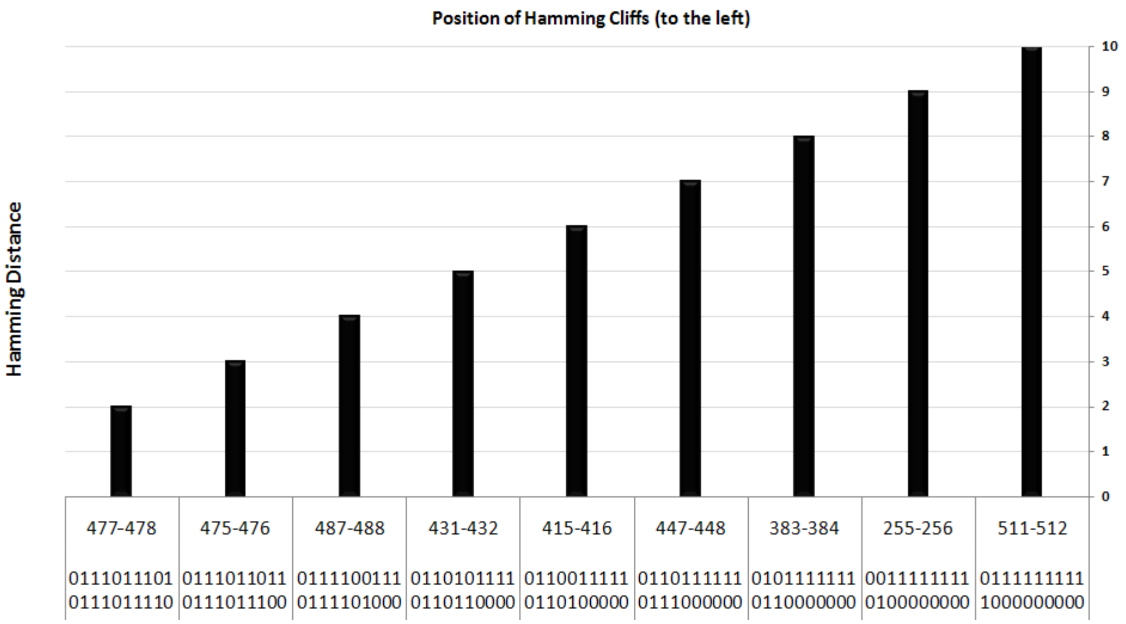
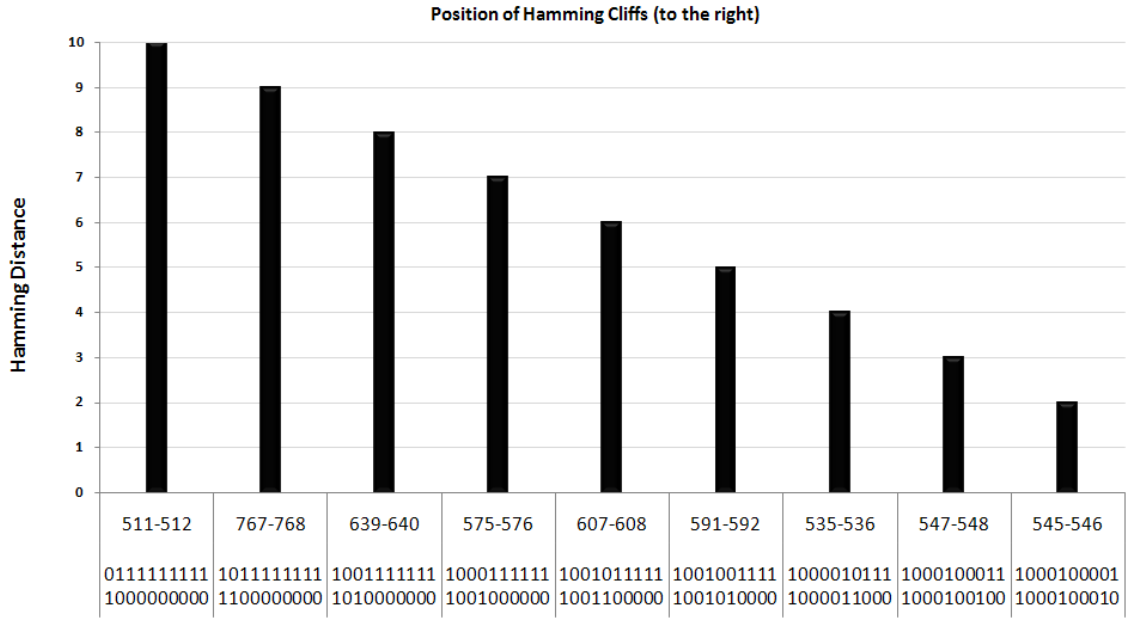

R₁/(R₁+R₂)
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0.00 0.10 0.20 0.30 0.40 0.50 0.60 0.70 0.80 0.90 1.00
r₁/(r₁+r₂)
R² = 0.98
R₁/R₂
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
0.00 1.00 2.00 3.00 4.00 5.00 6.00 7.00 8.00 9.00 10.00
r₁/r₂
R² = 0.99
log(R₁/R₂) = a log(r₁/r₂) + log b
log(R₁/R₂)
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
-1.5 -1 -0.5 0 0.5 1 1.5
log(r₁/r₂)
a = 0.81 (undermatching)
b = 0.83 (favors the 1st alt.)
R² = 0.952

Figure 8



Position of Hamming Cliffs (to the left)



Position of Hamming Cliffs (to the right)

Figure 9

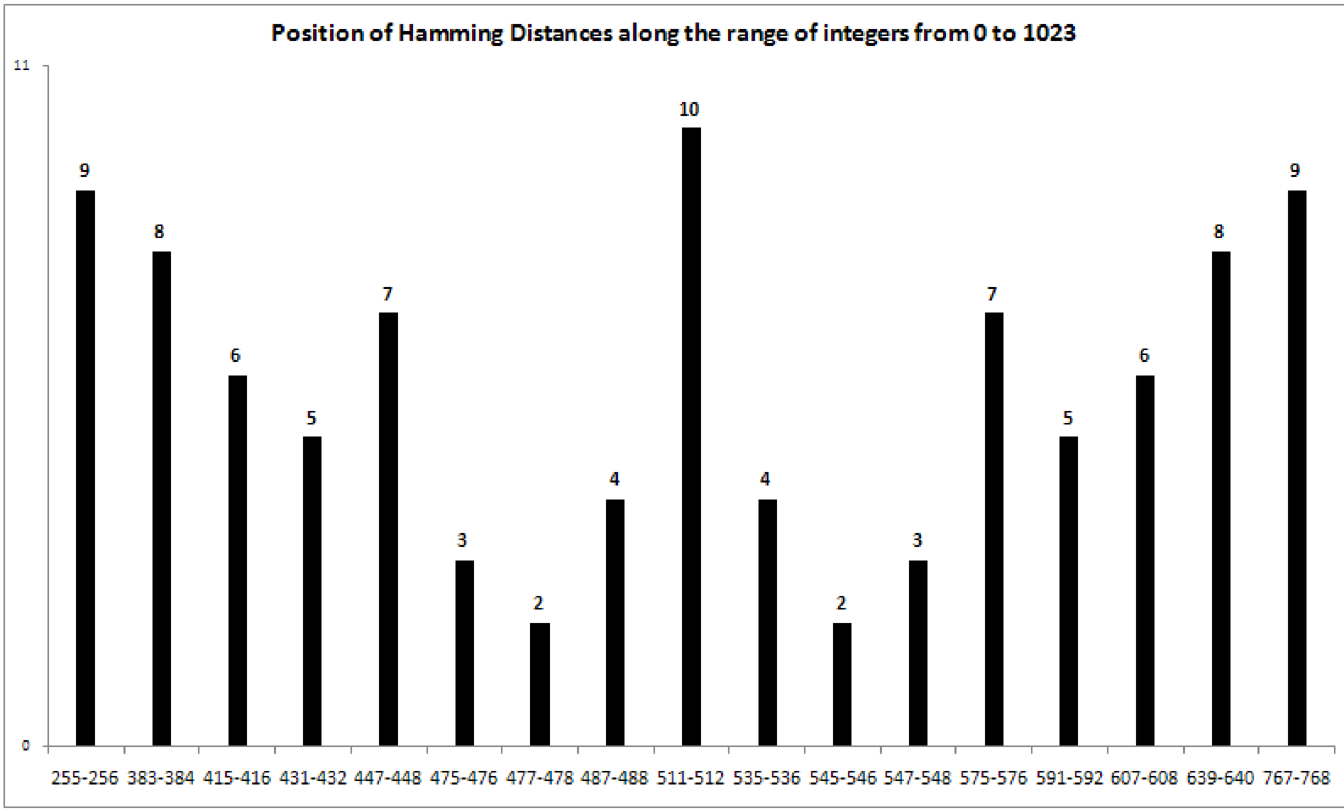
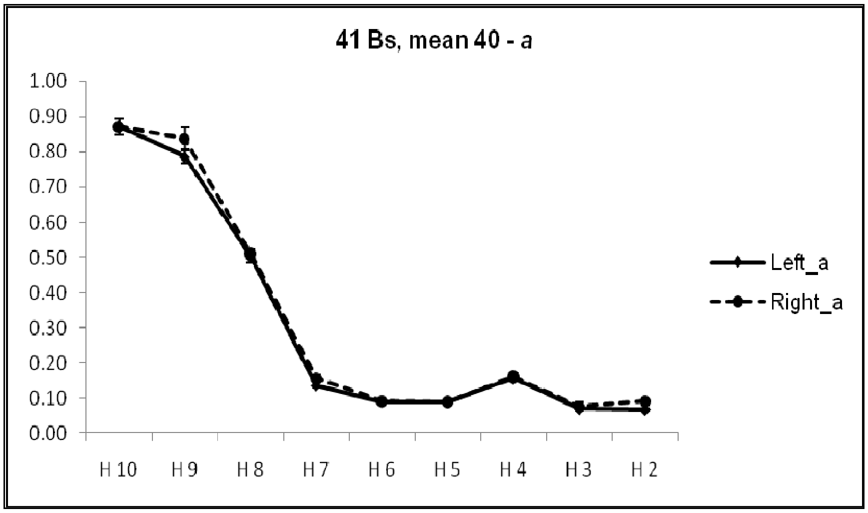

