

To the Graduate Council:

I am submitting herewith a thesis written by Mahendra Duwal Shrestha entitled “Analysis and Simulation Of A Simple Evolutionary System.” I have examined the final paper copy of this thesis for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Master of Science, with a major in Computer Science.

Michael D. Vose, Major Professor

We have read this thesis
and recommend its acceptance:

Michael D. Vose

Hairong Qi

Judy D. Day

Accepted for the Council:

Dixie Thompson

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(Original signatures are on file with official student records.)

Analysis and Simulation Of A Simple Evolutionary System

A Thesis Presented for
The Master of Science
Degree

The University of Tennessee, Knoxville

Mahendra Duwal Shrestha

May 2017

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To my loving

Father & Mother,

*Whose love, affection, encouragment, and support made me able to stand where I
am today*

Acknowledgements

I thank Michael D. Vose, Hairong Qi, and Judy D. Day for serving as my committee members. I am especially grateful to my academic advisor Michael D. Vose for suggesting the topic of this research and for giving so generously of his time. I have utterly enjoyed our many hours of discussion related to this thesis and learned a lot from this.

This research would not be complete without support of Sergey Gavrillets from Ecology and Evolutionary Biology, who funded most of my graduate tuition through assistantship, and also provided access to the computing cluster Volos for running simulations. I wish to thank Sergey Gavrillets for his support.

Finally, I wish to thank my family, especially cousin Reshma for putting up some encouraging words. Sometimes they had more belief in me than I had in myself.

“Truth is stranger than fiction.” - Mark Twain

Abstract

An infinite population model is considered for diploid evolution under the influence of crossing over and mutation. The evolution equations show how Vose's haploid model for Genetic Algorithms extends to the diploid case, thereby making feasible simulations which otherwise would require excessive resources. This is illustrated through computations confirming the convergence of finite diploid population short-term behaviour to the behaviour predicted by the infinite diploid model. The results show the distance between finite and infinite population evolutionary trajectories can decrease in practice like the reciprocal of the square root of population size.

Under necessary and sufficient conditions concerning mutation and crossover, infinite populations show oscillating behavior. We explore whether finite populations can also exhibit oscillation or approximate oscillation. Simulation results confirm that approximate finite population oscillation is possible.

We also investigate the robustness of finite population oscillation. Finite population evolution is modeled by a Markov chain. Necessary and sufficient conditions for infinite population oscillation concern mutation and crossover. We show that when the condition concerning mutation is violated, the Markov chain is regular, and perfect oscillation in finite population evolution should not occur. However, our simulation results show finite population exhibit approximate oscillating behavior even though the condition is violated.

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Chapter 1

Introduction

This thesis begins with notation that is used throughout this document.

1.1 Notation

Some standard mathematical notation as well as some non-standard mathematical notations are introduced here.

Angle brackets $\langle \cdots \rangle$ denote a tuple which is to be regarded as a column vector. The column vector of all 1s is denoted by $\mathbf{1}$. Transpose is indicated with superscript T . The standard vector norm is $\|x\| = \sqrt{x^T x}$. Modulus (or absolute value) is denoted by $|\cdot|$. When S is a set, $|S|$ denotes the cardinality of S .

The notation $O(f)$ denotes a function g (with similar domain and codomain as f), such that pointwise $g \leq cf$ for some constant c . The notation $\theta(f)$ is a function g such that pointwise $c_0 f \leq g \leq c_1 f$ for some constants c_0, c_1 . Curly brackets $\{\cdots\}$ are used as grouping symbols and to specify both sets and multisets. Square brackets $[\cdots]$ are, besides their standard use as specifying a closed interval of real numbers, used to denote an indicator function: if $expr$ is an expression which may be true or false, then $[expr]$ denotes 1 if $expr$ is true, and 0 otherwise; $[\cdots]$ is sometimes referred to as an *Iverson bracket*.

The supremum is the least upper bound, and is denoted by \sup . The infimum is the greatest lower bound, and is denoted by \inf .

The set of length ℓ binary strings is denoted by \mathcal{R} . It is a commutative ring under component-wise addition and multiplication modulo 2. If $x \in \mathcal{R}$, then it may be regarded as the vector $x = \langle x_0, x_1, \dots, x_{\ell-1} \rangle$. Denote the additive identity of \mathcal{R} by $\mathbf{0}$ and the multiplicative identity by $\mathbf{1}$. Let \bar{g} abbreviate $\mathbf{1} + g$. Except when explicitly indicated otherwise, operations acting on elements of \mathcal{R} are as defined in this paragraph. In particular, $g\bar{g} = \mathbf{0} = g + g$, $g^2 = g$, $g + \bar{g} = \mathbf{1}$ for all $g \in \mathcal{R}$.

1.2 Background

The genetic algorithm (GA) is inspired by nature, and seeks to evolve useful constructs. It is typically population based, and proceeds over a number of generations to evolve solutions to problems not yielding to other known methods. Basic elements of a GA are: selection according to fitness, crossover, and random mutation (see [Mitchell \(1999\)](#)). In the simplest case, population members are fixed-length binary strings. The fitness function assigns a score (fitness) to the elements (chromosomes) of the current population.

Selection: select population members in the current population for reproduction; those with higher fitness are more likely to be selected to reproduce.

Crossover: with some probability (the crossover rate), choose a random point in two parents (population members selected for reproduction) and exchange subsequences after that point to create two offspring.

Mutation: flip bits of an individual with some small probability, the mutation rate.

Figure [1.1](#) shows the procedural flow of a basic finite population genetic algorithm.



Figure 1.1: Finite GA

A simple Holland style genetic algorithm (see [Holland \(1992\)](#)):

1. Start with some initial population P containing r binary strings of length ℓ .
2. Choose (with replacement) parents u and v from the current population P (using any selection scheme).
 - a. Cross u and v to produce children u' and v' .
 - b. Mutate u' and v' with some probability to produce u'' and v'' .
 - c. Keep, with uniform probability, one of u'' and v'' for the next generation
3. If the next generation contains fewer than r members, repeat step 2.
4. Replace P by the new generation formed and go to step 2.

Each iteration of this process produces a generation. The process described above is repeated until the system stops to improve or some threshold is met.

The infinite population GA models a population as a probability vector \mathbf{p} where component \mathbf{p}_j can be interpreted as the proportion of string j in the population. If \mathcal{G} is the function mapping infinite population \mathbf{p} to the next generation, $\mathcal{G}(\mathbf{p})$ is a

probability vector such that

$\mathcal{G}(\mathbf{p})_j$ = the probability that string j occurs in the next generation.

The evolution of infinite population \mathbf{p} is the sequence

$$\mathbf{p} \rightarrow \mathcal{G}(\mathbf{p}) \rightarrow \mathcal{G}(\mathcal{G}(\mathbf{p})) \rightarrow \dots$$

Several people working in the 1950s and the 1960s – like Box (1957), Friedman (1959), Bledsoe (1961), Bremermann (1962), and Reed, Toombs and Baricelli (1967) – developed evolution-inspired algorithms, but little attention or theoretical analysis was given to them (see [Mitchell \(1999\)](#)). Genetic algorithms were popularized by Holland and his colleagues in the 1960s and the 1970s. Holland introduced a population-based algorithm with crossover and mutation, and promoted his schema theorem (see [Holland \(1992\)](#)) as a theoretical means to analyze on genetic algorithm dynamics. Holland’s Schema theorem provides a lower bound for schema survival in next generation.[‡] The schema theorem is an inequality however, and can not predict which strings are expected in the next generation. Bethke (see [Bethke \(1980\)](#)) gave equations computing the expected number of any string in the next generation. Goldberg (see [Goldberg \(1987\)](#)) used such equations to model the evolutionary trajectory of a two bit GA under crossover and proportional selection. Vose and Liepins (see [Vose and Liepins \(1991\)](#)) simplified and extended these equations by integrating mutation into the recombination of arbitrarily long binary strings. Although their model computes infinite population trajectories, given a *finite* population represented by vector \mathbf{p} (component \mathbf{p}_i is the proportion of string i in the *finite population*), the infinite population model computes the expected proportion

[‡]A schema is a template that identifies a set of strings in the population with similarities at certain string positions; it is made up of 1s, 0s, and *s where * is the ‘don’t care’ symbol that matches either 0 or 1.

$\mathcal{G}(\mathbf{p})_i$ of string i in the next generation. This is perhaps the most direct connection between the infinite population model and a finite population GA.

Nix and Vose (see [Nix and Vose \(1992\)](#)) explored issues regarding the relationship between the finite population GA and the infinite population model. For a mutation rate μ between 0 and 0.5, a finite population GA will form an ergodic Markov chain, visiting every state infinitely often in the long run. The short term trajectory followed by a finite population is related to the evolutionary path determined by the infinite population model. For large populations, the short term trajectory follows closely and with large probability, that path predicted by the infinite population model.

Vose compiled and extended previous work regarding the infinite population model in the book *Simple Genetic Algorithm: Foundations and Theory* (see [Vose \(1999\)](#)). In particular, he discussed how the Walsh transform can be applied to increase computational efficiency in calculating the infinite population model. There have been previous applications of the Walsh transform to GAs. Bethke first introduced the idea of using Walsh transforms to analyze GA fitness functions in terms of schemata (see [Bethke \(1980\)](#)). The idea was further developed in papers by Goldberg (see [Goldberg \(1989a\)](#), [Goldberg \(1989b\)](#)). However, such usage did not apply Walsh transforms to crossover, to mutation, or to any of their associated mathematical objects. In contrast, Vose and Liepins applied the Walsh transform directly to mutation and recombination, and proved that the twist M^* of the mixing matrix M is triangularized by the Walsh transform, and related eigenvalues of M^* to the stability of fixed points of \mathcal{G} (see [Vose and Liepins \(1991\)](#)).[§] In a related paper, Koehler (see [Koehler \(1994\)](#)) gives a congruence transformation defined by a lower triangular matrix that diagonalizes the mixing matrix (for 1-point crossover and mutation given by a rate) and proved a conjecture of Vose and Liepins concerning eigenvalues of M^* . Koehler, Bhattacharyya and Vose (see [Koehler et al. \(1997\)](#)) applied the Fourier

[§]The mixing matrix M has rows and columns indexed by chromosomes; entry $M_{i,j}$ is the probability that mixing parents i and j (mixing is the combined effect of crossover and mutation) will produce a child having all bits zero. The twist (M^*) of the mixing matrix M is defined by $(M^*)_{i,j} = M_{i+j,i}$.

transform in generalizing results established for binary GAs to strings over an alphabet of cardinality c (in the binary case, the Fourier transform is the Walsh transform). From a computational perspective, a major contribution of Vose and Wright (see [Vose and Wright \(1998\)](#)) was demonstrating that the mixing matrix is sparse in the Walsh basis, and the computational efficiency of computing $\mathcal{G}(\mathbf{p})$ can thereby be improved from $O(8^\ell)$ to $O(3^\ell)$ where ℓ is the chromosome length. The cost of moving from standard coordinates to the Walsh basis need not be a bottleneck; the fast Walsh transform (see [Shanks \(1969\)](#)) does that in $O(\ell 2^\ell)$ time.

1.3 Random Heuristic Search

The work presented in this thesis is based on *Random Heuristic Search (RHS)*, a general search method, defined upon the central concept of state and transition between states (see [Vose \(1999\)](#)). The simple genetic algorithm is a particular type of RHS. An instance of *RHS* is an initial collection of elements P (referred to as the initial population) chosen from some search space Ω , together with a stochastic transition rule τ , which from P will produce another collection P' ; iterating τ produces a sequence of generations.

Let n be the cardinality of Ω , let $\mathbf{1}$ denote the column vector of all 1s. The *simplex* is the set of population descriptors:

$$\Lambda = \{x = \langle x_0, \dots, x_{n-1} \rangle : \mathbf{1}^T x = 1, x_j \geq 0\}$$

Element $\mathbf{p} \in \Lambda$ corresponds to a population; p_j = the proportion in the population of the j th element of Ω . The cardinality of each population is a constant r , called the population size. Given r , a population descriptor \mathbf{p} unambiguously determines a population.

Given current population vector \mathbf{p} , the next population vector $\tau(\mathbf{p})$ cannot be predicted with certainty because τ is stochastic; it results from r independent,

identically distributed random choices. Let $\mathcal{G} : \Lambda \rightarrow \Lambda$ be a function that maps current population vector \mathbf{p} to a vector whose i th component is the probability that the i th element of Ω is chosen. Thus, $\mathcal{G}(\mathbf{p})$ specifies the distribution from which the aggregate of r choices forms the subsequent generation. The probability that population \mathbf{q} is the next population vector given current population (vector) \mathbf{p} is (see [Vose \(1999\)](#))

$$\begin{aligned} Q_{\mathbf{p},\mathbf{q}} &= r! \prod \frac{(\mathcal{G}(\mathbf{p})_j)^{r\mathbf{q}_j}}{(r\mathbf{q}_j)!} \\ &= \exp\left\{-r \sum \mathbf{q}_j \log \frac{\mathbf{q}_j}{\mathcal{G}(\mathbf{p})_j} - \sum (\log \sqrt{2\pi r\mathbf{q}_j} + \frac{1}{12r\mathbf{q}_j + \theta(r\mathbf{q}_j)})\right. \\ &\quad \left.+ O(\log r)\right\} \end{aligned} \quad (1.1)$$

where summation is restricted to indices for which $\mathbf{q}_j > 0$ and θ is a function such that $0 < \theta < 1$. Each random vector in the sequence $\mathbf{p}, \tau(\mathbf{p}), \tau^2(\mathbf{p}), \dots$ depends only on the value of the preceding one, which is a special situation. The sequence forms a Markov chain with transition matrix Q . The conceptualization of RHS can be replaced by a Markov chain model which makes no reference to sampling Ω ; from current population \mathbf{p} , produce \mathbf{q} with probability $Q_{\mathbf{p},\mathbf{q}}$. The expected next generation $\mathcal{E}(\tau(\mathbf{p}))$ is $\mathcal{G}(\mathbf{p})$ (see [Vose \(1999\)](#)). The expression

$$\sum \mathbf{q}_j \log \frac{\mathbf{q}_j}{\mathcal{G}(\mathbf{p})_j}$$

in (1.1) is the *discrepancy* of \mathbf{q} with respect to $\mathcal{G}(\mathbf{p})$. It is a measure of how far \mathbf{q} is from the expected next population $\mathcal{G}(\mathbf{p})$. Discrepancy is nonnegative and is zero only when \mathbf{q} is the expected next population. Hence the first factor

$$\exp\left\{-r \sum \mathbf{q}_j \log \frac{\mathbf{q}_j}{\mathcal{G}(\mathbf{p})_j}\right\}$$

in (1.1) indicates the probability that \mathbf{q} is the next generation decays exponentially, with constant r , as the discrepancy between \mathbf{q} and $\mathcal{G}(\mathbf{p})$ increases. The expression

$$\sum (\log \sqrt{2\pi r \mathbf{q}_j} + \frac{1}{12r \mathbf{q}_j + \theta(r \mathbf{q}_j)})$$

measures the *dispersion* of the population vector \mathbf{q} and the second factor in (1.1)

$$\exp\{-\sum (\log \sqrt{2\pi r \mathbf{q}_j} + \frac{1}{12r \mathbf{q}_j + \theta(r \mathbf{q}_j)})\}$$

indicates the probability that \mathbf{q} is the next generation decays exponentially with increasing dispersion. As Vose stated in his book (see [Vose \(1999\)](#)):

The combined effect of the two influences of discrepancy and dispersion is that random heuristic search favors a less disperse population near the expected next generation. In particular, if the current population is near the expected next generation, then the first factor does not contribute a strong bias for change. When $\mathcal{G}(\mathbf{p})$ is nearly the initial population \mathbf{p} , the influence of discrepancy favors \mathbf{p} as the next generation since the alternatives, being lattice points, are constrained to be some distance away from the expected next generation. This phenomenon is expressed quantitatively by theorem 3.4. Moreover, the second factor may exert a stabilizing effect provided the current population has low dispersion compared to the alternatives

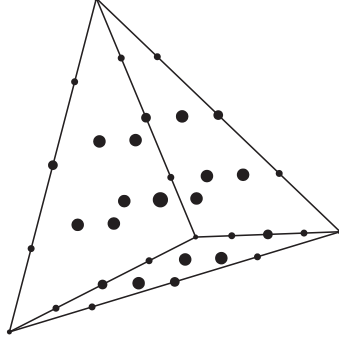


Figure 1.2: Population points

Figure 1.2 illustrates population points in a simplex for $\ell = 2, r = 4$. Finite populations are represented by dots, where smaller dots have lower dispersion and larger dots have higher dispersion. The diagram also illuminates that finite populations are constrained to occupy lattice points within Λ . As population size $r \rightarrow \infty$, the lattice points become dense in Λ , which corresponds to the fact that an infinite population can be (represented by) any point of Λ .

The variance of the next generation (with respect to the expected population) (see Vose (1999)) is

$$\mathcal{E}(\|\tau(\mathbf{p}) - \mathcal{G}(\mathbf{p})\|^2) = \frac{1 - \|\mathcal{G}(\mathbf{p})\|^2}{r} \quad (1.2)$$

It follows from Chebyshev's inequality (see Wikipedia (2016a)) that

$$P(\|\tau(\mathbf{p}) - \mathcal{G}(\mathbf{p})\| \geq \epsilon) \leq \frac{1 - \|\mathcal{G}(\mathbf{p})\|^2}{r\epsilon^2} \quad (1.3)$$

where P above denotes probability and $\epsilon > 0$ is arbitrary.