Position of Hamming Distances along the range of integers from 0 to 1023
11
0
9
8
6
5
7
3
2
4
10
4
2
3
7
5
6
8
9
255-256
383-384
415-416
431-432
447-448
475-476
477-478
487-488
511-512
535-536
545-546
547-548
575-576
591-592
607-608
639-640
767-768

Figure 10


41 Bs, mean 40 - *a*
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
H 10
H 9
H 8
H 7
H 6
H 5
H 4
H 3
H 2
Left_a
Right_a

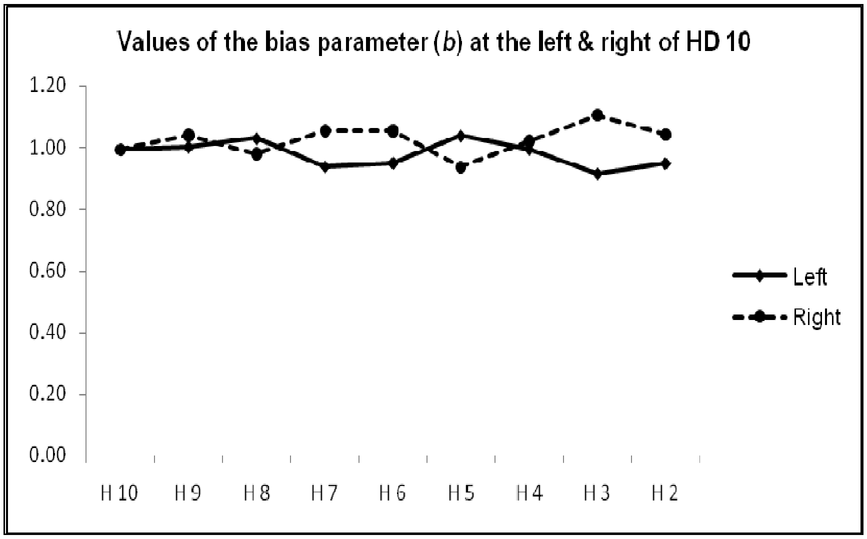

Values of the bias parameter (*b*) at the left & right of HD 10
1.20
1.00
0.80
0.60
0.40
0.20
0.00
H 10
H 9
H 8
H 7
H 6
H 5
H 4
H 3
H 2
Left
Right

Figure 11

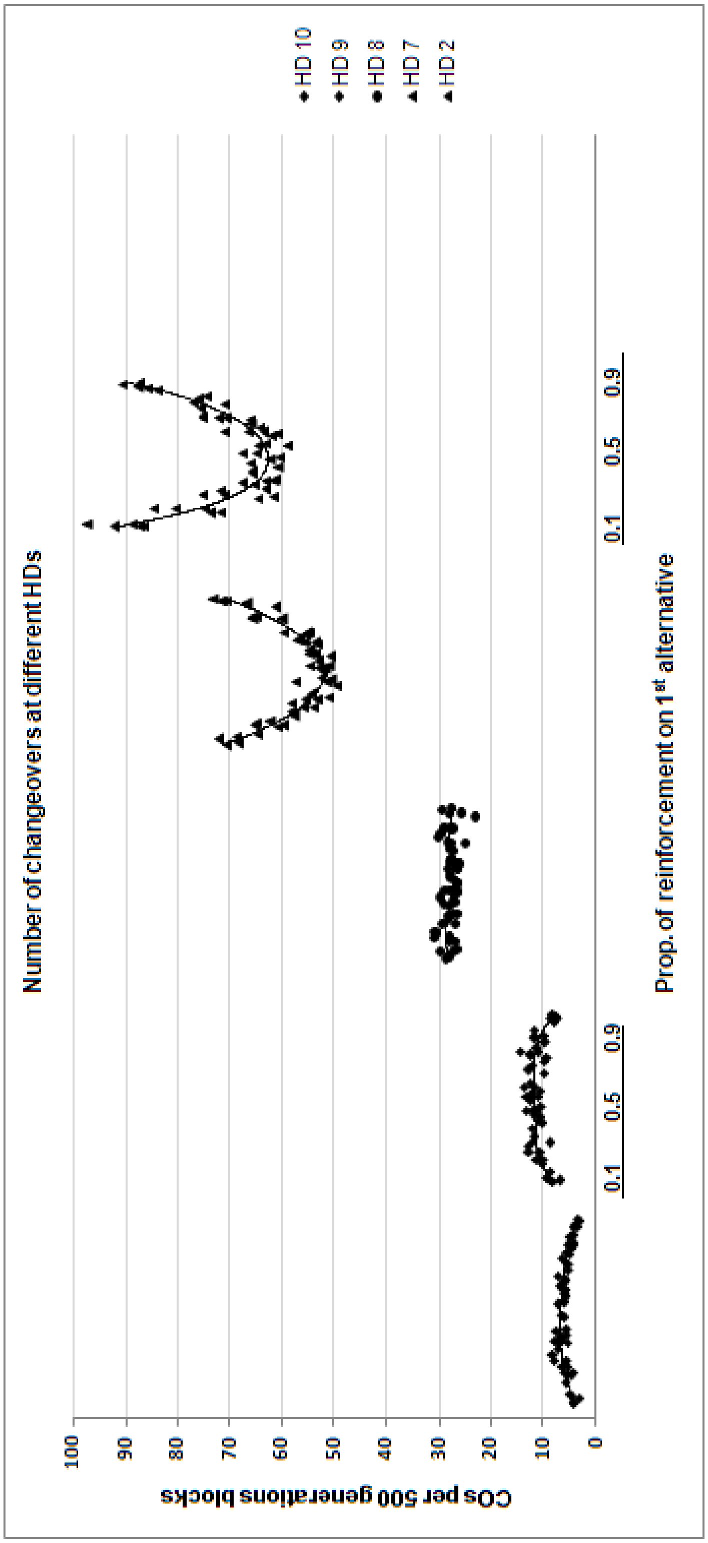

Number of changeovers at different HDs
COs per 500 generations blocks
100
90
80
70
60
50
40
30
20
10
0
0.1
0.5
0.9
0.1
0.5
0.9
Prop. of reinforcement on 1st alternative
HD 10
HD 9
HD 8
HD 7
HD 2

Figure 12

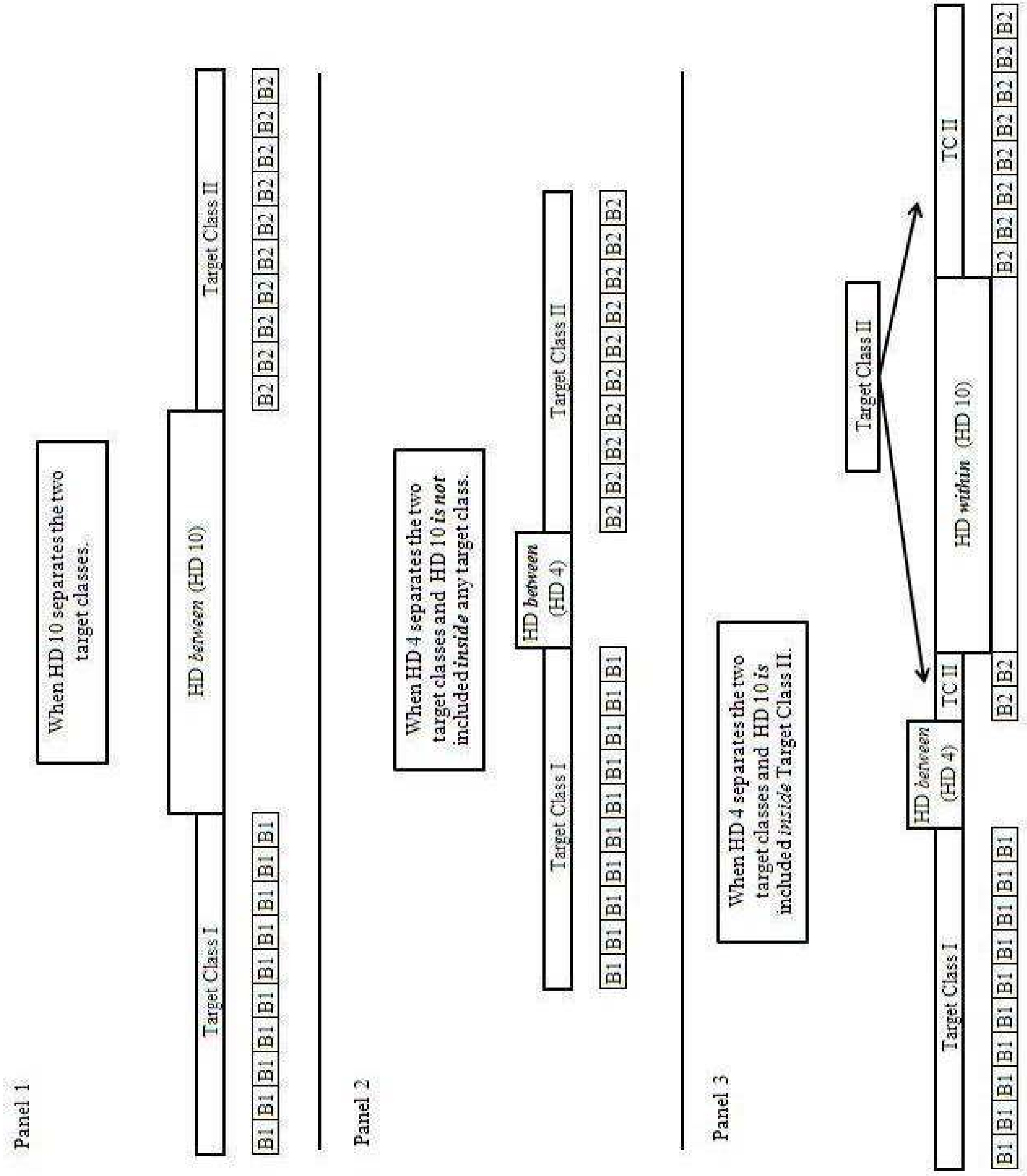

Panel 1
When HD 10 separates the two target classes.
Target Class I
HD *between* (HD 10)
Target Class II
B1
B2
Panel 2
When HD 4 separates the two target classes and HD 10 ***is not*** included ***inside*** any target class.
Target Class I
HD ***between*** (HD 4)
Target Class II
B1
B2
Panel 3
When HD 4 separates the two target classes and HD 10 *is* included *inside* Target Class II.
Target Class I
HD *between* (HD 4)
TC II
HD ***within*** (HD 10)
TC II
Target Class II
B1
B2

Figure 13

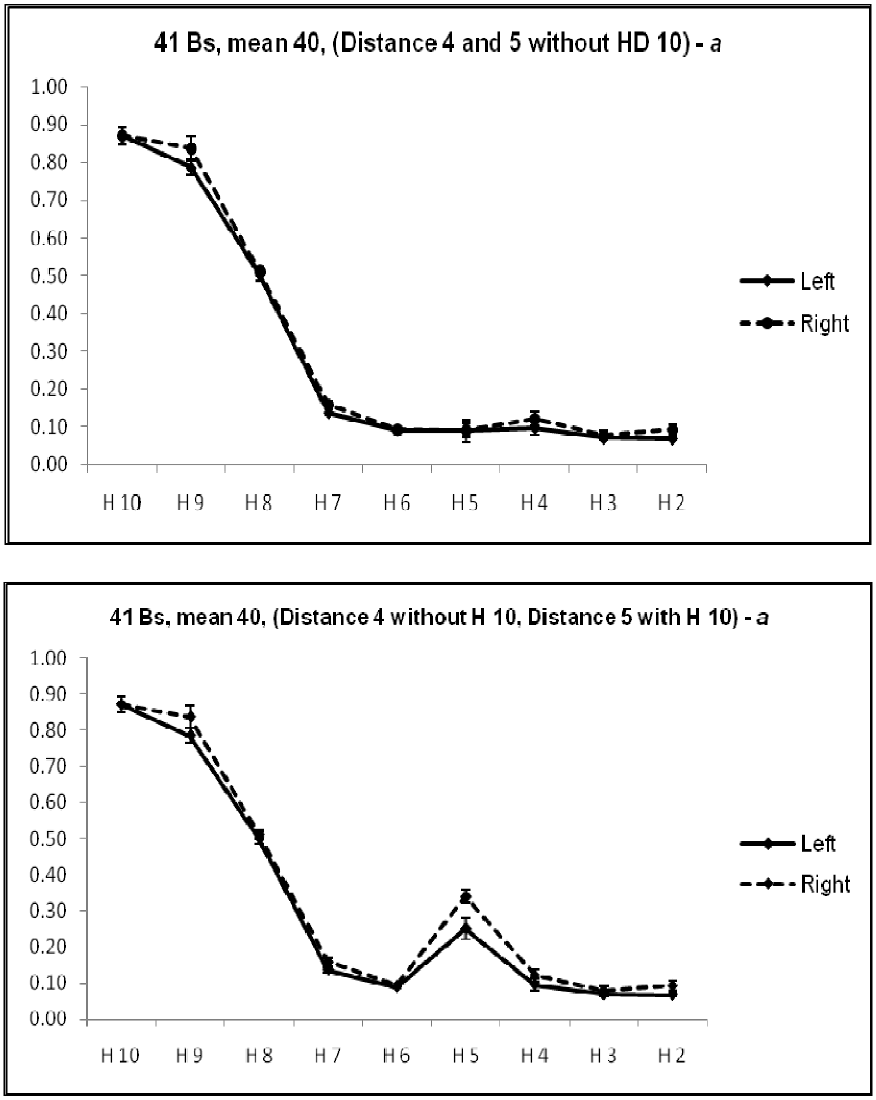

41 Bs, mean 40, (Distance 4 and 5 without HD 10) - *a*
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
H 10
H 9
H 8
H 7
H 6
H 5
H 4
H 3
H 2
Left
Right
41 Bs, mean 40, (Distance 4 without H 10, Distance 5 with H 10) - *a*
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
H 10
H 9
H 8
H 7
H 6
H 5
H 4
H 3
H 2
Left
Right