Let $f(r)$ be a function which grows arbitrarily slowly, such that

$$\lim_{r \rightarrow \infty} f(r) = \infty$$

and

$$\lim_{r \rightarrow \infty} f(r)/\sqrt{r} = 0.$$

If

$$\epsilon = f(r)/\sqrt{r} \tag{1.4}$$

then (1.3) becomes

$$\lim_{r \rightarrow \infty} P(\|\tau(\mathbf{p}) - \mathcal{G}(\mathbf{p})\| \geq \epsilon) \leq \lim_{r \rightarrow \infty} \frac{1 - \|\mathcal{G}(\mathbf{p})\|^2}{f(r)^2} = 0$$

Therefore, $\tau(\mathbf{p})$ converges in probability to $\mathcal{G}(\mathbf{p})$ as the population size increases, and τ corresponds to \mathcal{G} in the infinite population case. Moreover, 1.4 suggests that the expected distance between finite and infinite population in the next generation might decrease as $1/\sqrt{r}$.

In figure 1.2, finite population points can be only at certain points, but infinite population points can be anywhere in the simplex. Theorem 3.1 in 'The Simple Genetic Algorithm: Foundations and Theory' states (see Vose (1999)):

If $\mathbf{p}, \mathbf{q} \in \Lambda$ are arbitrary population vectors for population size r , and $\boldsymbol{\xi}$ denotes an arbitrary element of Λ , then

$$\inf_{\mathbf{p} \neq \mathbf{q}} \|\mathbf{p} - \mathbf{q}\| = \sqrt{2}/r \tag{1.5}$$

$$\sup_{\boldsymbol{\xi}} \inf_{\mathbf{p}} \|\boldsymbol{\xi} - \mathbf{p}\| = O(1/\sqrt{r}) \tag{1.6}$$

where the constant (in the "big oh") is independent of the dimension n of Λ .

From 1.6, the distance between an infinite population $\boldsymbol{\xi}$ and finite population p is $O(1/\sqrt{r})$. This suggests that the distance between $\tau(\mathbf{p})$ and $\mathcal{G}(\mathbf{p})$ might decrease as $1/\sqrt{r}$.

Let η be the random variable $\|\mathbf{q} - \mathcal{G}(\mathbf{p})\|$, and let $\phi(x) = x^2$. It follows from Jensen's Inequality (see Wikipedia (2016b)) that since ϕ is a convex function,

$$\phi(\mathcal{E}(\eta)) \leq \mathcal{E}(\phi(\eta))$$

Therefore,

$$\mathcal{E}(\|\mathbf{q} - \mathcal{G}(\mathbf{p})\|) = \mathcal{E}(\eta) \leq \sqrt{\mathcal{E}(\eta^2)} = \frac{\sqrt{1 - \|\mathcal{G}(\mathbf{p})\|^2}}{\sqrt{r}} \quad (1.7)$$

This suggests that the distance between $\tau(\mathbf{p})$ and $\mathcal{G}(\mathbf{p})$ might decrease as $1/\sqrt{r}$.

1.4 Research Problems

- Equations 1.4, 1.6, and 1.7 all suggest that the distance between $\tau(\mathbf{p})$ and $\mathcal{G}(\mathbf{p})$ might decrease as $1/\sqrt{r}$. The first research question to consider is whether that rate of decrease is exhibited in practice. We investigate the rate of decrease with experiments in Chapter 2.
- An instance of RHS is *focused* if \mathcal{G} is continuously differentiable, and for every $\mathbf{p} \in \Lambda$ the sequence

$$\mathbf{p}, \mathcal{G}(\mathbf{p}), \mathcal{G}^2(\mathbf{p}), \dots$$

converges. In this case, \mathcal{G} is also called *focused*, and the path determined by following at each generation what τ is expected to produce will lead to some fixed point ω

$$\mathcal{G}(\omega) = \lim_{n \rightarrow \infty} \mathcal{G}^n(\mathbf{p}) = \omega.$$

When specialized to a simple GA (the details are explained in Chapter 2), it turns out that \mathcal{G} is focused under certain conditions, but under other conditions the sequence $\mathbf{p}, \mathcal{G}(\mathbf{p}), \mathcal{G}^2(\mathbf{p}), \dots$ converges to a periodic orbit which oscillates between fixed points of \mathcal{G}^2 (see Vose (1999)). If a finite population GA follows the infinite population GA closely, and if infinite populations oscillate under certain conditions, then finite populations might also show oscillating behavior. The second research question to consider is whether such finite population oscillation is exhibited in practice. We investigate finite population oscillation with experiments in Chapter 3.

- The third research question concerns the robustness of finite population oscillation. Consider the lattice points in the simple Λ which represent finite populations (for some fixed population size r) and let \mathbf{P}_j denote the j th population represented by the j th lattice point. Let $\boldsymbol{\pi}^k$ be the probability vector having as j th component the probability that \mathbf{P}_j is the k th generation. If $\boldsymbol{\pi}^0$ is the initial population distribution, the steady state distribution $\boldsymbol{\pi}$ is given by (see Häggström (2002))

$$\boldsymbol{\pi} = \lim_{k \rightarrow \infty} \boldsymbol{\pi}^k = \lim_{k \rightarrow \infty} \boldsymbol{\pi}^0 Q^k \quad (1.8)$$

assuming the limit exists. The j th component π_j can be interpreted as the proportion of time that a GA spends in population \mathbf{P}_j . If transition matrix Q is irreducible[¶] and aperiodic^{||}, then the Markov chain is regular (see Iosifescu (1980)), the steady state distribution $\boldsymbol{\pi}$ exists, and it has positive components (see Minc (1988)). The solution to equation 1.8 satisfies

$$\boldsymbol{\pi} = \boldsymbol{\pi} Q \quad (1.9)$$

where $\boldsymbol{\pi}$ is normalized so that its components sum to one. If GA were to perfectly oscillate between two populations \mathbf{P}_i and \mathbf{P}_j , then $\pi_i^k = 1$ (other components are 0) when k is odd, and $\pi_j^k = 1$ (other components are 0) when k is even. Therefore, perfect oscillation should not occur. In Chapter 4, we investigate oscillation behavior of finite populations when the Markov chain is regular. The third research question concerns whether finite population approximate oscillation can be exhibited in practice when the Markov chain is regular and infinite population trajectories have no periodic orbit.

[¶]A Markov chain is said to be *irreducible* if it is possible to get to any state from any state.

^{||}A Markov chain is *aperiodic* if it can return to state i at irregular times.

- The fourth research question also concerns the robustness of finite population oscillation. Can finite population approximate oscillation be exhibited in practice when infinite population trajectories have no periodic orbit due to the crossover distribution violating the condition required for infinite population oscillation?

Chapter 2

Extending A Genetic Algorithm Model To The Diploid Case

This chapter describes a simple Markov model for evolution under the influence of crossing over and mutation; it is a non-overlapping, generational, infinite population model under the assumption of *complete panmixia* (random mating) and no selective pressure. This chapter shows how diploid evolution equations can be represented by haploid equations and can be specialized to Vose's infinite population model, which is a haploid model.

A basic syntactic model for haploid and diploid genomes is first considered. Then the mechanics of how the next generation is obtained from current generation are defined abstractly in procedural terms, which serves to motivate the equations governing evolution. Next evolution equations are developed corresponding to the procedural description defining evolution for a population of diploid genomes. Observations concerning the form and symmetry of those equations directly lead to decoupling from the diploid case a haploid model sufficient to determine evolutionary trajectories for the diploid case. Mask based mutation and crossover operators are used to specialize haploid equations to Vose's infinite haploid population model. Analytical and computational simplification resulting from specialization to Vose's

infinite population model are explained and used in experimental simulation and study of convergence of finite population short-term behavior to behavior predicted by infinite population model. The results confirm that the distance between the short-term evolutionary trajectory of finite diploid populations and the evolutionary trajectory of infinite diploid populations can in practice decrease like the inverse of the square root of population size. Our first research question is thereby answered affirmatively.

2.1 Model

A haploid genome g is defined syntactically as a length ℓ binary string. A collection of h chromosomes may be modeled by partitioning g into h segments (of arbitrary lengths ℓ_1, \dots, ℓ_h ; thus $\ell = \ell_1 + \dots + \ell_h$).

A diploid genome $\alpha = \langle \alpha_0, \alpha_1 \rangle$ is likewise defined syntactically as a pair of length ℓ binary strings. Although simple, that syntax is flexible and possesses significant modeling power by means of tailoring partitioning to application. We concentrate on the abstract level, considering the evolution of a non-overlapping, generational, infinite population model assuming panmixia and no selective pressure. We are not concerned with whether and how partitioning is defined as it is irrelevant to the development.

Following Hardy (see [Hardy \(1908\)](#)), the model q^n at generation n is a vector having for component q_α^n the prevalence of diploid α (the probability of selecting α at generation n , assuming unbiased selection).[‡] Ordered diploid $\gamma = \langle \gamma_0, \gamma_1 \rangle$ is produced for generation $n + 1$ according to following procedural description.

Assuming independent selection events:

- From parent α — selected with probability q_α^n — obtain gamete γ_0
- From parent β — selected with probability q_β^n — obtain gamete γ_1

[‡]The representation here is the conceptual equivalent of Hardy's model.

Following Gieringer (see [Geiringer \(1944\)](#)), let the transmission function $t_\alpha(g)$ be the probability that gamete g is produced from parental genome α . It follows from the above that the equation determining the next generation q^{n+1} is

$$q_\gamma^{n+1} = \sum_\alpha q_\alpha^n t_\alpha(\gamma_0) \sum_\beta q_\beta^n t_\beta(\gamma_1) \quad (2.1)$$

It should be appreciated that the Mendelian (see [Mendel \(1865\)](#)) laws of segregation[§] and independent assortment[¶] need not be respected by the transmission function.

The right hand side of (2.1) is invariant under interchange of the summation variables α and β , which is equivalent to interchanging γ_0 and γ_1 . This symmetry reflects the fact that which haploid of γ is designated as γ_0 is arbitrary,

$$q_{\langle\gamma_0, \gamma_1\rangle}^{n+1} = q_{\langle\gamma_1, \gamma_0\rangle}^{n+1}$$

The model corresponding to (2.1) is low-level in the sense that it regards $\langle\gamma_0, \gamma_1\rangle$ and $\langle\gamma_1, \gamma_0\rangle$ as distinct when $\gamma_1 \neq \gamma_0$. A higher-level model based on sets is easily obtained,

$$q_{\{\gamma_0, \gamma_1\}} = \begin{cases} 2q_{\langle\gamma_0, \gamma_1\rangle} & \text{if } \gamma_0 \neq \gamma_1 \\ q_{\langle\gamma_0, \gamma_1\rangle} & \text{otherwise} \end{cases}$$

which is in agreement with Hardy (see [Hardy \(1908\)](#)).

2.2 Reduction

Evolution equation (2.1) may be reduced to the haploid case. Its right hand side is the product of two summations; denote the first by $p_{\gamma_0}^{n+1}$ and the second by $p_{\gamma_1}^{n+1}$ so that

$$q_{\langle\gamma_0, \gamma_1\rangle}^{n+1} = p_{\gamma_0}^{n+1} p_{\gamma_1}^{n+1} \quad (2.2)$$

[§]Alleles of a given locus segregate into separate gametes.

[¶]Alleles of one gene sort into gametes independently of the alleles of another gene.

where for any haploid γ_0 ,

$$p_{\gamma_0}^{n+1} = \sum_{\alpha} q_{\alpha}^n t_{\alpha}(\gamma_0) \quad (2.3)$$

It suffices to determine the evolution of the distributions p^n . Uncoupling p from q using (2.3), and equation (2.2) with superscript n — instantiate the n in (2.2) with $n - 1$ — yields the evolution equation

$$\begin{aligned} p_{\gamma_0}^{n+1} &= \sum_{\alpha_0, \alpha_1} q_{\langle \alpha_0, \alpha_1 \rangle}^n t_{\langle \alpha_0, \alpha_1 \rangle}(\gamma_0) \\ &= \sum_{\alpha_0, \alpha_1} p_{\alpha_0}^n p_{\alpha_1}^n t_{\langle \alpha_0, \alpha_1 \rangle}(\gamma_0) \end{aligned} \quad (2.4)$$

The p^n are in fact distributions; summing equation (2.2) with superscript n yields

$$1 = \sum_{\alpha} q_{\alpha}^n = \sum_{\alpha_0, \alpha_1} p_{\alpha_0}^n p_{\alpha_1}^n = \left(\sum_{\alpha_0} p_{\alpha_0}^n \right)^2$$

The weighted count of haploid g in generation n is

$$\sum_{\alpha_0, \alpha_1} q_{\langle \alpha_0, \alpha_1 \rangle}^n ([g = \alpha_0] + [g = \alpha_1]) \quad (2.5)$$

$$= \sum_{\alpha_0, \alpha_1} p_{\alpha_0}^n p_{\alpha_1}^n [g = \alpha_0] + \sum_{\alpha_0, \alpha_1} p_{\alpha_0}^n p_{\alpha_1}^n [g = \alpha_1] \quad (2.6)$$

$$= 2p_g^n \quad (2.7)$$

Hence the (normalized) prevalence of haploid g in generation n is the g th component of the distribution p^n . Moreover, (2.5) and (2.2) show (for $n > 0$) invertibility of the map

$$\pi : \mathbf{q}^n \longmapsto \mathbf{p}^n$$

Evolution equation (2.4) in matrix form is

$$p'_g = p^T M_g p \quad (2.8)$$

where current state p (generation n) and next state p' (generation $n + 1$) are column vectors, and the g th transmission matrix is

$$\left(M_g\right)_{u,v} = t_{\langle u,v \rangle}(g) \quad (2.9)$$

(vectors and matrices are indexed by haploids — length ℓ binary strings).

2.3 Specialization

This section summarizes from the development in Vose (see [Vose \(1999\)](#)). It specializes the haploid evolution equations in the previous section to a context where mask-based crossing over and mutation operators are used, leading to Vose’s infinite population model for Genetic Algorithms. Whereas in previous sections *component* referred to a component of a distribution vector q^n or p^n , in this section a component is either a probability (when when speaking of a component of a distribution vector), or a bit (when speaking of a component of a haploid).

2.3.1 Mutation

Mutation simulates low probability errors in chromosome duplication. Mutation provides a mechanism to inject new strings into the next generation. The symbol μ denotes mutation distribution describing the probability μ_i with which $i \in \Omega$ is selected to be a mutation mask. The result of mutating g is $g + i$ with probability μ_i . Mutating g using mutation mask i alters the bits of g in those positions the mutation mask i is 1. If g should mutate to g' with probability ρ , let

$$\mu_{g+g'} = \rho$$

Given distribution μ , mutation is the stochastic operator sending g to g' with probability $\mu_{g+g'}$. Abusing notation, $\mu \in [0, 0.5)$ is regarded as a *mutation rate* which implicitly specifies distribution μ according to the rule (see [Vose and Wright](#)

(1998))

$$\mu_i = (\mu)^{1^T i} (1 - \mu)^{\ell - 1^T i}$$

2.3.2 Crossover

Crossover refers to crossing over (also termed recombination) between two chromosomes (strings in our case). Crossover like mutation also provides a mechanism for injection of new strings into the next generation population. Geiringer (see Geiringer (1944)) used crossover masks to generate offsprings from parent chromosomes in absence of mutation and selection. Let χ_m be the probability distribution with which m is selected to be a crossover mask. Following Geiringer (see Geiringer (1944)), if crossing over u and v should produce u' and v' with probability ρ , let

$$\chi_m = \rho$$

where m is 1 at components which u' inherits from u , and 0 at components inherited from v . It follows that

$$\begin{aligned} u' &= mu + \overline{m}v \\ v' &= mv + \overline{m}u \end{aligned}$$

Given distribution χ , crossover is the stochastic operator which sends u and v to u' and v' with probability $\chi_m/2$.

Abusing notation, χ can be considered as a *crossover rate* that specifies the distribution χ given by the rule (see Vose and Wright (1998))

$$\chi_i = \begin{cases} \chi^{c_i} & \text{if } i > 0. \\ 1 - \chi + \chi^{c_0} & \text{if } i = 0. \end{cases}$$

where $c \in \Lambda$ is referred to as *crossover type*. Classical crossover types include *1-point crossover* and *uniform crossover*. For *1-point crossover*,

$$c_i = \begin{cases} 1/(\ell - 1) & \text{if } \exists k \in (0, \ell). i = 2^k - 1. \\ 0 & \text{otherwise.} \end{cases}$$

and for uniform crossover, $c_i = 2^{-\ell}$.

2.3.3 Mixing Matrix

The combined action of mutation and crossover is referred to as *mixing*. The *mixing matrix* M is the transmission matrix corresponding to the additive identity of \mathcal{R}

$$M = M_{\mathbf{0}}$$

Crossover and mutation are defined in a manner respecting arbitrary partitioning and arbitrary linkage to preserve the ability to endow abstract syntax with specialized semantics. Groups of loci can mutate and crossover with arbitrarily specified probabilities as discussed in above sections. For mutation distribution $\boldsymbol{\mu}$ and crossover distribution $\boldsymbol{\chi}$, the transmission function can be expressed as (see [Vose and Wright \(1998\)](#))

$$t_{\langle u, v \rangle}(g) = \sum_{i \in \mathcal{R}} \sum_{j \in \mathcal{R}} \sum_{k \in \mathcal{R}} \boldsymbol{\mu}_i \boldsymbol{\mu}_j \frac{\boldsymbol{\chi}_k + \boldsymbol{\chi}_{\bar{k}}}{2} [k(u + i) + \bar{k}(v + j) = g] \quad (2.10)$$

Here a child gamete g is produced via mutation and then crossover (which are operators that commute).