Figure 14

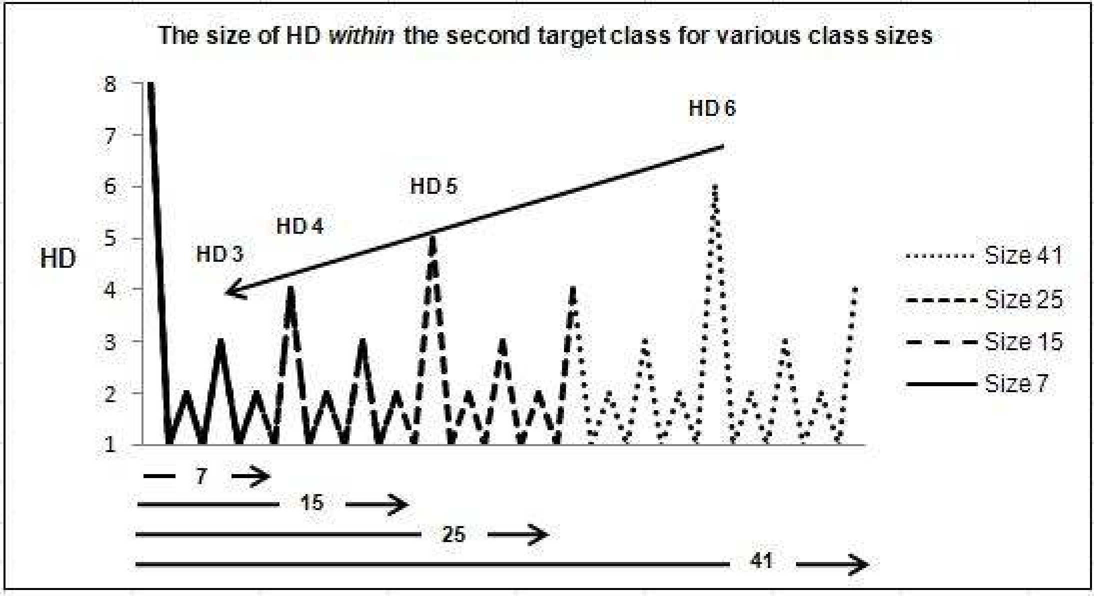
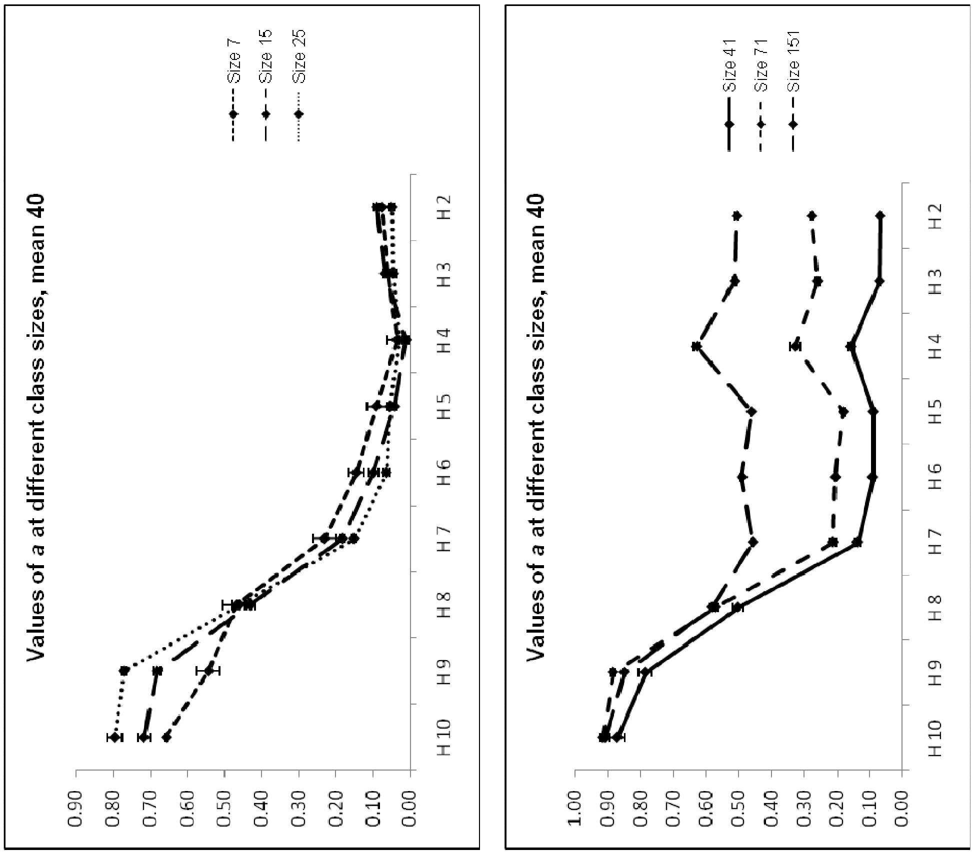

The size of HD *within* the second target class for various class sizes
HD
8
7
6
5
4
3
2
1
HD 3
HD 4
HD 5
HD 6
Size 41
Size 25
Size 15
Size 7
7
15
25
41

Figure 15


Values of *a* at different class sizes, mean 40
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
H10
H9
H8
H7
H6
H5
H4
H3
H2
Size 7
Size 15
Size 25
Values of *a* at different class sizes, mean 40
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
H10
H9
H8
H7
H6
H5
H4
H3
H2
Size 41
Size 71
Size 151

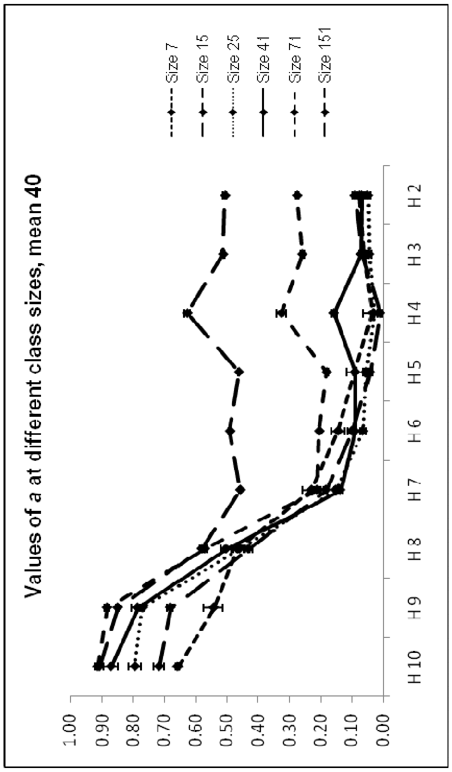

Values of a at different class sizes, mean 40
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
H10
H9
H8
H7
H6
H5
H4
H3
H2
Size 7
Size 15
Size 25
Size 41
Size 71
Size 151