The mixing matrix M is a fundamental object, because (2.10) implies that evolution equation (2.8) can be expressed in the form

$$p'_g = (\sigma_g p)^T M (\sigma_g p) \quad (2.11)$$

where the permutation matrix σ_g is defined by component equations

$$(\sigma_g)_{u,v} = [u + v = g]$$

2.4 Walsh Transform

If $n \in \mathcal{R}$ and $t \in \mathcal{R}$, and N is the cardinality of \mathcal{R} , the Walsh matrix is defined by

$$W_{n,t} = N^{-1/2}(-1)^{n^T t} \quad (2.12)$$

where $N^{-1/2}$ can be thought of as a normalization factor.

The matrix is symmetric, i.e.,

$$W_{n,t} = W_{t,n}$$

and it has entries satisfying

$$W_{n,t+k} = N^{1/2} W_{n,t} W_{n,k}; \quad k \in \mathcal{R}.$$

The practical importance of this symmetry is that the transform and inverse are the same mathematical operation, and *Walsh matrix* is its own inverse,

$$W = W^{-1}.$$

Given vector w and matrix A , let \hat{w} and \hat{A} denote the Walsh transform of w and A respectively. Then $\hat{w} = Ww$ and $\hat{A} = WAW$ (see [Beauchamp \(1975\)](#)).

2.4.1 Fast Walsh Transform

Computation of the discrete Walsh transform given by equation (2.12) might take n^2 operations if implemented naively. An algorithm using $O(n \log_2 n)$ operations is the

Fast Walsh transform (FWT). Shanks (see [Shanks \(1969\)](#)) described FWT algorithm which is analogous to Cooley-Tukey algorithm (see [Cooley and Tukey \(1965\)](#)) for fast Fourier transformation. The algorithm for FWT can be translated into pseudocode as:

```

1: procedure FWT
2:    $n = 2^d \leftarrow$  size of array  $X$  where  $d$  is positive integer
3:   for  $i = 0$  to  $d - 1$  do
4:      $m = n/2^i$ 
5:      $z = m/2$ 
6:     for  $j = 0$  to  $2^i - 1$  do
7:       for  $k = 0$  to  $z - 1$  do
8:          $t1 = m \times j + k$ 
9:          $t2 = m \times j + z + k$ 
10:         $a = X[t1]$ 
11:         $b = X[t2]$ 
12:         $X[t1] = a + b$ 
13:         $X[t2] = a - b$ 
14:      end for
15:    end for
16:  end for
17:  return  $X$ 
18: end procedure

```

Algorithm 1: FWT pseudocode

2.4.2 Walsh Transform Adaptation

We adapt Walsh transform methods which have already been established for Vose’s haploid model (see [Vose and Wright \(1998\)](#)) for computing evolutionary trajectories, making feasible computation-based comparisons between finite and infinite diploid population short-term evolutionary behavior. Evolution equation (2.11), specialized to Vose’s infinite population model without selection, is simplified by changing basis to diagonalize the σ_g . Columns of the Walsh matrix W form the orthonormal basis — the *Walsh basis* — which simultaneously diagonalizes the σ_g . Expressed in the

Walsh basis (see [Vose and Wright \(1998\)](#)), the mixing matrix takes the form

$$\widehat{M}_{u,v} = 2^{\ell-1} [uv = \mathbf{0}] \widehat{\mu}_u \widehat{\mu}_v \sum_{k \in \overline{u+v}\mathcal{R}} \chi_{k+u} + \chi_{k+v} \quad (2.13)$$

and equation (2.11) takes the form

$$\widehat{p}'_g = 2^{\ell/2} \sum_{i \in g\mathcal{R}} \widehat{p}_i \widehat{p}_{i+g} \widehat{M}_{i,i+g} \quad (2.14)$$

where $g\mathcal{R} = \{gi \mid i \in \mathcal{R}\}$ (for any $g \in \mathcal{R}$).

The mapping from generation n to generation $n + 1$, determined in natural coordinates by equation (2.8) in terms of the transmission function (2.9), and given in Walsh coordinates by equation (2.14) in terms of the mixing matrix (2.13), is Markovian; the next state p' depends only upon the current state p . Let \mathcal{M} represent the mixing transformation,

$$p' = \mathcal{M}(p) \quad (2.15)$$

and let $\mathcal{M}^n(p)$ denote the n -fold composition of \mathcal{M} with itself; thus generation $n + 1$ is described by

$$p^{n+1} = \mathcal{M}^n(p^1)$$

where $p^1 = \pi(q^1)$. We have little to say about the matrix of the Markov chain corresponding to the mixing transformation \mathcal{M} , because it is uncountable; each state is a distribution vector p describing a population. However, that is not an obstacle to computing evolutionary trajectories; (2.15) can be computed in Walsh coordinates relatively efficiently via (2.13) and (2.14).

2.5 Distance

Let vector \mathbf{f} represent a finite diploid population; component \mathbf{f}_α is the prevalence of diploid α . Let the support $S_{\mathbf{f}}$ of \mathbf{f} be the set of diploids occurring in the population

represented by \mathbf{f} ,

$$S_{\mathbf{f}} = \{\alpha \mid \mathbf{f}_{\alpha} > 0\}$$

Let \mathbf{q} similarly represent an infinite diploid population (see section 2.1). As points in $\mathbb{R}^{2^{\ell} \times 2^{\ell}}$, the Euclidean distance between \mathbf{f} and \mathbf{q} is

$$\|\mathbf{f} - \mathbf{q}\| = \sum_{\alpha}^{\frac{1}{2}} (\mathbf{f}_{\alpha} - \mathbf{q}_{\alpha})^2$$

Whereas a naive computation of this distance involves $2^{\ell} \cdot 2^{\ell}$ terms, leveraging equation (2.2) can significantly reduce the number of terms involved. Note that

$$\|\mathbf{f} - \mathbf{q}\|^2 = \sum_{\alpha \notin S_{\mathbf{f}}} (\mathbf{f}_{\alpha} - \mathbf{q}_{\alpha})^2 + \sum_{\alpha \in S_{\mathbf{f}}} (\mathbf{f}_{\alpha} - \mathbf{q}_{\alpha})^2 \quad (2.16)$$

Using equation (2.2) — $\mathbf{q}_{\alpha} = \mathbf{p}_{\alpha_0} \mathbf{p}_{\alpha_1}$ (suppressing superscripts to streamline notation) — together with the fact that $\mathbf{f}_{\alpha} = 0$ in every term of the first sum above, the first sum reduces to

$$\begin{aligned} \sum_{\langle \alpha_0, \alpha_1 \rangle \notin S_{\mathbf{f}}} (\mathbf{p}_{\alpha_0} \mathbf{p}_{\alpha_1})^2 &= \sum_{\langle \alpha_0, \alpha_1 \rangle} (\mathbf{p}_{\alpha_0})^2 (\mathbf{p}_{\alpha_1})^2 - \sum_{\langle \alpha_0, \alpha_1 \rangle \in S_{\mathbf{f}}} (\mathbf{p}_{\alpha_0} \mathbf{p}_{\alpha_1})^2 \\ &= \sum_g^2 (\mathbf{p}_g)^2 - \sum_{\alpha \in S_{\mathbf{f}}} (\mathbf{q}_{\alpha})^2 \end{aligned} \quad (2.17)$$

It follows from (2.16) and (2.17) that

$$\begin{aligned} \|\mathbf{f} - \mathbf{q}\|^2 &= \sum_g^2 (\mathbf{p}_g)^2 + \sum_{\alpha \in S_{\mathbf{f}}} (\mathbf{f}_{\alpha} - \mathbf{q}_{\alpha})^2 - \sum_{\alpha \in S_{\mathbf{f}}} (\mathbf{q}_{\alpha})^2 \\ &= \sum_g^2 (\mathbf{p}_g)^2 + \sum_{\alpha \in S_{\mathbf{f}}} \mathbf{f}_{\alpha} (\mathbf{f}_{\alpha} - 2\mathbf{q}_{\alpha}) \end{aligned} \quad (2.18)$$

which involves $2^{\ell} + |S_{\mathbf{f}}|$ terms, assuming that $S_{\mathbf{f}}$ is known as a byproduct of computing

f. Therefore, (2.18) computes distance between finite and infinite population efficiently.

2.6 Simplification

Computations in the haploid case are simplified by equations (2.13) and (2.14) which follow from specializing to Vose’s infinite population model and computing in the Walsh basis. Time switching between the standard basis and the Walsh basis is negligible; the fast Walsh transform (in dimension n) has complexity $n \log n$ (see Shanks (1969)).

Only one mixing matrix as opposed to 2^ℓ matrices is needed to compute the next generation; evolution equation (2.14) references the same matrix for every g , whereas evolution equation (2.8) depends upon a different matrix M_g for each choice of g . The matrix is computed by a single sum as opposed to a triple sum; compare equation (2.13) with equation (2.10). Also, the relevant quadratic form is computed with a single sum as opposed to a double sum; computing via (2.14) is linear time in the size of $g\mathcal{R}$ (for each g) as opposed to the quadratic time computation (for each g) represented by equation (2.8).

From a computational standpoint, the best-case scenario is where recomputation of the matrices mentioned in the previous paragraph is obviated by sufficient memory. The reduction from 2^ℓ matrices to one matrix helps significantly in that regard. To demonstrate this advantage in concrete terms, consider genomes of length $\ell = 14$. Using 2^{14} matrices each of which contains $2^{14} \times 2^{14}$ entries of type `double` requires 32 terabytes, whereas the mixing matrix at 2 gigabytes fits easily within the memory of a laptop. Moreover, for a population size of $N \leq 2^{20}$, the distance computation described in the previous section reduces the number of terms involved by a factor of $2^{28}/(2^{14} + 2^N) > 252$.

2.7 Convergence

This section presents a cursory numerical investigation of the convergence of finite diploid population short-term behaviour to that of the infinite diploid population model as described in section 2 (the underlying haploid model for the infinite population case is described in section 2.1).

Equations (2.2), (2.13), (2.14), (2.18) were employed to efficiently compute the distance

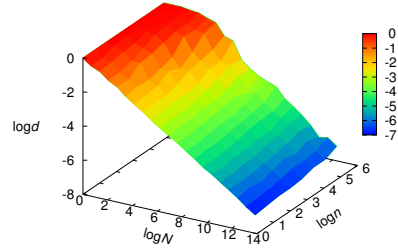
$$d = \|\mathbf{f}^n - \mathbf{q}^n\|$$

where \mathbf{f}^n and \mathbf{q}^n represent finite and infinite diploid populations (respectively) at generation $n \in \{1, 2, 4, 8, 16, 32, 64, 128\}$, beginning from a random initial population ($\mathbf{f}^0 = \mathbf{q}^0$). Genome lengths $\ell \in \{4, 6, 8, 10, 12, 14\}$ and population sizes $N = 2^i$ for integer $0 \leq i \leq 20$ were considered. The crossover distribution χ corresponds to independent assortment of bits, and the mutation distribution μ corresponds to independent bit mutation probability 0.001,

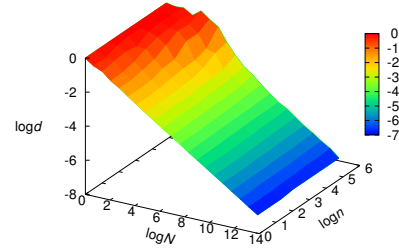
$$\chi_m = 2^{-\ell}, \quad \mu_g = (0.001)^{\mathbf{1}^T g} (0.999)^{\ell - \mathbf{1}^T g}$$

(subscripts above on the left hand side of an equality are interpreted on the right hand side of the equality as column vectors in \mathbb{R}^ℓ). The finite population case is computed using the itemized procedural definition given in section 2.1; the transmission function (2.10) corresponds to μ and χ above (bits mutate independently and are freely assorted).

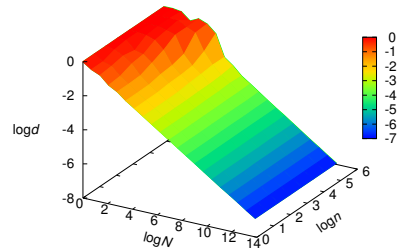
The data, presented in six surface graphs in **Figure 2.1** and organized by genome length, shows a near linear dependence of $\log d$ on $\log N$. As expected, the graphs show smoothing with increasing genome length (the computation of d involves averaging over ℓ components), and also with increased population size (as explained in Vose (1999), the initial transient of a finite haploid population trajectory converges as $N \rightarrow \infty$ to the corresponding infinite population model).



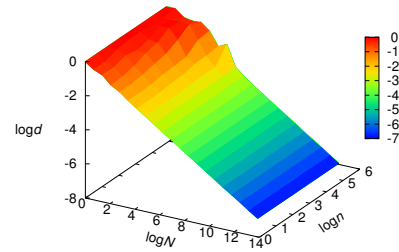
(a) $\ell = 4$.



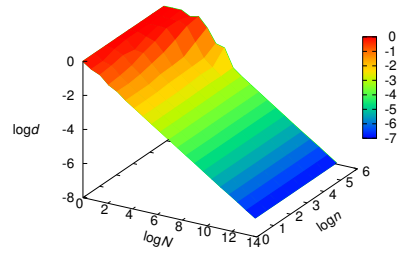
(b) $\ell = 6$.



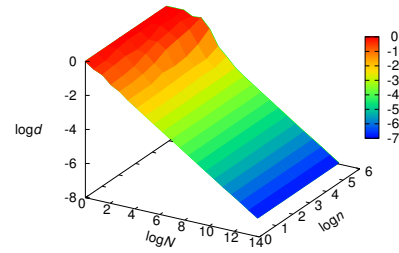
(c) $\ell = 8$.



(d) $\ell = 10$.



(e) $\ell = 12$.



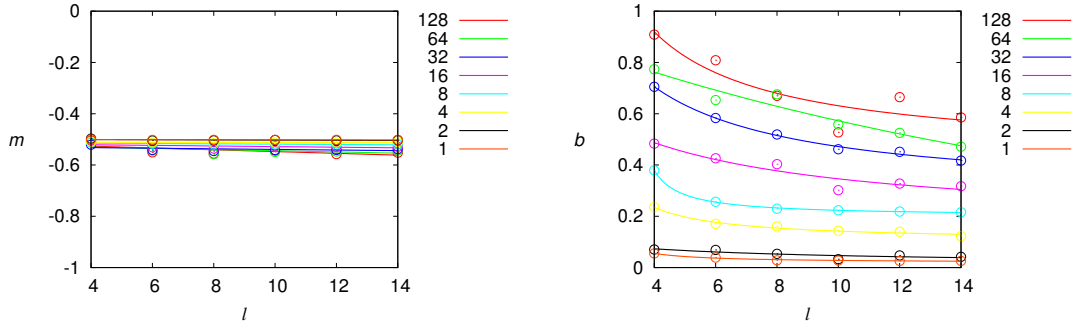
(f) $\ell = 14$.

Figure 2.1: Convergence of finite population behaviour: d is distance between finite population \mathbf{f}^n and infinite population \mathbf{q}^n at generation n , population size N , for genome length ℓ (bits).

Of particular interest is the linear trend exhibited above. The slope m and intercept b of the regression line

$$\log d = m \log N + b \quad (2.19)$$

was computed using the data above; each was plotted against genome length ℓ and organized by generation n . The resulting graphs are displayed below.



(a) Slope m , genome length ℓ .

(b) Intercept b , genome length ℓ .

Figure 2.2: Regression parameters: multi-plot of slope m and intercept b for generation $n \in \{1, 2, 4, 8, 16, 32, 64, 128\}$.

Taking the exponential of the regression line (2.19) yields the estimate $d \approx N^m e^b$.

Slopes of the regression lines shown in **Figure 2.2** are approximately -0.5 , indicating

$$d \approx k/\sqrt{N}. \quad (2.20)$$

Equation 2.20 agrees with (1.3), (1.7) and theorem 3.1 from 'The Simple Genetic Algorithm: Foundations and Theory' (see Vose (1999)) which gives the bound for the expected rate of convergence for the single-step haploid case; the distance is inversely proportional to square root of population size. The consistent convergence rate across multiple generations shown in Figure (2.1) is somewhat surprising, simulation results above indicate it may persist to generation $n = 128$.

The intercept graphs in **Figure 2.2 b** show the constant of proportionality $k = e^b$ decreases monotonically with genome length ℓ , and increases monotonically with generation n . The increase in k for larger n seems to be a manifestation of the growing nonlinearity uniformly exhibited by the plots in **Figure 2.1** as n increases. It seems likely that the nonlinearity results from genetic drift experienced by finite populations (see [Crow and Kimura \(1970\)](#)).

2.8 Summary

We began with a description of simple diploid Markov model under mutation and crossover with no selective pressure. The model was reduced to the haploid case and specialized using mask based recombination operators to show Vose’s infinite population model can be extended to the diploid case. Using computational benefits of this reduction, we showed via experiment and regression of the resulting data that distance between finite diploid population and infinite diploid population can indeed decrease like $1/\sqrt{N}$ in practice. That rate of decrease is consistent with the single step-step convergence bounds predicted by Vose’s infinite population model for the haploid case.

Chapter 3

Oscillation

This chapter investigates the qualitative similarity between finite population short-term behavior and infinite population evolutionary limits predicted by Vose. It uses computation to verify predicted infinite population limits and presents necessary and sufficient conditions for convergence to periodic orbits. We compute mutation distribution μ and crossover distribution χ to satisfy those conditions. Through experiments, we explore our second research question: can finite populations exhibit oscillation behavior in practice?

3.1 Limits

Vose states that under mild assumptions on mutation (explained later), infinite populations converge under repeated application of \mathcal{M} in the absense of selective pressure. Vose mentions that periodic orbits are possible, but populations converge under repeated application of \mathcal{M}^2 and the limits $\mathbf{p}^* = \lim_{n \rightarrow \infty} \mathcal{M}^{2n}(\mathbf{p})$ and $\mathbf{q}^* = \lim_{n \rightarrow \infty} \mathcal{M}^{2n+1}(\mathbf{q})$ exist (see [Vose \(1999\)](#)).

Following Vose (see [Vose \(1999\)](#)), let $S_g = g\mathcal{R}/\{\mathbf{0}, g\}$, and let $|g|$ be the number of non zero bits in g . If $\hat{\mathbf{p}}$ represents the current population in Walsh coordinates,

then the next generation $\widehat{\mathbf{p}}'_g$ (expressed in Walsh coordinates) is

$$\widehat{\mathbf{p}}'_g = \begin{cases} 2^{\ell/2} & \text{if } g = 0 \\ x_g \widehat{\mathbf{p}}_g + y_g(\widehat{\mathbf{p}}_g) & \text{otherwise} \end{cases}$$

where

$$x_g = 2\widehat{\mathcal{M}}_{g,0}, \quad y_g(z) = 2^{\ell/2} \sum_{i \in S_g} z_i z_{i+g} \widehat{\mathcal{M}}_{i,i+g}.$$

Moreover,

$$\begin{aligned} |g| = 1 &\implies y_g = 0 \\ |g| > 0 &\implies |x_g| \leq 1 \\ |x_g| = 1 &\implies y_g = 0 \end{aligned}$$

With above notations, the limits can be expressed in the Walsh basis by recursive equations (see [Vose \(1999\)](#))

$$\widehat{\mathbf{p}}^*_g = \begin{cases} (x_g y_g(\widehat{\mathbf{p}}^*) + y_g(\widehat{\mathbf{q}}^*)) / (1 - x_g^2) & \text{if } |x_g| < 0 \\ \widehat{p}_g & \text{otherwise} \end{cases} \quad (3.1)$$

$$\widehat{\mathbf{q}}^*_g = \begin{cases} (x_g y_g(\widehat{\mathbf{q}}^*) + y_g(\widehat{\mathbf{p}}^*)) / (1 - x_g^2) & \text{if } |x_g| < 0 \\ \widehat{\mathcal{M}(\mathbf{p})}_g & \text{otherwise} \end{cases} \quad (3.2)$$

If $x_g \neq -1$ for all g , then $\mathbf{p}^* = \mathbf{q}^* = \lim_{n \rightarrow \infty} \mathcal{M}(\mathbf{p})$ is the limit of mixing. In other cases, mixing converges to a periodic orbit oscillating between \mathbf{p}^* and $\mathbf{q}^* = \mathcal{M}(\mathbf{p}^*)$.

Limits $\widehat{\mathbf{p}}^*_g$ and $\widehat{\mathbf{q}}^*_g$ can be computed considering g th components in order of increasing $|g|$. The necessary and sufficient condition for the sequence

$$\mathbf{p}, \mathcal{M}(\mathbf{p}), \mathcal{M}^2(\mathbf{p}), \dots$$

to converge to a periodic orbit is that for some g

$$-1 = \sum_j (-1)^{g^T j} \mu_j = - \sum_{k \in \bar{g}\mathcal{R}} \chi_{k+g} + \chi_k \quad (3.3)$$

3.2 Mutation and Crossover Distributions

The following describes the generation of mutation and crossover distributions that satisfy equation 3.3 for evolution to converge to a periodic orbit. Let μ and χ represent mutation and crossover distributions (respectively), and let $U01()$ return a random number between 0 and 1. For any $g \in \mathcal{R}$, $g \neq 0$, and for all $j \in \mathcal{R}$,

$$\mu_j = \begin{cases} U01() & \text{if } g^T j \text{ is odd} \\ 0 & \text{otherwise} \end{cases} \quad (3.4)$$

Normalization yields μ (the mutation distribution),

$$\mu_j := \mu_j / \sum_{j \in \mathcal{R}} \mu_j.$$

Moreover, μ satisfies condition 3.3.

Condition $k \in \bar{g}\mathcal{R}$ in equation 3.3 is

$$k = \bar{g}i \text{ for some } i \in \mathcal{R}$$

Multiplying through by \bar{g} yields

$$\bar{g}k = \bar{g}\bar{g}i = i = k$$

The crossover distribution can therefore be generated as follows. For all $k \in \mathcal{R}$,

$$\begin{aligned}\chi_k &= U01() \text{ if } \bar{g}k = k \\ \chi_{k+g} &= U01() \text{ if } \bar{g}k = k \\ \chi_k &= 0 \text{ otherwise.}\end{aligned}\tag{3.5}$$

Normalization yields χ (the crossover distribution),

$$\chi_k := \chi_k / \sum_{k \in \mathcal{R}} \chi_k.$$

Moreover, χ_k satisfies condition 3.3.

3.3 Initial Population

To investigate oscillation in infinite population and finite population behavior, it is desirable to have the same or corresponding initial populations.

For string length ℓ , the number of possible haploids is $x = 2^\ell$. Let array \mathbf{t} represent a population of size N as follows: \mathbf{t}_j is the j th population member (some element of $\{0, \dots, x-1\}$ where elements are base 2 length ℓ binary strings). Array \mathbf{t} is generated from a random vector \mathbf{u} of size x as follows.

$$\begin{aligned}\mathbf{u}_i &= U01(); & i = 0, \dots, x-1 \\ \mathbf{t}_j &= randp(\mathbf{u}); & j = 0, \dots, N-1\end{aligned}$$

where $randp(\mathbf{u})$ returns random index i into array \mathbf{u} with probability \mathbf{u}_i .

Let \mathbf{c}_i be the count of haploid member i in population \mathbf{t} ,

$$\mathbf{c}_i = \sum_{j=0}^{N-1} [\mathbf{t}_j = i]; \quad i = 0, \dots, x-1$$

The infinite population vector \mathbf{p} has i th component

$$p_i = \frac{c_i}{N}.$$

This randomly generated infinite haploid population vector \mathbf{p} is used to obtain a diploid infinite population vector \mathbf{q} , and finite population vectors \mathbf{s} and \mathbf{f} as follows.

Infinite diploid population \mathbf{q} is calculated corresponding to initial haploid population \mathbf{p} as

$$q_{i,j} = p_i p_j; \quad (0 \leq i, j < x)$$

The finite haploid population members are the elements of array \mathbf{t} , the corresponding finite haploid population vector \mathbf{s} is identical to \mathbf{p} . Let \mathbf{v} be a finite diploid population member array of dimension two and of size N^2 whose diploid member $\mathbf{v}[i][j]$ at index $[i][j]$ is

$$\mathbf{v}[i][j] = \langle \mathbf{t}_i, \mathbf{t}_j \rangle \quad 0 \leq i, j < N$$

The finite diploid population (proportion) vector \mathbf{f} corresponding to finite diploid population member array \mathbf{v} is identical to \mathbf{q} .

Thus, initial infinite haploid population vector \mathbf{p} corresponds to initial infinite diploid population vector \mathbf{q} , and to initial finite haploid population vector \mathbf{s} with population size N and population member array \mathbf{t} , and to initial finite diploid population vector \mathbf{f} with population size N^2 and population member array \mathbf{v} .

3.4 Oscillation

Crossover distribution χ and mutation distribution μ satisfying condition (3.3) are considered to investigate oscillating behavior near predicted infinite population evolutionary limits.

Infinite haploid population evolutionary limits \mathbf{p}_h^* and \mathbf{q}_h^* were computed using equations (3.1) and (3.2). Infinite diploid population evolutionary limits \mathbf{p}_d^* and \mathbf{q}_d^* are obtained as follows

$$\begin{aligned}(\mathbf{p}_d^*)_{\langle \gamma_0, \gamma_1 \rangle} &= (\mathbf{p}_h^*)_{\gamma_0} (\mathbf{p}_h^*)_{\gamma_1} \\ (\mathbf{q}_d^*)_{\langle \gamma_0, \gamma_1 \rangle} &= (\mathbf{q}_h^*)_{\gamma_0} (\mathbf{q}_h^*)_{\gamma_1}\end{aligned}$$

where $\gamma = \langle \gamma_0, \gamma_1 \rangle$ is a diploid genome.

For every genome length ℓ , the same initial population (calculated as described in (3.3)) was used for the infinite population and all sizes of finite populations considered. Genome lengths $\ell \in \{8, 10, 12, 14\}$ were used. Base population size of $N_0 = 64$ was used for the finite haploid case to compute initial population vector. The population sizes considered for plotting graphs were $N \in \{N_0^2, 10N_0^2, 20N_0^2\}$. To study oscillation in finite populations, the distances of \mathbf{p}^n and \mathbf{s}^n to haploid evolutionary limits \mathbf{p}_h^* and \mathbf{q}_h^* were plotted and the distances of \mathbf{q}^n and \mathbf{f}^n to diploid evolutionary limits \mathbf{p}_d^* and \mathbf{q}_d^* were plotted.

According to the results and conclusions from chapter 2, the expected distance d between finite population of size N and infinite population is

$$d \approx 1/\sqrt{N}$$

Table 3.1: Expected single step distance d for population size N

| | | | |
|-----|--------|--------|--------|
| N | 4096 | 40960 | 81920 |
| d | 0.0156 | 0.0049 | 0.0035 |

The distance between finite population and infinite population, for both haploid and diploid cases, were also plotted.

3.4.1 Haploid Population

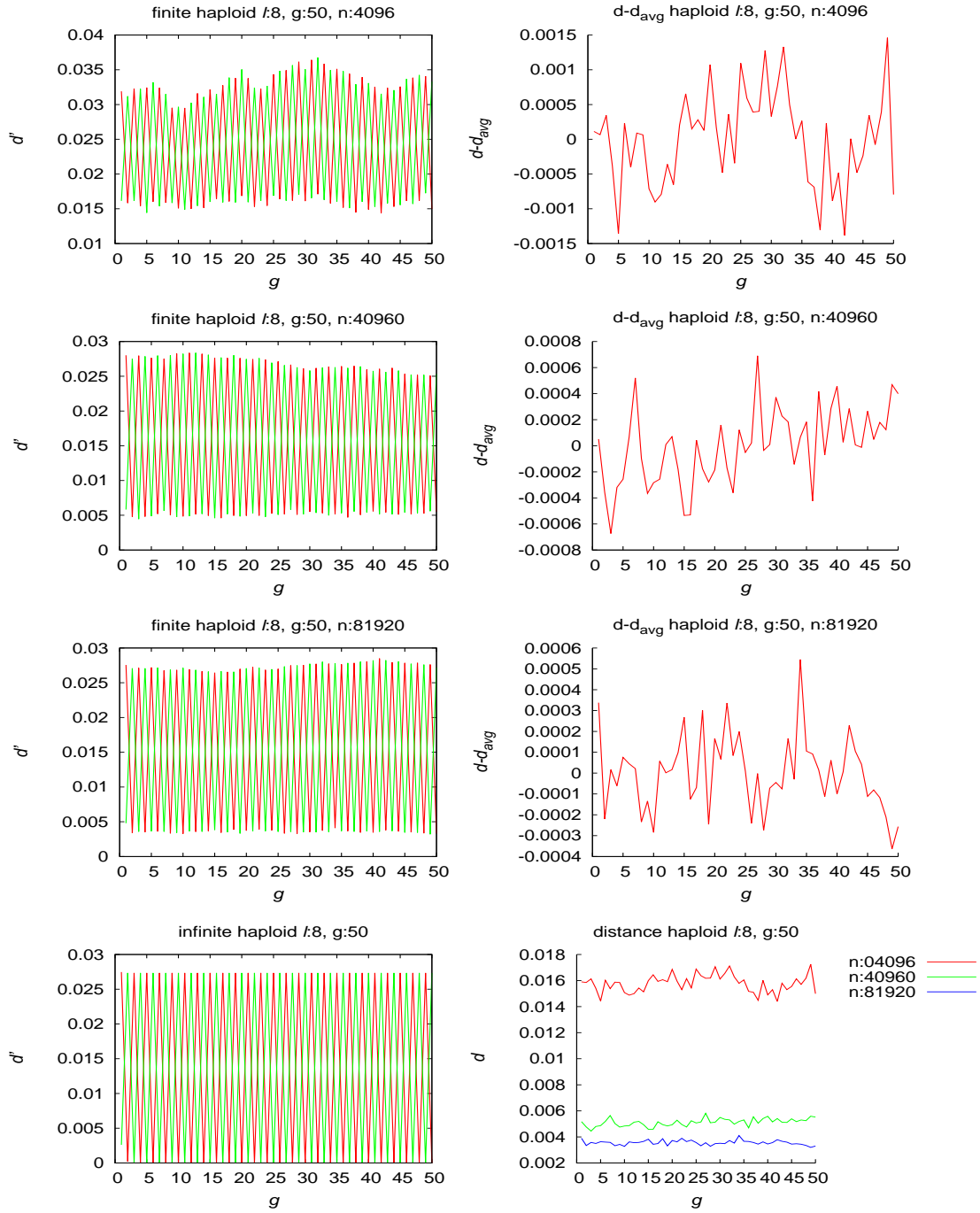


Figure 3.1: Infinite and finite haploid population oscillation behavior for genome length $\ell = 8$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

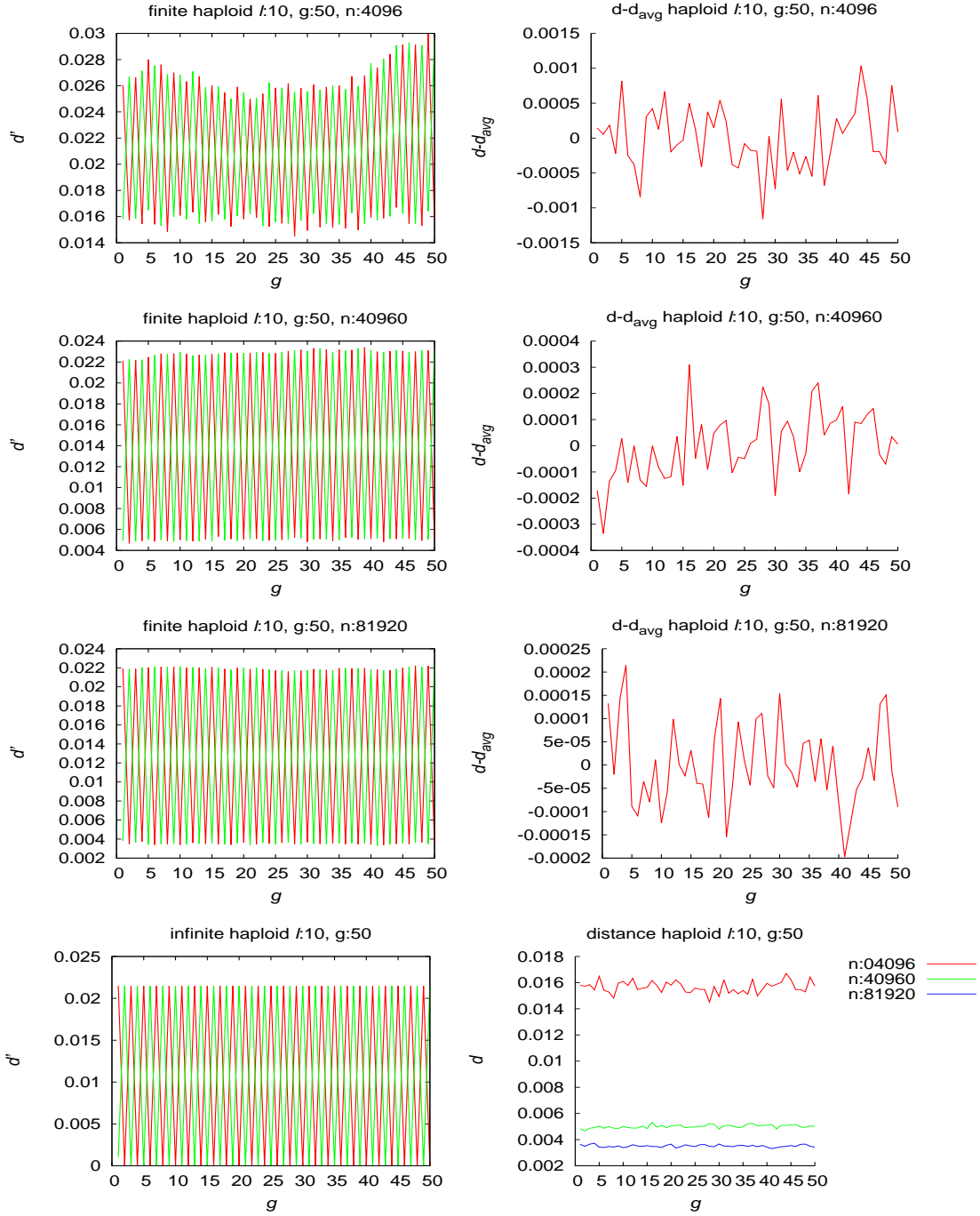


Figure 3.2: Infinite and finite haploid population oscillation behavior for genome length $\ell = 10$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