Figure 16

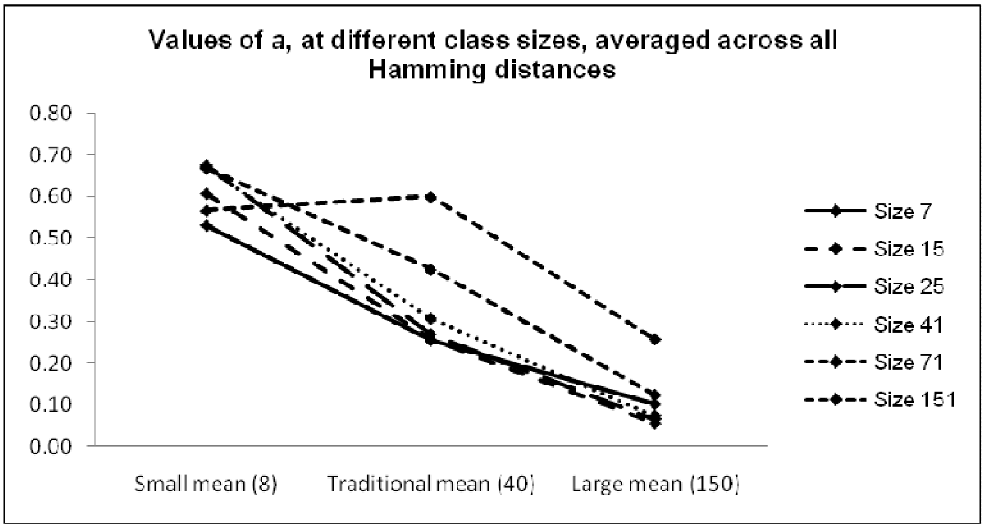
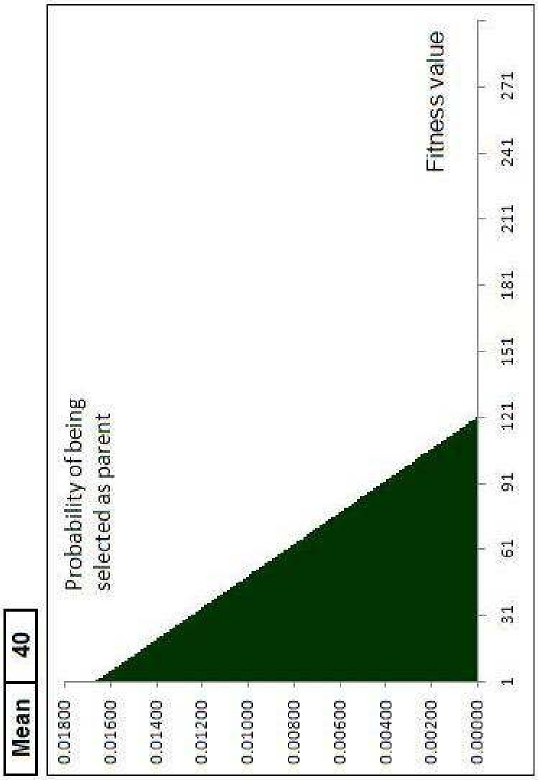
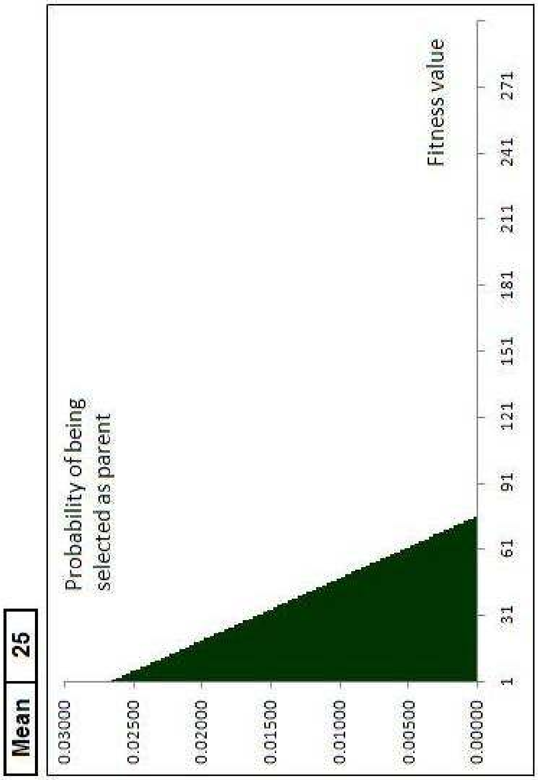
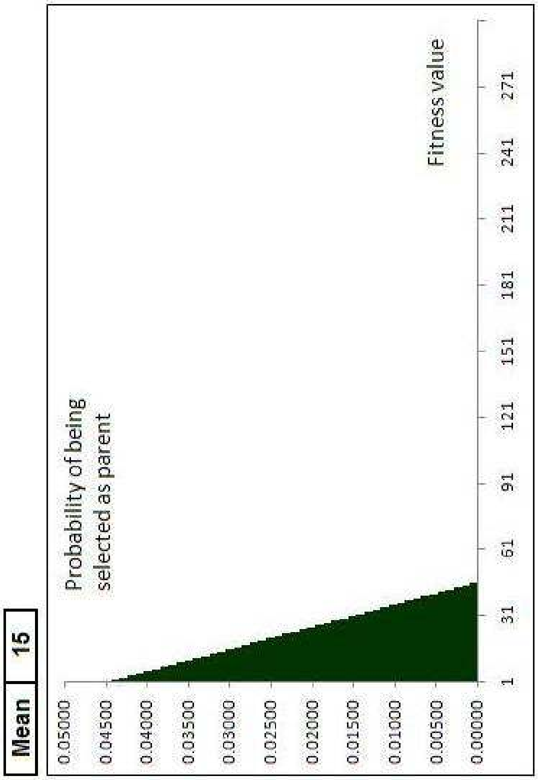

Values of a, at different class sizes, averaged across all Hamming distances
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
Small mean (8)
Traditional mean (40)
Large mean (150)
Size 7
Size 15
Size 25
Size 41
Size 71
Size 151

Figure 17


Mean
40
Probability of being selected as parent
Fitness value
0.01800
0.01600
0.01400
0.01200
0.01000
0.00800
0.00600
0.00400
0.00200
0.00000
1
31
61
91
121
151
181
211
241
271


Mean
25
Probability of being selected as parent
Fitness value
0.03000
0.02500
0.02000
0.01500
0.01000
0.00500
0.00000
1
31
61
91
121
151
181
211
241
271


Mean
15
Probability of being selected as parent
Fitness value
0.05000
0.04500
0.04000
0.03500
0.03000
0.02500
0.02000
0.01500
0.01000
0.00500
0.00000
1
31
61
91
121
151
181
211
241
271

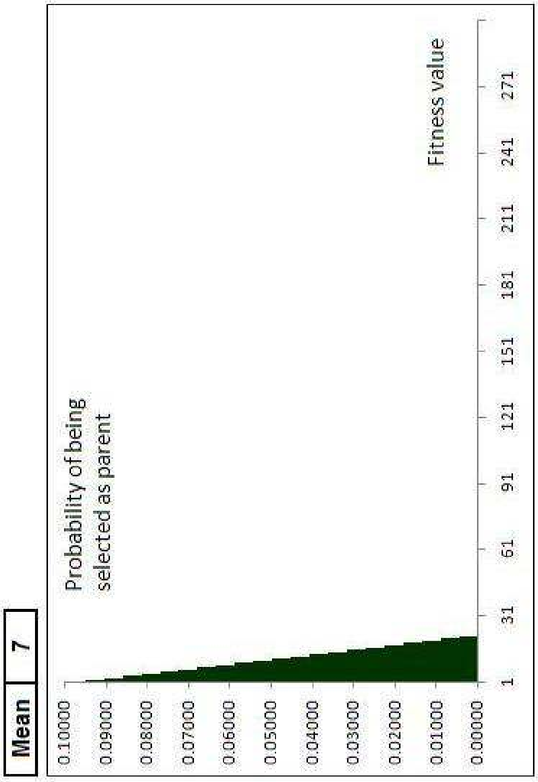

Mean
7
Probability of being selected as parent
Fitness value
0.10000
0.09000
0.08000
0.07000
0.06000
0.05000
0.04000
0.03000
0.02000
0.01000
0.00000
1
31
61
91
121
151
181
211
241
271

Figure 18

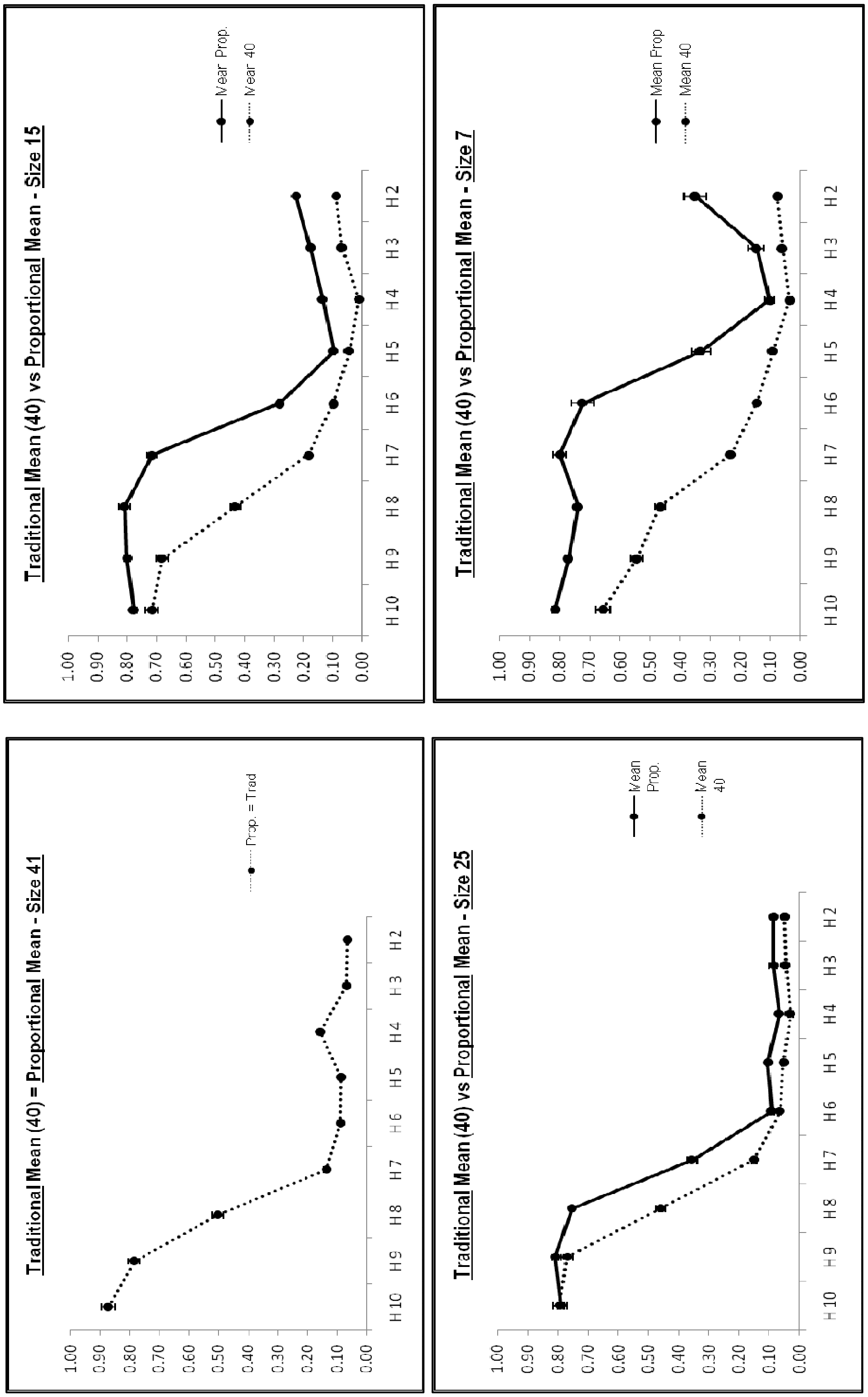

Traditional Mean (40) = Proportional Mean - Size 41
Prop. = Trad
Traditional Mean (40) vs Proportional Mean - Size 15
Mean Prop.
Mean 40
Traditional Mean (40) vs Proportional Mean - Size 25
Mean Prop.
Mean 40
Traditional Mean (40) vs Proportional Mean - Size 7
Mean Prop
Mean 40
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
H10
H9
H8
H7
H6
H5
H4
H3
H2

Figure 19

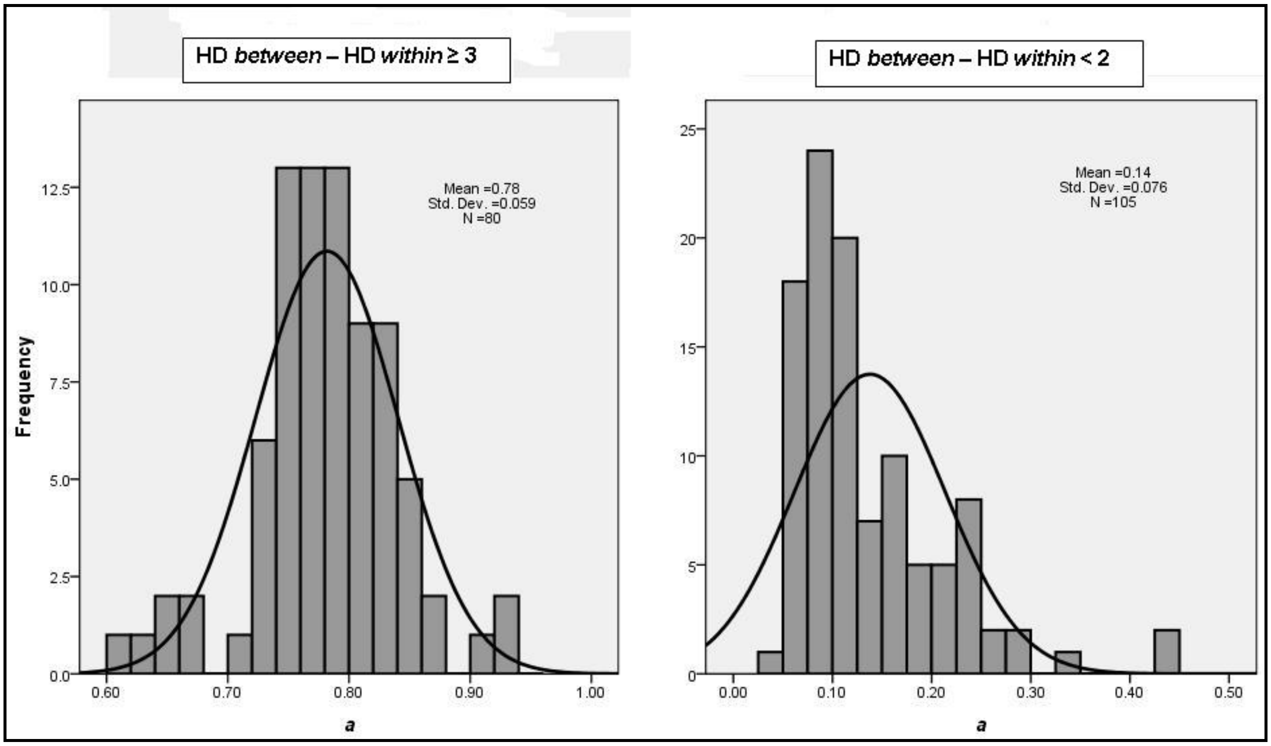
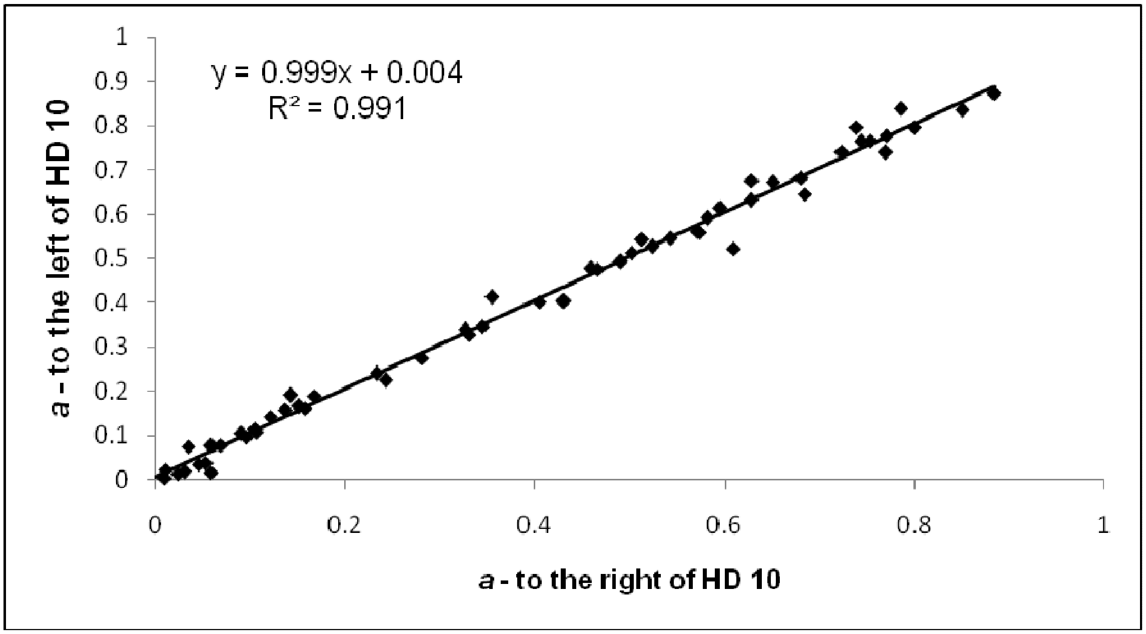

HD *between* – HD *within* ≥ 3
Frequency
12.5
10.0
7.5
5.0
2.5
0.0
0.60
0.70
0.80
0.90
1.00
a
Mean =0.78
Std. Dev. =0.059
N =80
HD *between* – HD *within* < 2
25
20
15
10
5
0
0.00
0.10
0.20
0.30
0.40
0.50
a
Mean =0.14
Std. Dev. =0.076
N =105