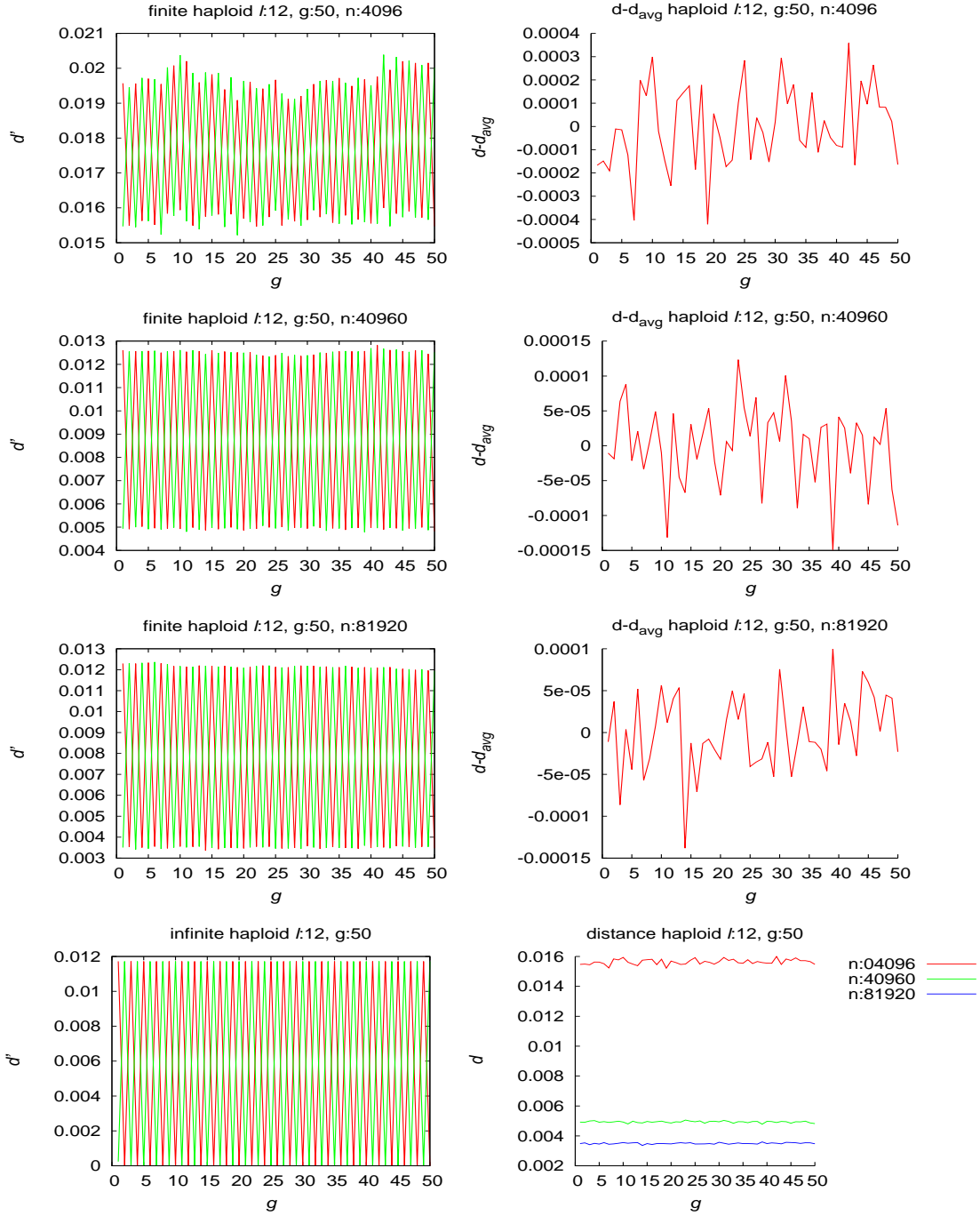


Figure 3.3: Infinite and finite haploid population oscillation behavior for genome length $\ell = 12$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

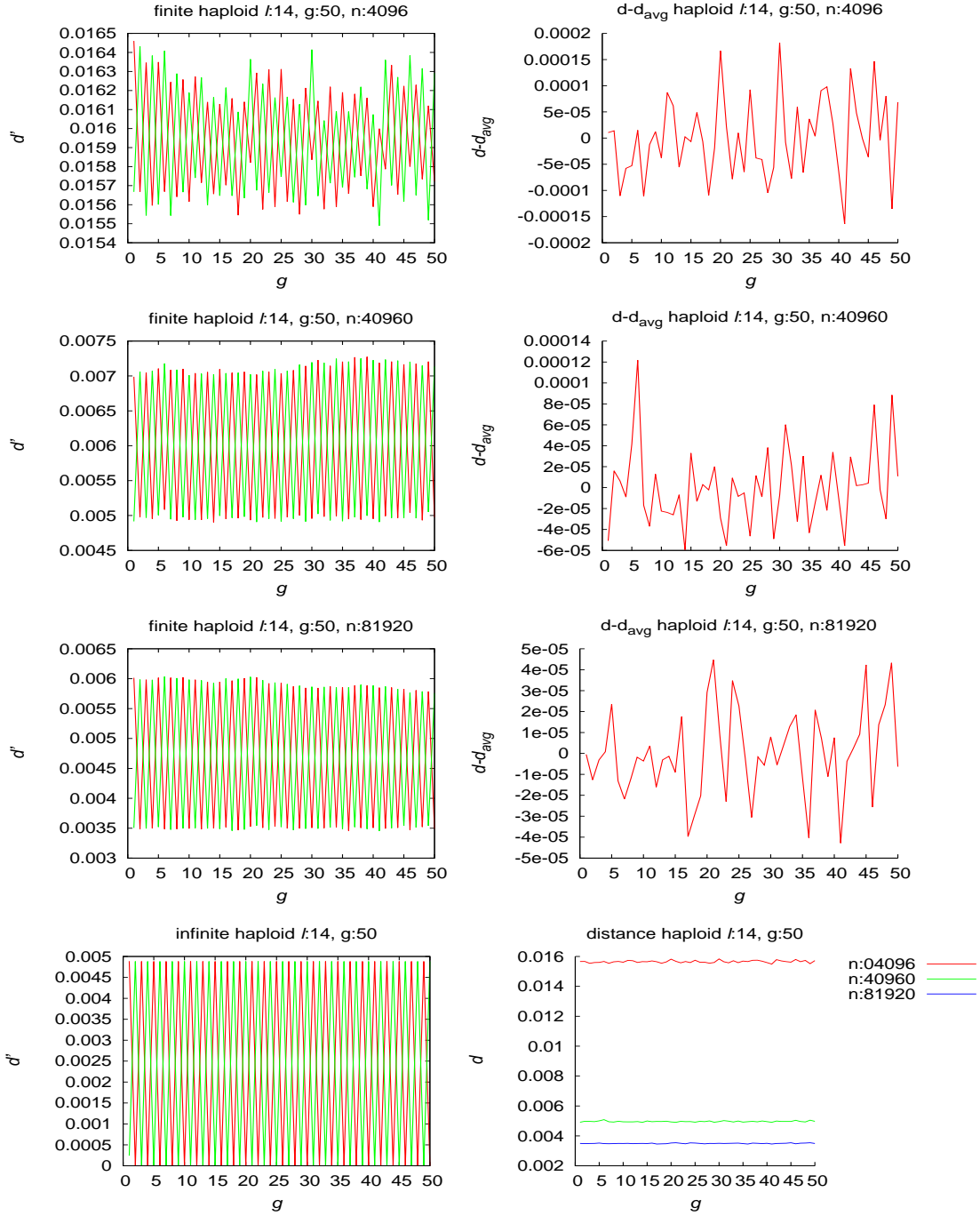


Figure 3.4: Infinite and finite haploid population oscillation behavior for genome length $\ell = 14$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

Figures 3.1, 3.2, 3.3 and 3.4 show oscillations in finite haploid populations, and distances between finite haploid populations and infinite haploid populations arranged by genome length ℓ in ascending order. In each figure for unique genome length ℓ , sub-figures are arranged by population size N . In each figure, the first three rows of sub-figures in the left column show distance d' of finite population to limits, the sub-figure in fourth row of the left column shows distance d' of infinite population to limits. These sub-figures depict oscillating behavior of both infinite and finite haploid populations when condition 3.3 is met. As population size increases, oscillation approaches the behavior exhibited by infinite population.

In each figure (3.1, 3.2, 3.3, and 3.4), the first three graphs in the right column show distance variation (difference of distance d and average distance d_{avg}) where d is distance between haploid finite and infinite populations and d_{avg} is average value of d . The graph in the fourth row of the right column combines distance plots between finite and infinite populations for sizes ($N = N_0^2, 10N_0^2, 20N_0^2$). The resulting graphs show distance decreases as population size increases, consistent with results from section 2.1. The graphs of $d - d_{avg}$ decrease in amplitude as population size increases. For fixed finite population size, as ℓ increases, the distance graphs become smoother, and amplitude of oscillations decrease.

Distance data obtained from simulations for haploid populations are summarized in table 3.2, which tabulates average distance between finite and infinite populations for population sizes $N = 4096$, $N = 40960$ and $N = 81920$.

Results from table 3.2 show average distance between finite and infinite population closely follows the expected single step distance. The distance decreases as $1/\sqrt{N}$.

Table 3.2: Distance measured for haploid population: N is population size, ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0158 | 0.0051 | 0.0035 |
| 10 | 0.0157 | 0.0050 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

3.4.2 Diploid Population

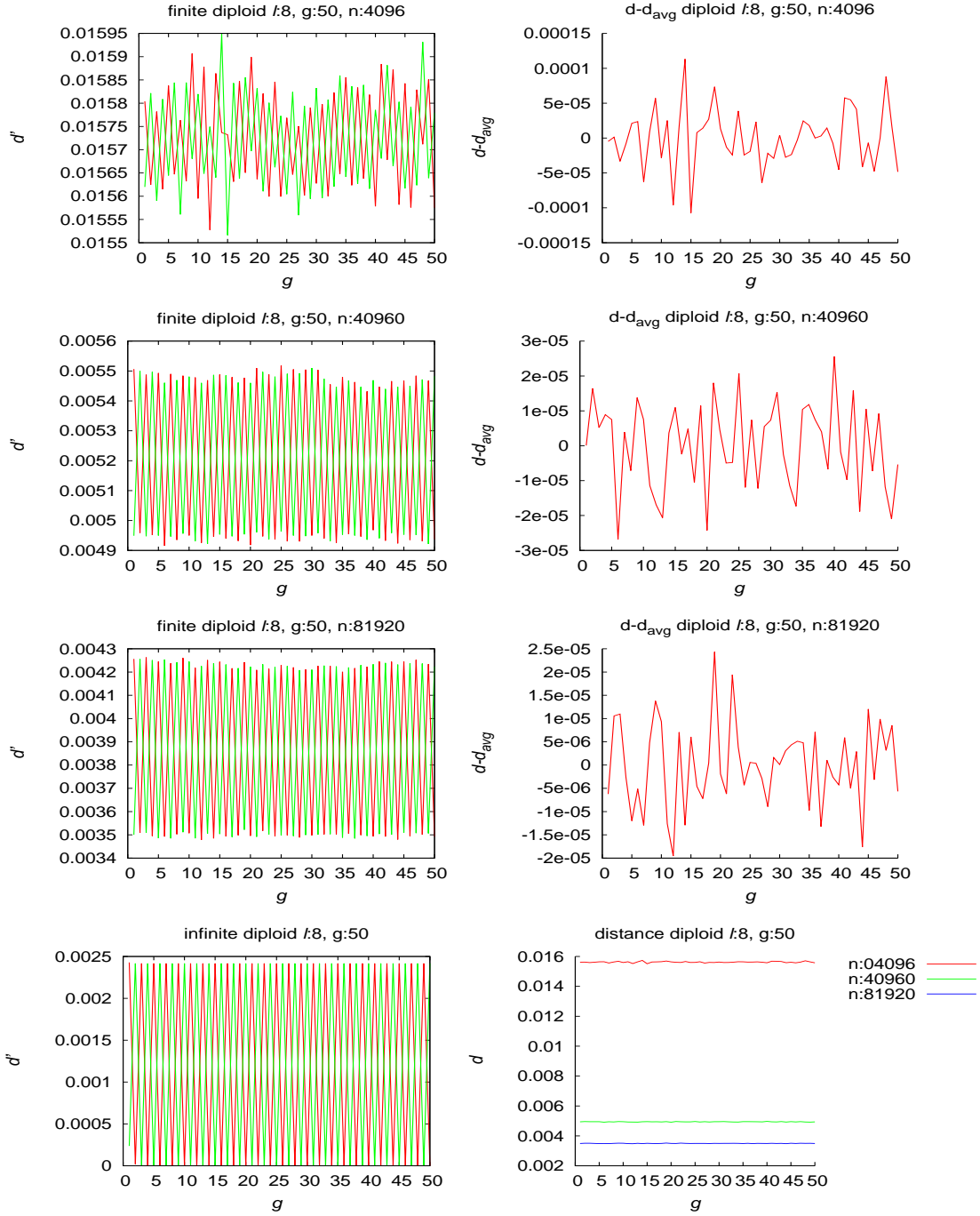


Figure 3.5: Infinite and finite diploid population oscillation behavior for genome length $\ell = 8$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

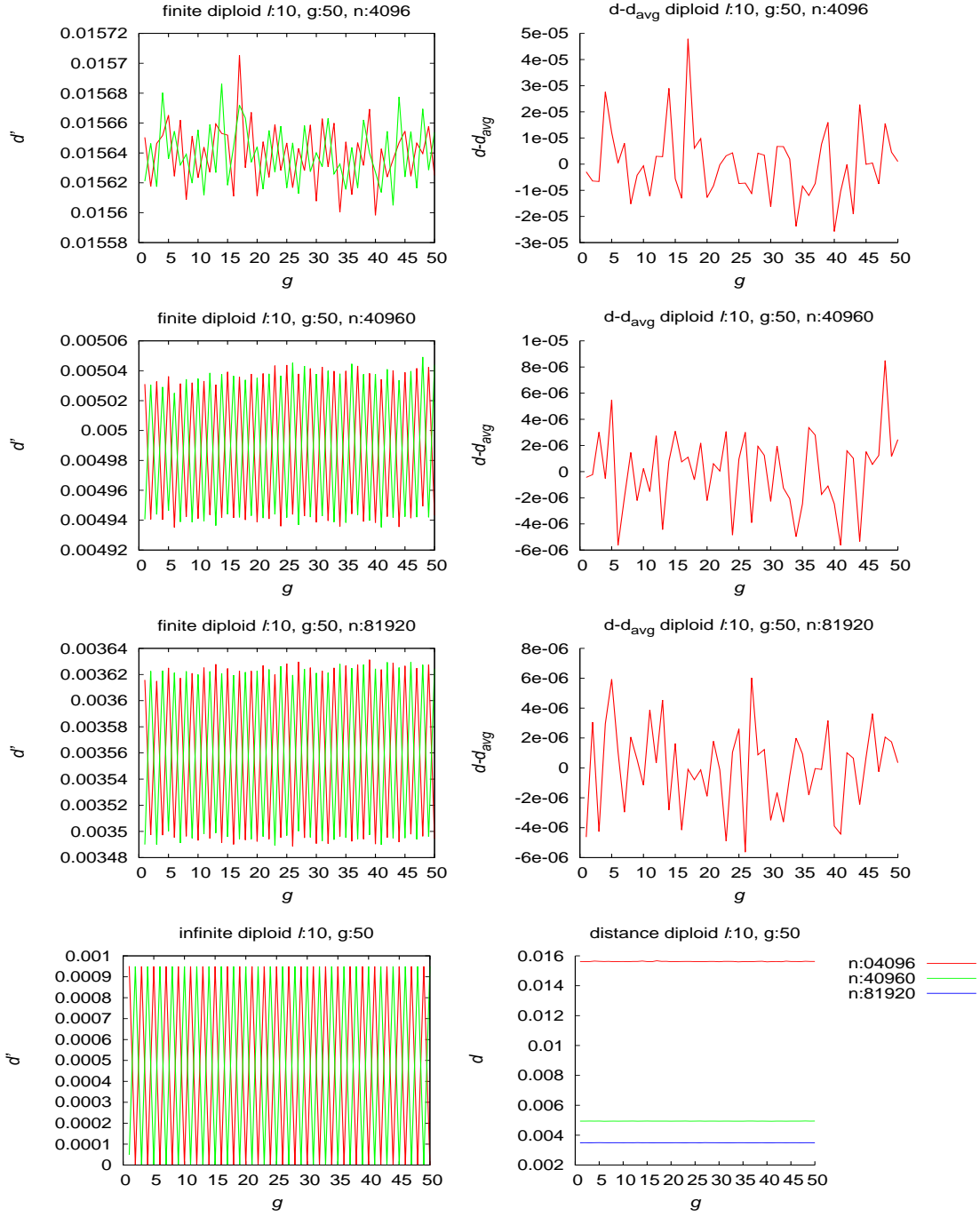


Figure 3.6: Infinite and finite diploid population oscillation behavior for genome length $\ell = 10$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

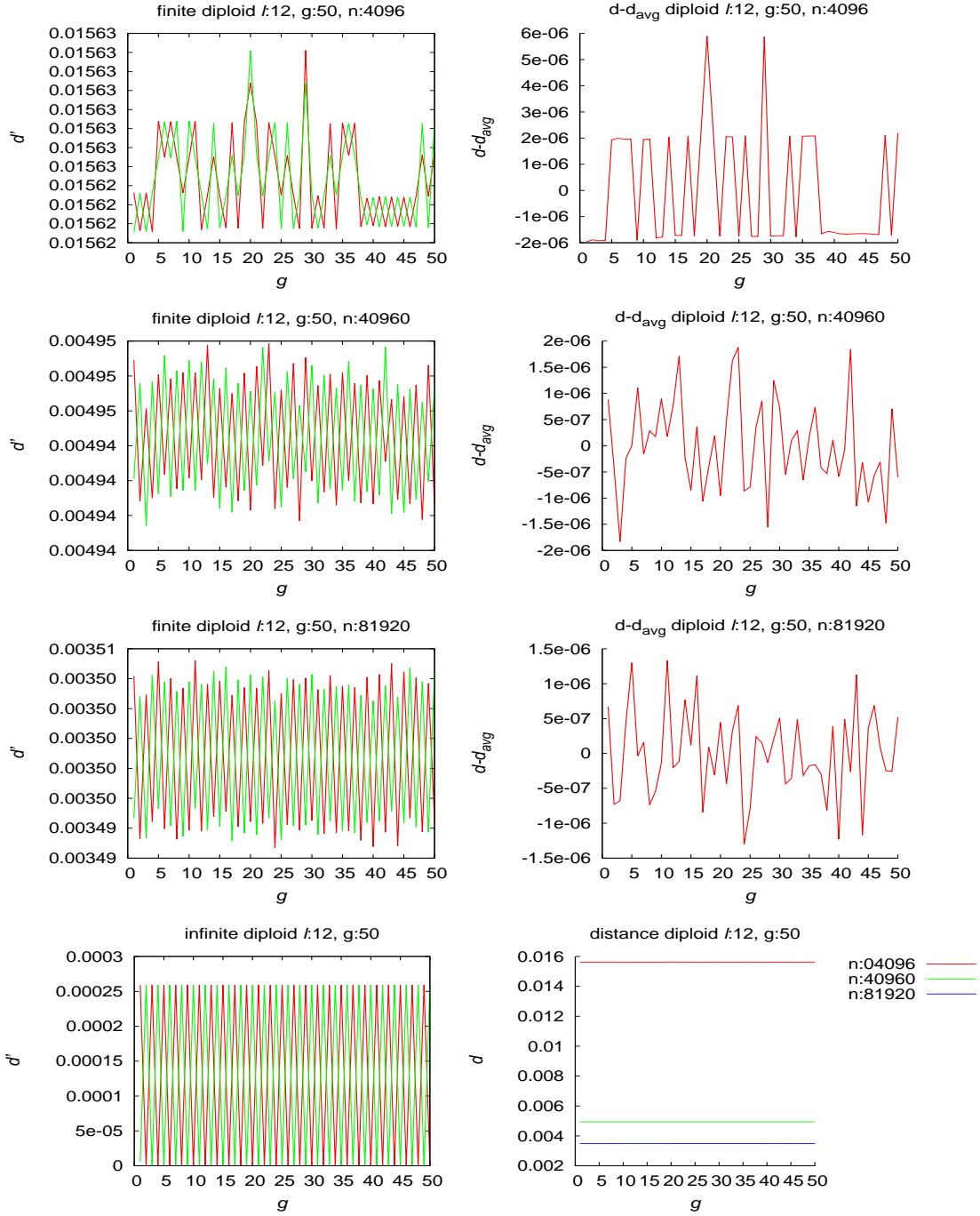


Figure 3.7: Infinite and finite diploid population oscillation behavior for genome length $\ell = 12$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

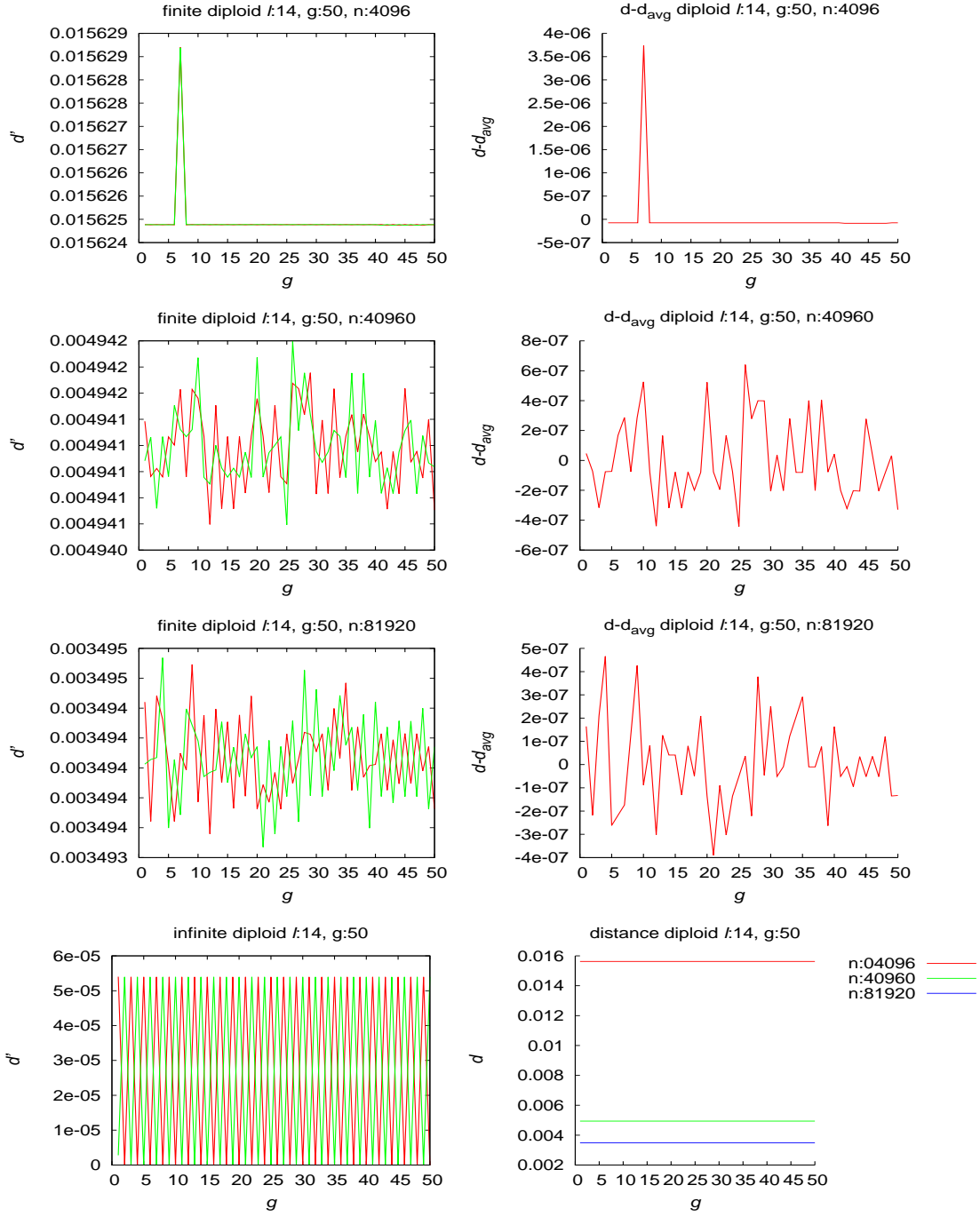


Figure 3.8: Infinite and finite diploid population oscillation behavior for genome length $\ell = 14$: In left column, d' is distance of finite population of size n or infinite population to limits for g generations. In right column, d is distance of finite population to infinite population for g generations and d_{avg} is average distance.

Figures 3.5, 3.6, 3.7 and 3.8 show oscillations in finite diploid populations, and distances between finite diploid populations and infinite diploid populations arranged by genome length ℓ in ascending order. In each figure for unique genome length ℓ , sub-figures are arranged by population size N . In each figure, the first three rows of sub-figures in the left column show distance d' of finite population to limits, the sub-figure in fourth row of the left column shows distance d' of infinite population to limits. These sub-figures depict oscillating behavior of both infinite and finite diploid populations when condition 3.3 is met. Like in haploid population case, as population size increases, oscillation approaches the behavior exhibited by infinite population.

In each figure (3.5, 3.6, 3.7, and 3.8), the first three graphs in the right column show distance variation (difference of distance d and average distance d_{avg}) where d is distance between diploid finite and infinite populations and d_{avg} is average value of d . The graph in the fourth row of the right column combines distance plots between finite and infinite populations for sizes ($N = N_0^2, 10N_0^2, 20N_0^2$). The graphs show distance decreases as population size increases, consistent with results from section 2.1. The graphs of $d - d_{avg}$ decrease in amplitude as population size increases. For fixed finite population size, as ℓ increases, the distance graphs become smoother, and amplitude of oscillations decrease.

Distance data obtained from simulations for diploid populations are summarized in table 3.3, which tabulates average distance between finite and infinite populations for population sizes $N = 4096$, $N = 40960$ and $N = 81920$.

Results from table 3.3 show average distance between finite and infinite population closely follows the expected single step distance. The distance decreases as $1/\sqrt{N}$.

3.5 Discussion

For same genome length ℓ and same size finite populations, graph showing distance between finite diploid population and infinite population is smoother than graph showing distance between finite haploid population and infinite population. Average

Table 3.3: Distance measured for diploid population: N is population size, ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0049 | 0.0035 |
| 10 | 0.0156 | 0.0049 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

oscillation amplitude is plotted for both haploid and diploid populations as surface graphs in figures 3.9a and 3.9b.

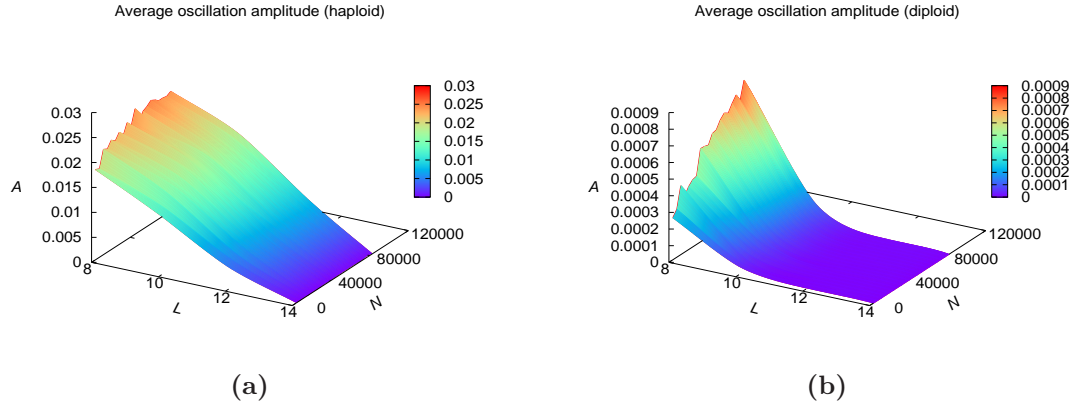


Figure 3.9: Average oscillation amplitude: A is average amplitude of oscillation, L is genome length ℓ , and N is population size

Oscillation amplitude increases with increase in population size for both haploid and diploid populations, and better oscillations are observed with larger population size for a given ℓ . Also amplitude of oscillation decreases with increase in ℓ value for same population size, and since total genome length of diploid population is twice that of haploid population, amplitude of oscillation of diploid population is smaller than haploid population of same population size and same value of ℓ . So for longer genome length ℓ , larger population size is needed to observe clear oscillations.

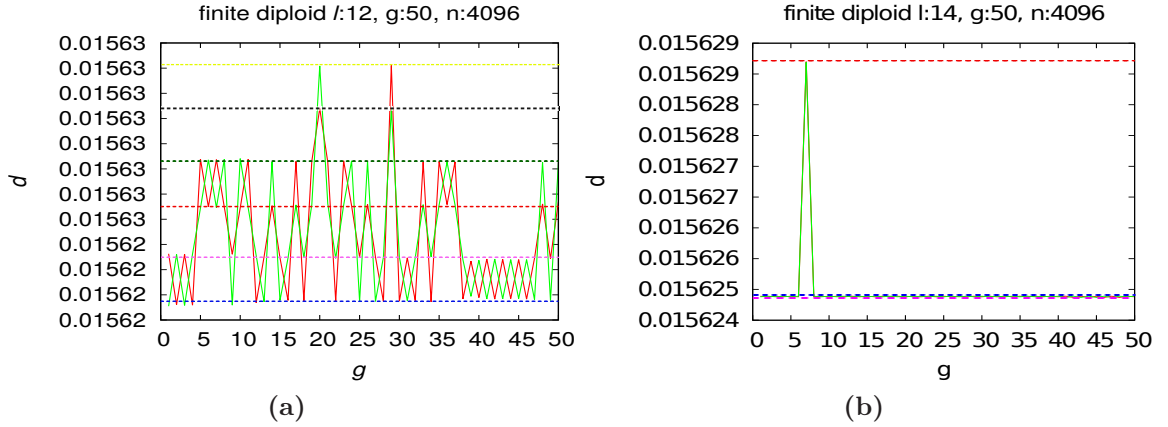


Figure 3.10: Finite diploid population oscillation for $\ell = 12$ & 14 and $N = 4096$

For the diploid case, when genome length ℓ is longer ($\ell = 12$ and 14 in our simulation), and population size is small (like $N = 4096$ in our simulation), finite population has tendency to jump between different levels. Figures 3.10a and 3.10b show such tendency for $\ell = 12$ and $\ell = 14$. Very good oscillations with tiny amplitude were observed in temporarily stable states in these cases. Figure 3.11 shows magnified scale oscillations for $\ell = 14$ when high peak is omitted from the plot of 3.10b. As string length increases, the number of fixed points also increases, and finite populations tend to stay near fixed points (see Vose (1999)). With many fixed points available, there are several regions for finite populations to prefer. But when population size is large, finite populations intend to follow the infinite population, and infinite population tends to converge to a single fixed point or oscillate between two fixed points, and thus, larger populations have lower tendency to jump between different levels.

3.6 Summary

In this chapter, we described infinite population limits predicted by Vose, and conditions for convergence to periodic orbits. Mutation distributions and crossover

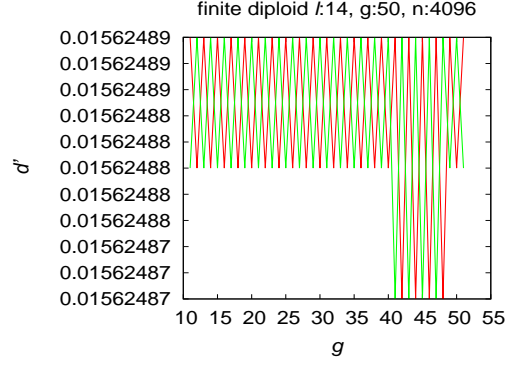


Figure 3.11: Finite diploid population oscillation for $\ell = 14$ and $N = 4096$ from 10 to 50 generations

distributions were computed to satisfy the conditions for infinite populations to converge to periodic orbits. Through experiment, we showed finite populations can also oscillate. Moreover, the distance between finite populations and infinite populations can in practice decrease as $1/\sqrt{N}$ as the populations size increases, which is in agreement with previous results from chapter 2.

Chapter 4

Violation in Mutation Distribution

The results from chapter 3 show that oscillation occurs when the crossover distribution χ , and the mutation distribution μ satisfy condition 3.3. This chapter explores the robustness of finite population oscillation when condition 3.3 is violated for μ . The violation in μ makes the Markov chain representing finite population regular (sometimes called ergodic). Does approximate oscillation in finite populations occur in practice when the Markov chain is regular and infinite population trajectories have no periodic orbit?

Error ϵ is introduced into the mutation distribution μ so as to violate condition 3.3; this guarantees that infinite population trajectories have no periodic orbit. Consequently, $\mathbf{p}^* = \mathbf{q}^* = \mathbf{z}^*$. Violation of condition 3.3 for the mutation distribution makes the Markov chain regular. The initial population is computed using same procedure as described in section 3.3. To explore the effects of the degree of violation of condition 3.3 in μ , different values of ϵ are used in experiments. String length $\ell \in \{8, 10, 12, 14\}$ are considered for simulation. Going forward, we use ‘limit \mathbf{z}^* ’ to denote evolutionary limit when mutation distribution μ violates condition 3.3, and ‘non-violation limits \mathbf{p}^* and \mathbf{q}^* ’ to denote limits without violation.