Figure 20


y = 0.999x + 0.004
R² = 0.991
a - to the left of HD 10
a - to the right of HD 10
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.2
0.4
0.6
0.8
1

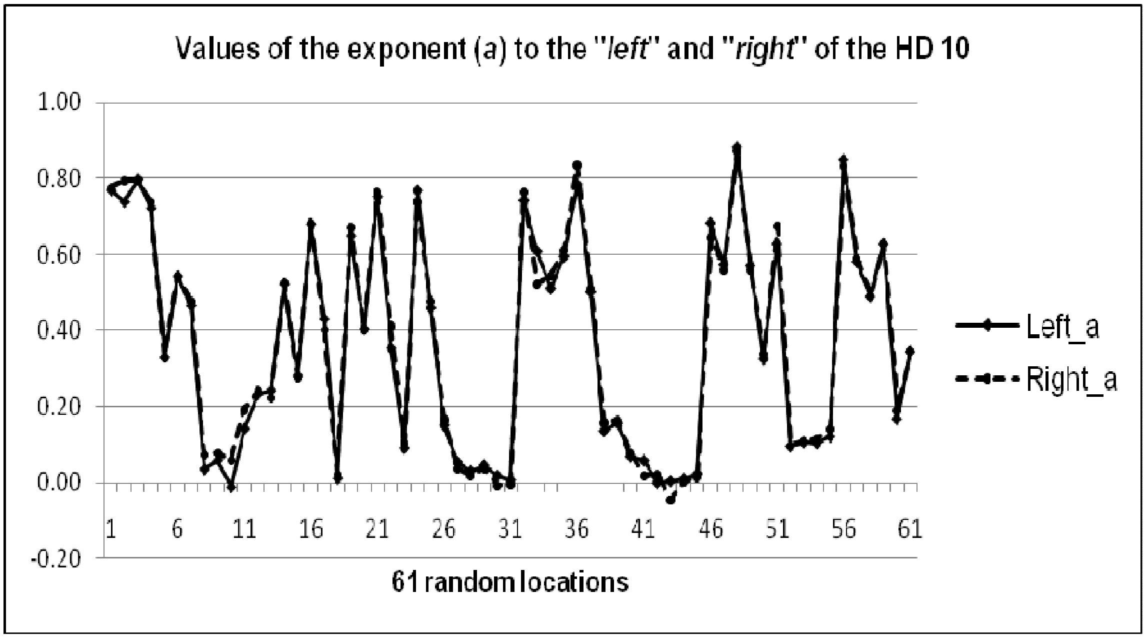

Values of the exponent (a) to the "left" and "right" of the HD 10
1.00
0.80
0.60
0.40
0.20
0.00
-0.20
1
6
11
16
21
26
31
36
41
46
51
56
61
61 random locations
Left_a
Right_a