4.1 Violation

The mutation distribution μ is modified as follows

$$\mu_i = (1 - \epsilon)\mu_i; \quad i = \{0, 1, 2, \dots, 2^\ell - 1\}.$$

Thus summing components of μ distribution yields,

$$1 - \epsilon = \sum_{i=0}^{2^\ell-1} \mu_i$$

Then set

$$\mu_0 = \epsilon$$

The modified mutation distribution μ is normalized such that $\sum \mu_i = 1$. The modification described above makes it possible for any population member to mutate to any other population member. Let us explore for two cases of g in 3.3:

1. When g is all 1s:

Any mask with a 1 at position k ($0 \leq k < \ell$) and 0 at all other positions can mutate the k th bit, and since the all 0s mask has positive probability, strings have an option to not mutate. This makes possible for any string to mutate to any other string. Let us take an example with $\ell = 8$. Let $g = 11111111$. Then, mask $i = 00000100$ will have positive probability according to condition 3.3. Mask i can be used to mutate the sixth bit of a population member. More generally, any bit has the option of mutating or not, so any string can mutate to any other.

2. When g has atleast one 0:

Any mask with a 1 at position k and 0 at all other positions will have positive probability if g also is 1 at position k . Thus any bit where g is 1 has the option of mutating or not. Any mask with 1 in just one of the positions where g has 1s and also 1 in just one of the positions where g has 0s can be used to mutate a bit where g is 0. Let us take an example with $\ell = 8$. Let $g = 11001111$. Then, mask

$i = 00000100$ will have positive probability according to condition 3.3. Also mask $j = 00010100$ will have positive probability. Mask i can be used to mutate the sixth bit, and masks i and j will result in mutating the fourth bit. More generally, any bit has the option of mutating or not, so any string can mutate to any other. Since any population can therefore mutate to any other population (this may involve many generations because there are many population members which may need to be mutated), the Markov chain is irreducible.

The Markov chain is also aperiodic. We prove this by simple induction. Let $S(n)$ be the assertion that population P can be returned to in n generations. Our base case is $n = 1$. The GA can stay in its original state P if no mutation or crossover events occur. Population P has option to not mutate to any other population, since all 0s mutation mask has positive probability. Moreover, the all 0s crossover mask can have positive probability since that is compatible with condition 3.3. So $S(n)$ is true. Now, assume $S(k)$ is true. Therefore, population P can be returned to in $n = k$ generations. In the $k + 1$ th generation, population P has the option to stay in state P . So $S(k + 1)$ is also true and that completes the inductive proof. Since any population state can be returned to in any period of time, the Markov chain is aperiodic.

Because the Markov chain formed by GA after violation in μ is irreducible and aperiodic, the Markov chain is regular (see Iosifescu (1980)), and a steady state distribution with positive components exists for the GA (see Minc (1988)).

Simulations were repeated with the violations in (3.3) described above for the mutation distribution. The distances of both infinite and finite populations to limit z^* were plotted. The distances of both infinite and finite populations to non-violation limits p^* and q^* were also plotted.

4.1.1 Haploid Population $\sim \epsilon : 0.01$

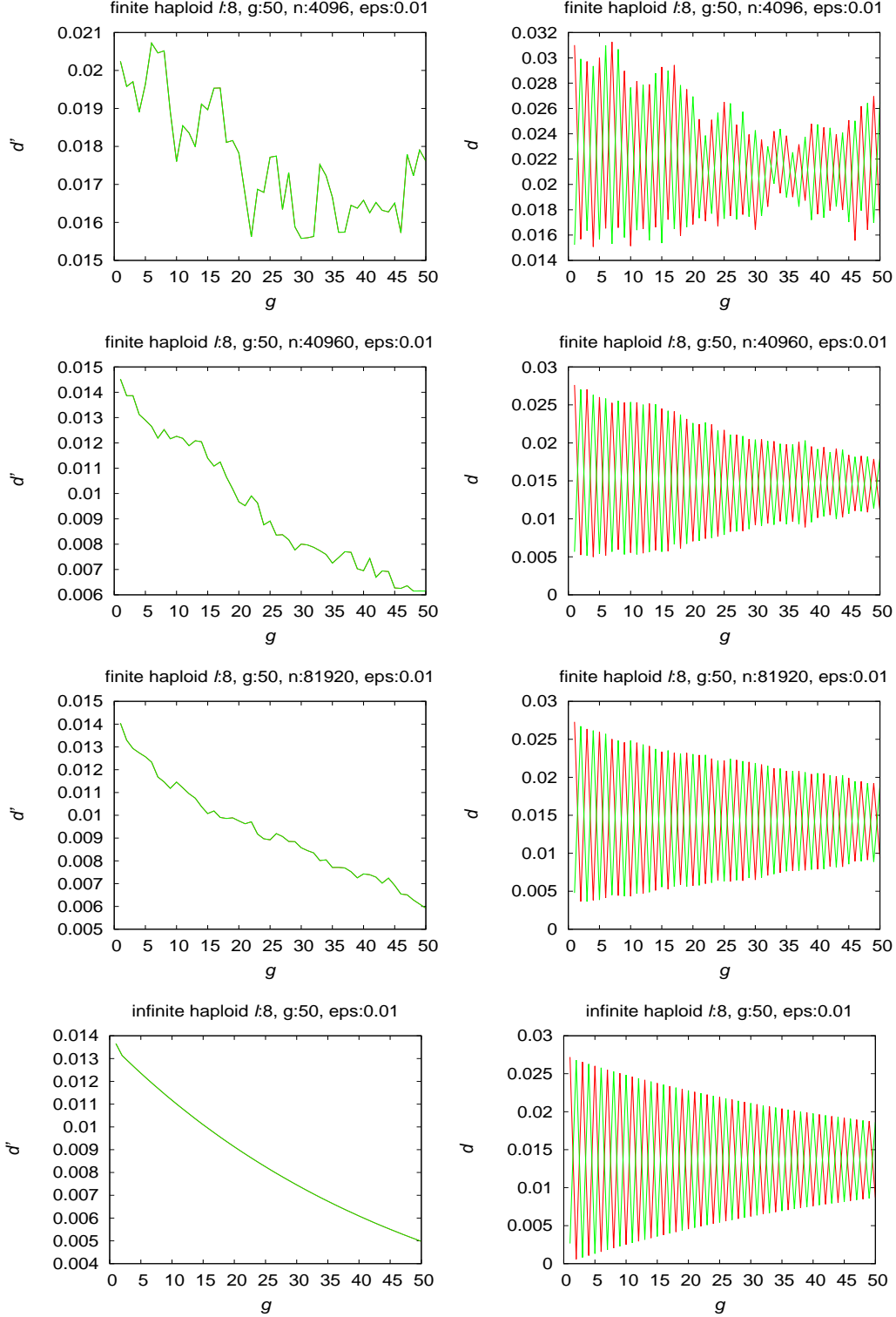


Figure 4.1: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 8$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

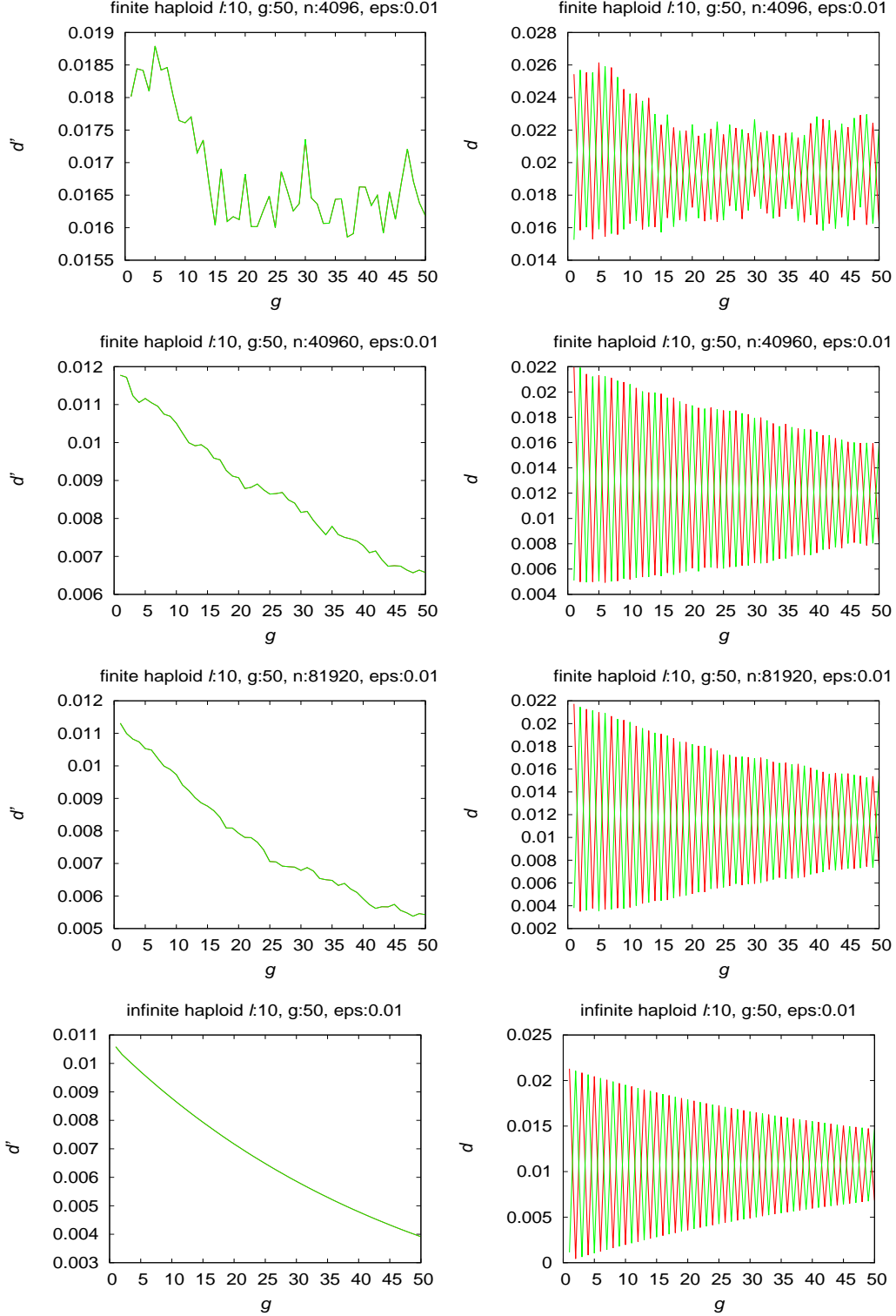


Figure 4.2: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 10$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 56

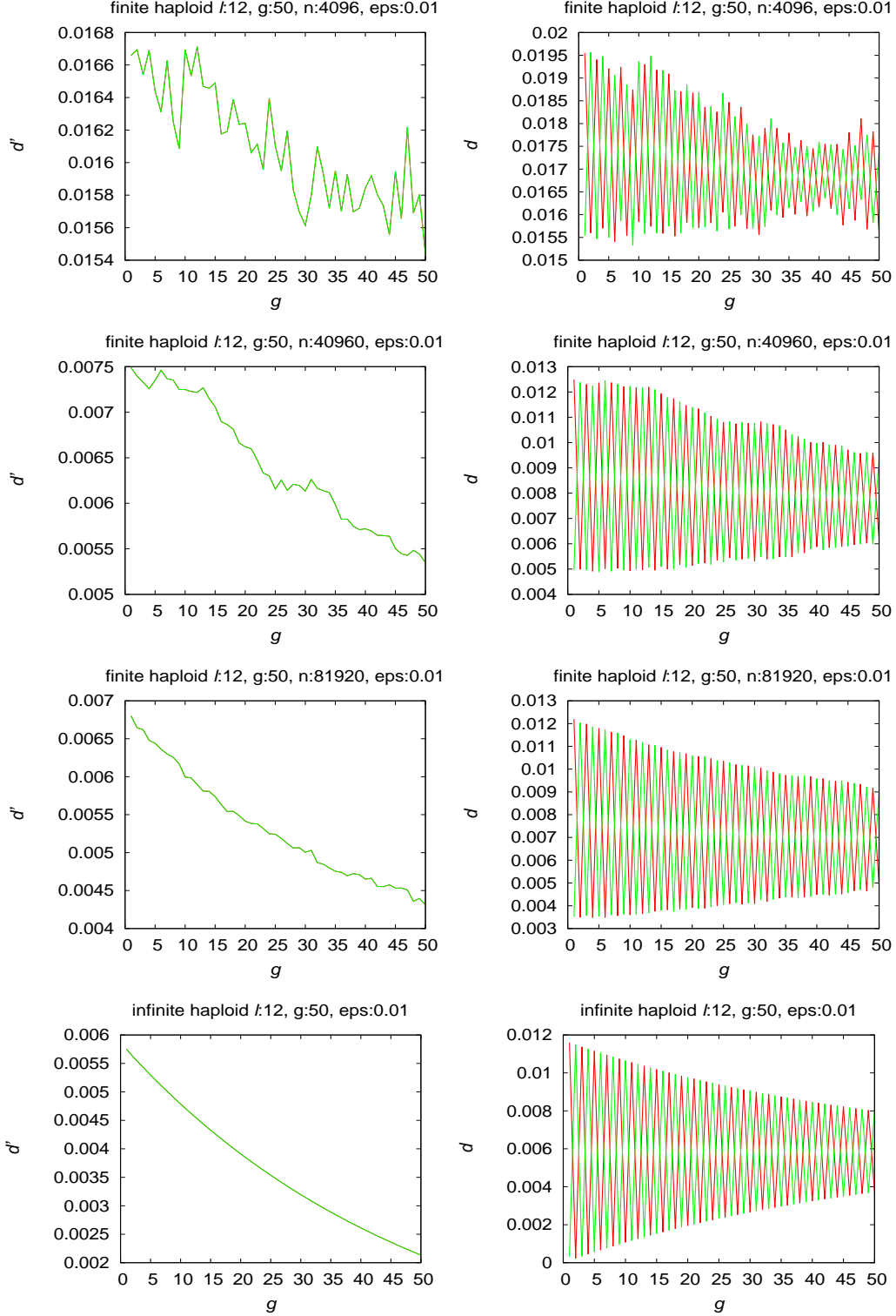


Figure 4.3: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 12$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

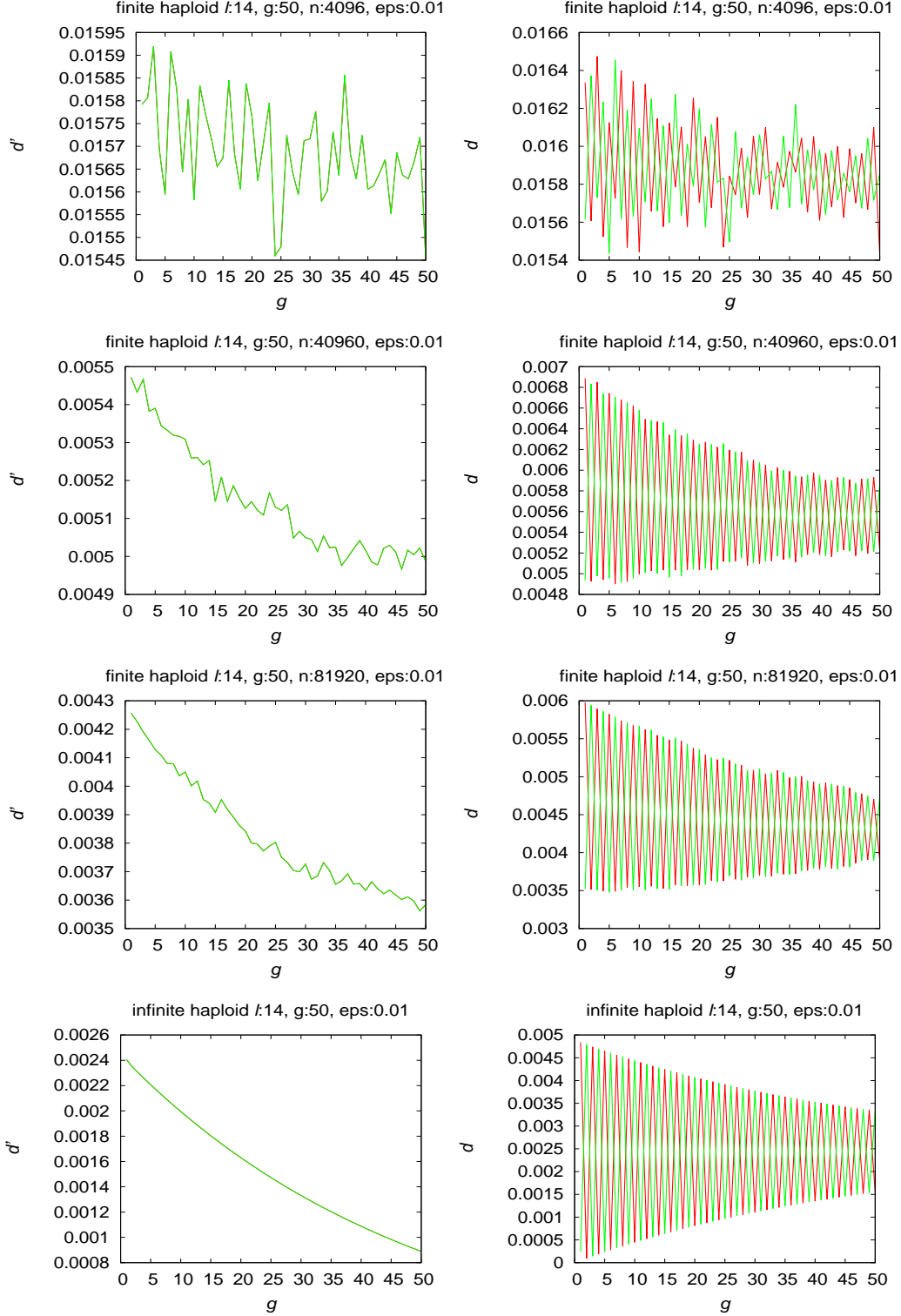


Figure 4.4: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 14$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

The right column in figures 4.1 through 4.4 shows distance of finite and infinite haploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.01$. Those graphs indicate oscillating behavior of haploid population given violation. Both finite and infinite populations oscillate given violation. Oscillations are sharper. Since the value of ϵ is small, damping of ripples is slow. The all zeros mask created in mutation distribution with $\epsilon = 0.01$ have small probability of being used during mutation, and when it is not used, behavior should be consistent with the behavior without violation. Moreover, ϵ is so small that infinite population oscillation does not die out completely in 50 generations.