Figure 21

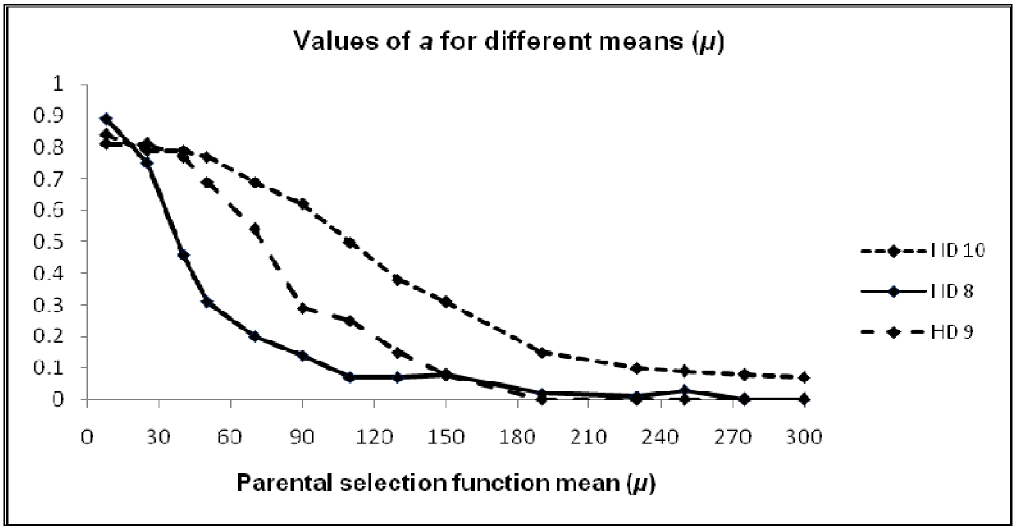


Figure 22

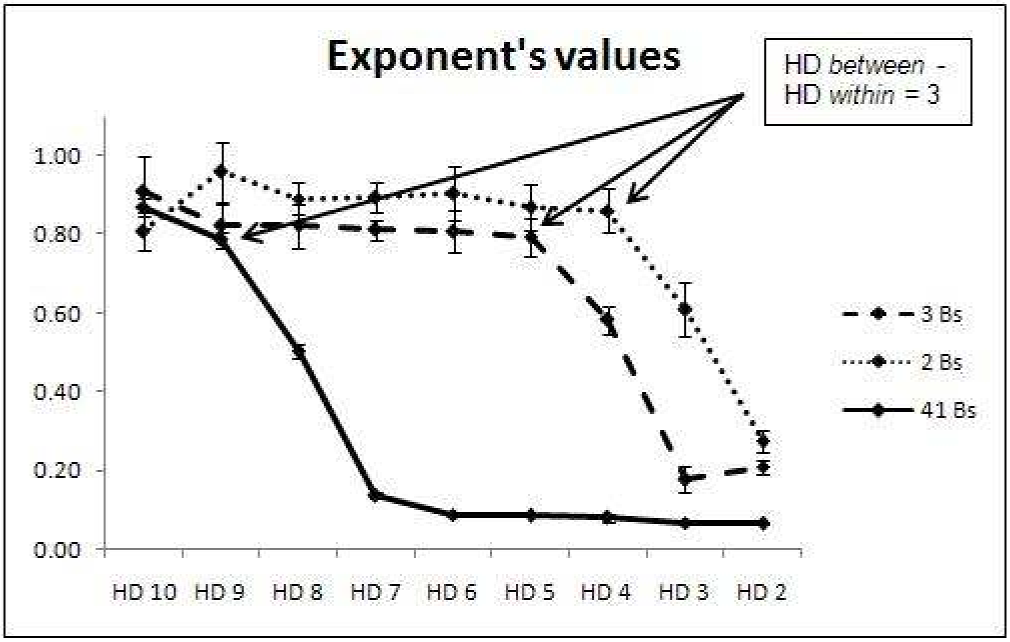


Figure 23

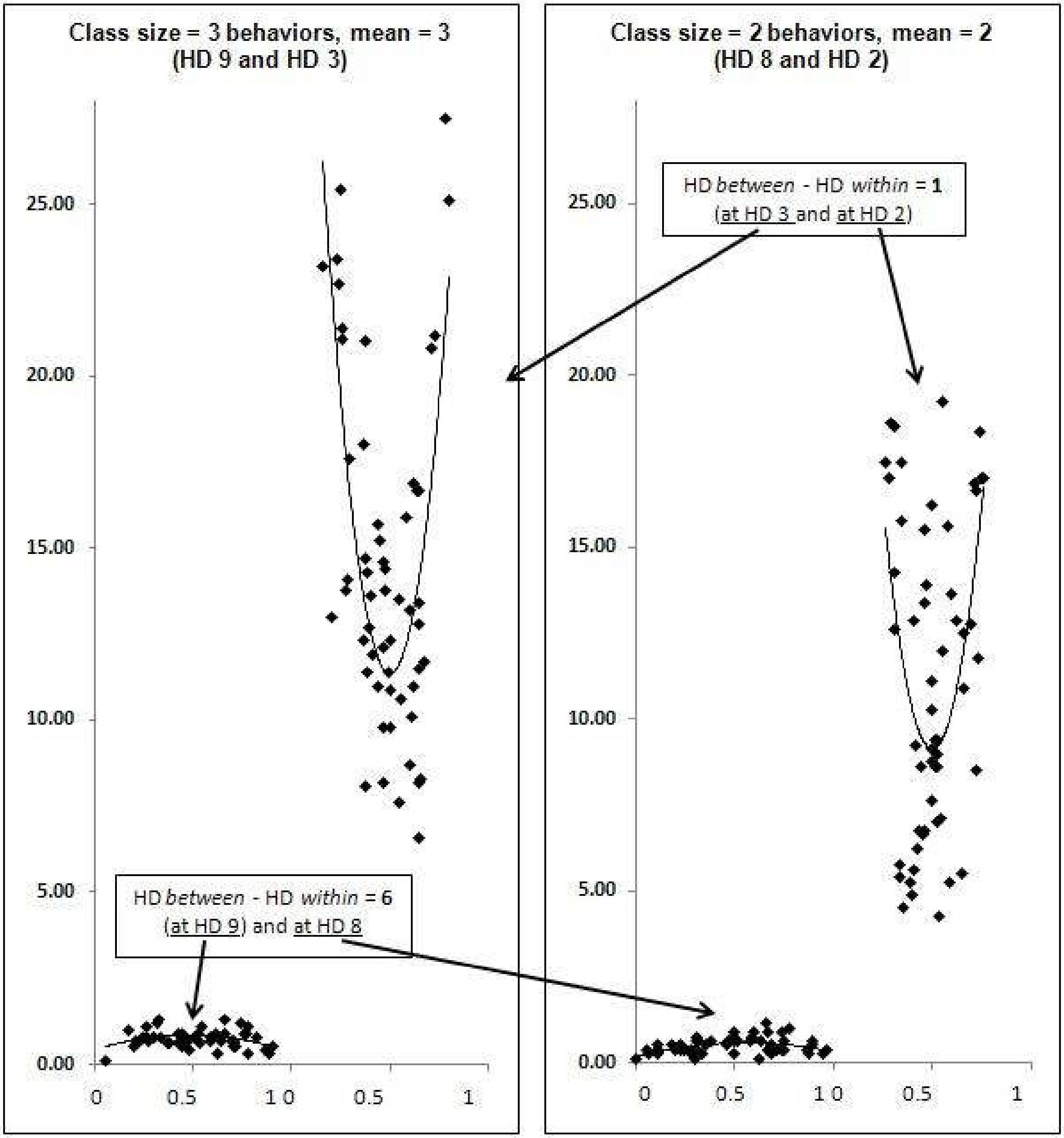
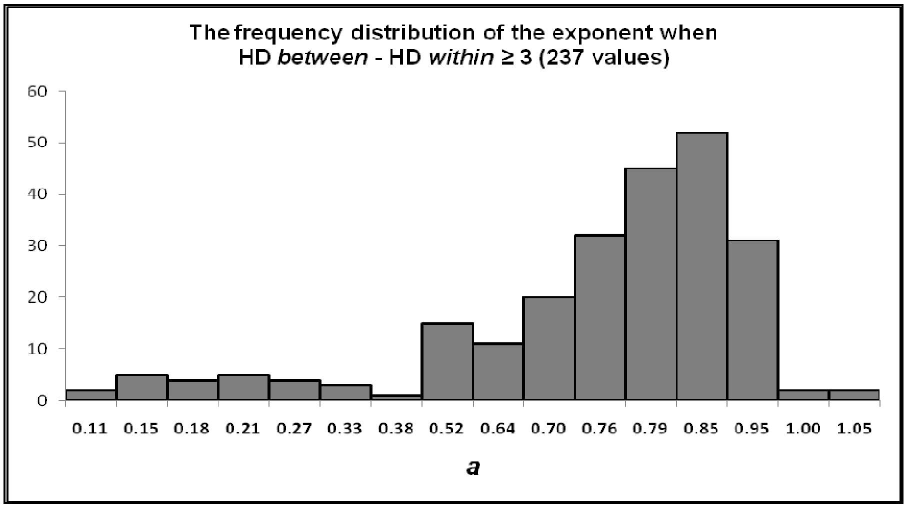
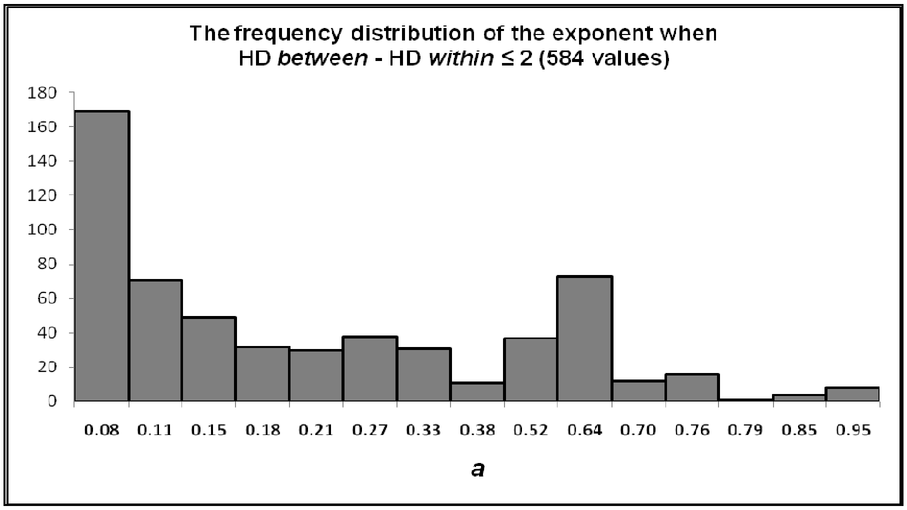
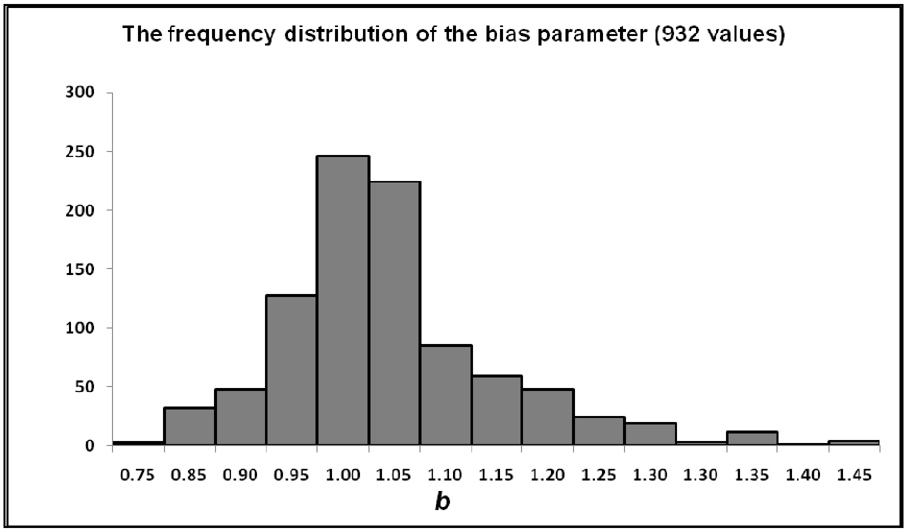

Class size = 3 behaviors, mean = 3
(HD 9 and HD 3)
Class size = 2 behaviors, mean = 2
(HD 8 and HD 2)
HD between - HD within = 1
(at HD 3 and at HD 2)
HD between - HD within = 6
(at HD 9) and at HD 8
25.00
20.00
15.00
10.00
5.00
0.00
0
0.5
1 0
0.5
1

Figure 24


The frequency distribution of the exponent when
HD *between* - HD *within* ≥ 3 (237 values)
60
50
40
30
20
10
0
0.11
0.15
0.18
0.21
0.27
0.33
0.38
0.52
0.64
0.70
0.76
0.79
0.85
0.95
1.00
1.05
a


The frequency distribution of the exponent when
HD *between* - HD *within* ≤ 2 (584 values)
180
160
140
120
100
80
60
40
20
0
0.08
0.11
0.15
0.18
0.21
0.27
0.33
0.38
0.52
0.64
0.70
0.76
0.79
0.85
0.95
a


The frequency distribution of the bias parameter (932 values)
300
250
200
150
100
50
0
0.75
0.85
0.90
0.95
1.00
1.05
1.10
1.15
1.20
1.25
1.30
1.30
1.35
1.40
1.45
b