The left column of figures 4.1 through 4.4 shows distance of finite and infinite haploid populations to limit \mathbf{z}^* (limit with violation in mutation distribution $\boldsymbol{\mu}$) when $\epsilon = 0.01$. The distance between finite population and limit \mathbf{z}^* (limit with violation in $\boldsymbol{\mu}$ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population reach large number. Average distance data for haploid population in case of violation in $\boldsymbol{\mu}$ distribution with $\epsilon = 0.01$ for different finite population size N are tabulated in table 4.1.

Table 4.1: Distance measured for violation in $\boldsymbol{\mu}$ with $\epsilon = 0.01$ for haploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0176 | 0.0094 | 0.0093 |
| 10 | 0.0168 | 0.0088 | 0.0077 |
| 12 | 0.0161 | 0.0064 | 0.0053 |
| 14 | 0.0157 | 0.0051 | 0.0038 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

From table 4.1, average distance calculated for finite population size 4096 is 0.0165, for size 40960 is 0.0074 and for size 81920 is 0.0065. These results show average distance between finite population and limit \mathbf{z}^* approach the expected single step

distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance decreased as genome length ℓ increased for all sizes of finite haploid populations with $\epsilon = 0.01$.

4.1.2 Haploid Population $\sim \epsilon : 0.1$

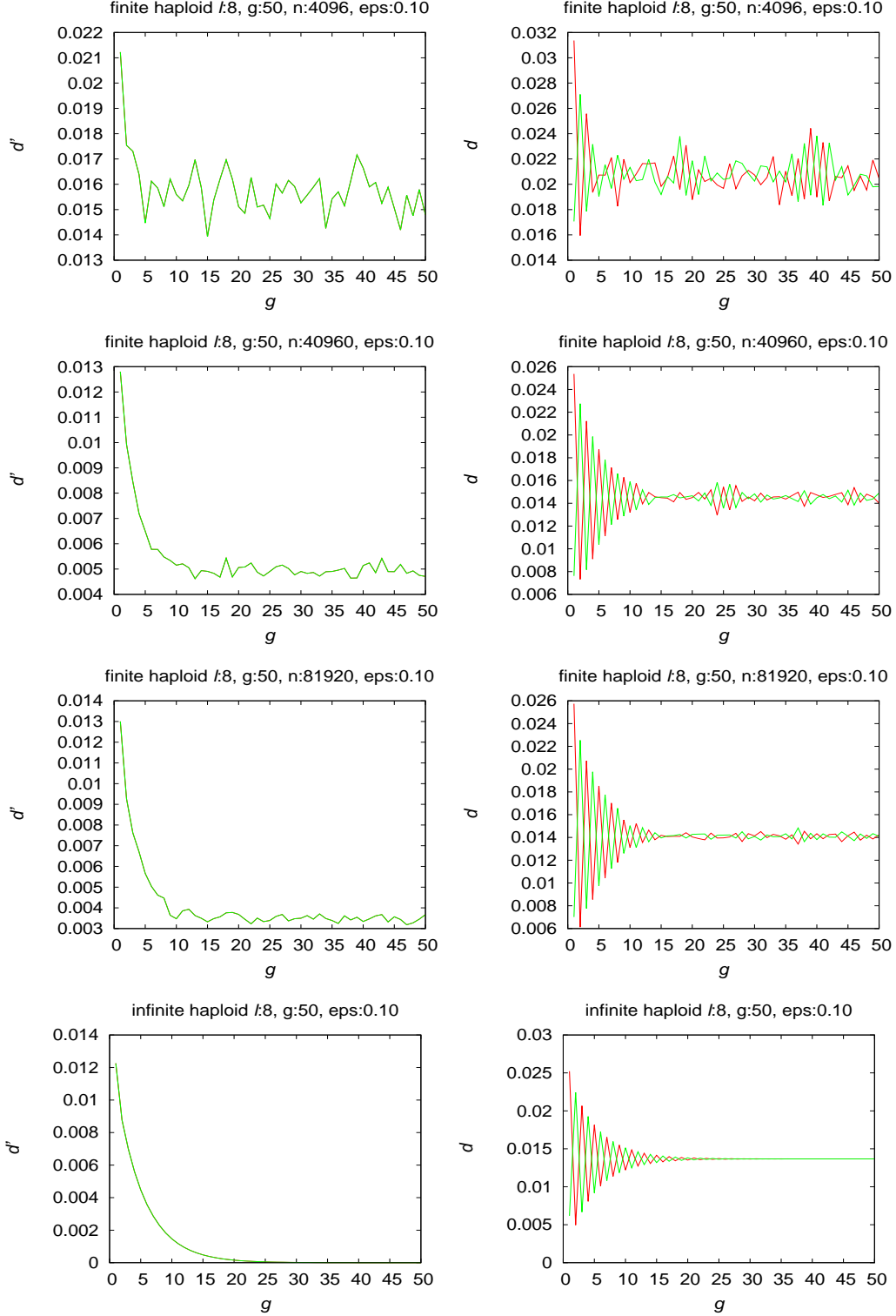


Figure 4.5: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 8$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 61

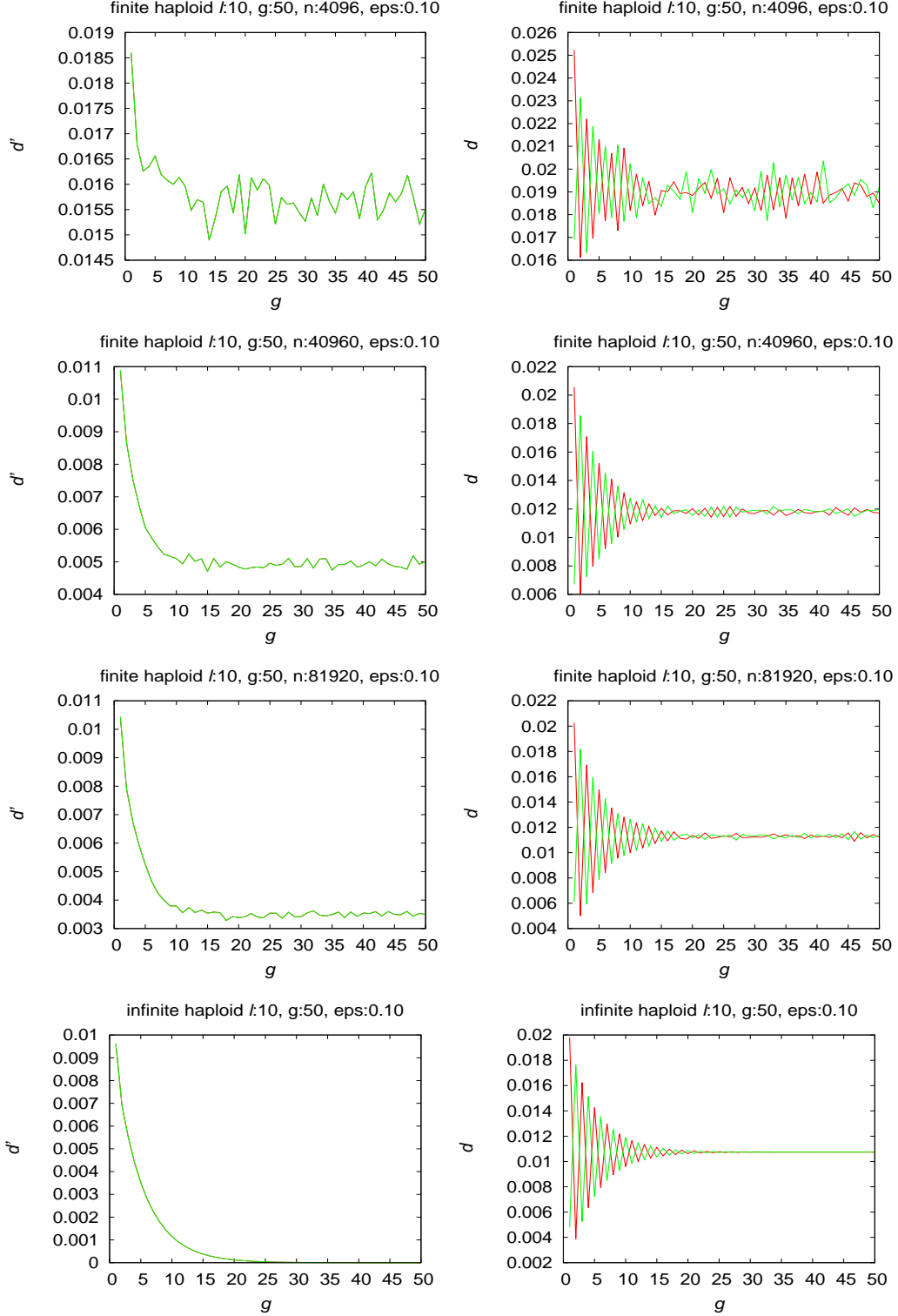


Figure 4.6: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 10$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 62

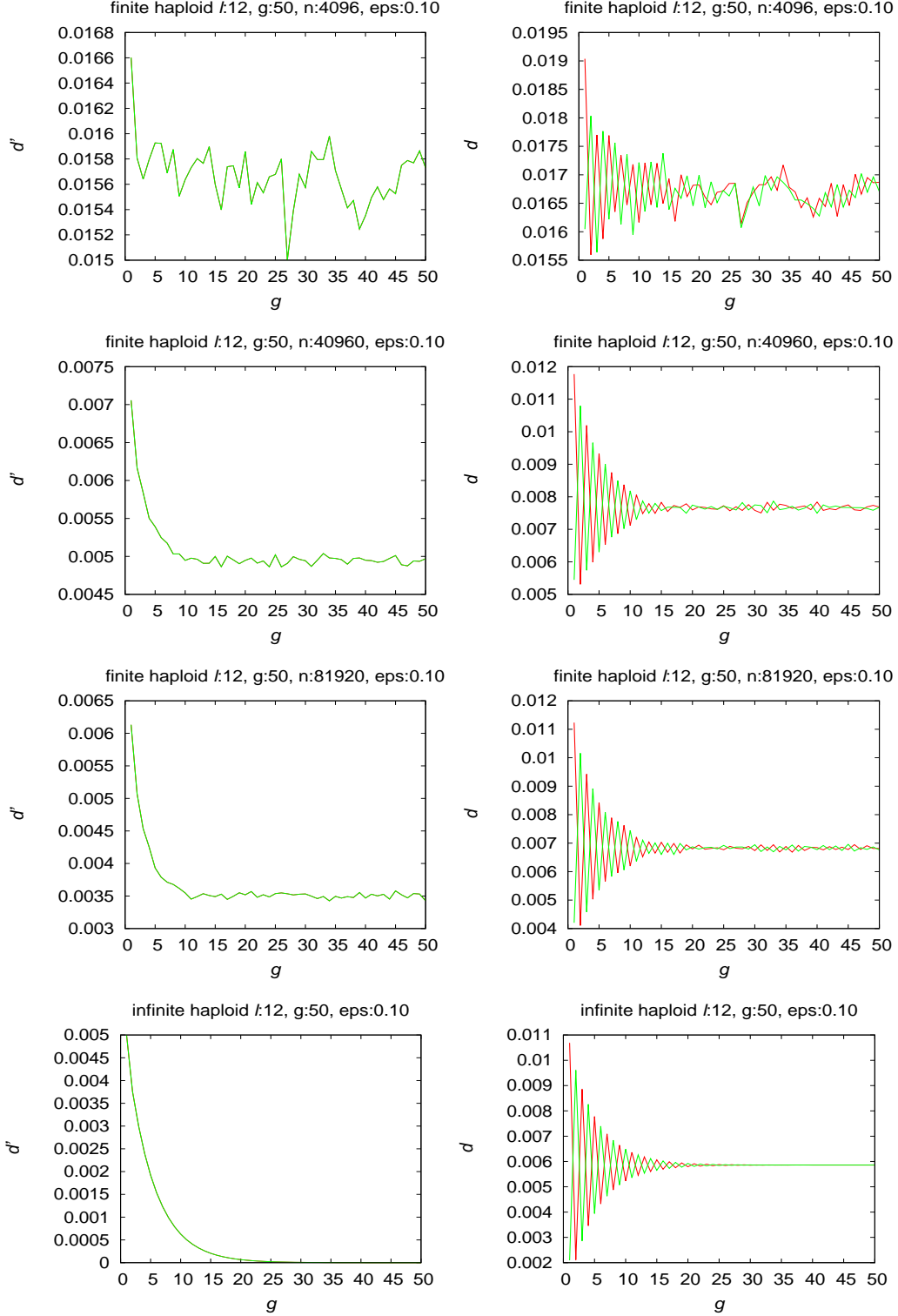


Figure 4.7: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 12$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 63

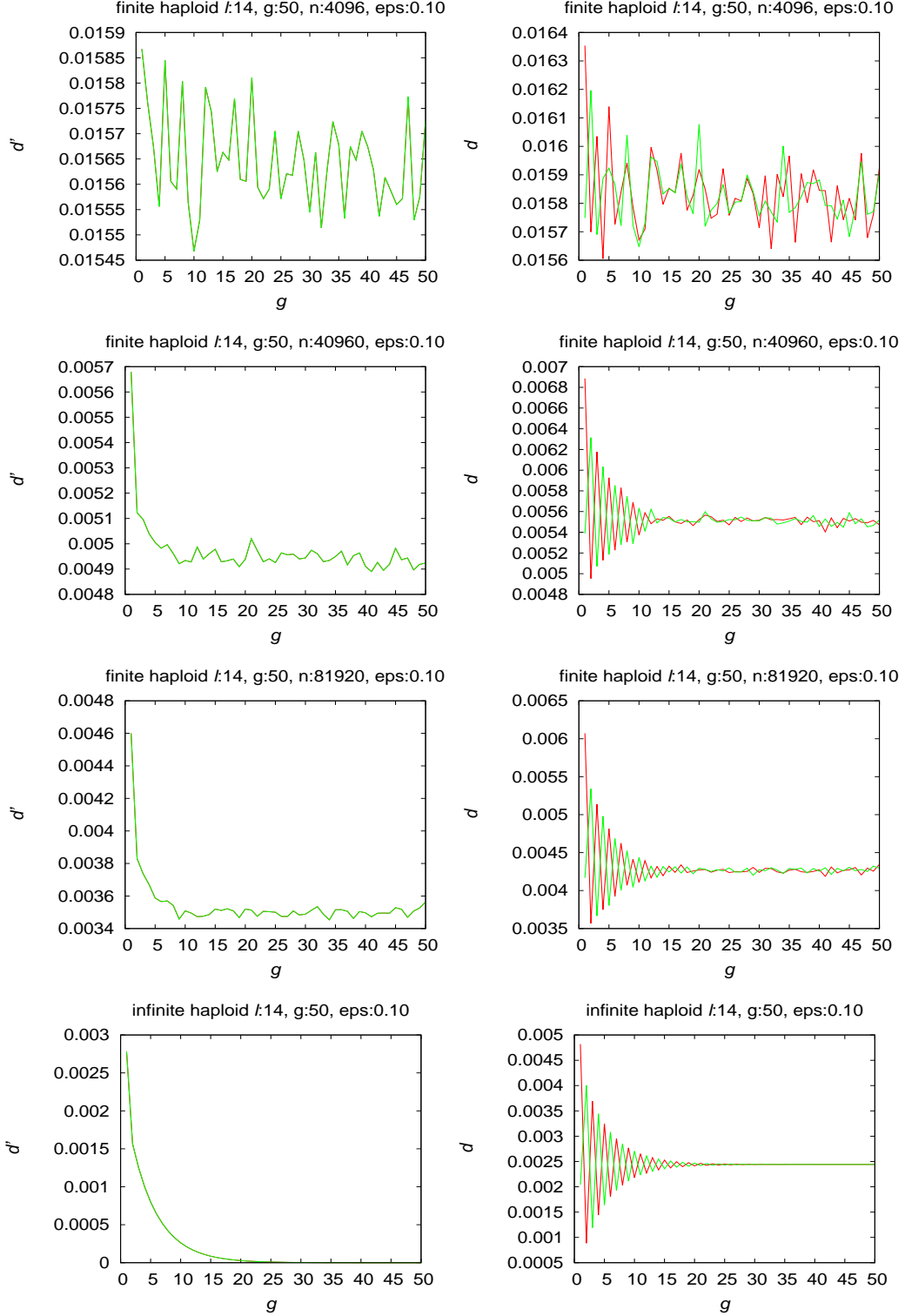


Figure 4.8: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 14$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

The right column in figures 4.5 through 4.8 shows distance of finite and infinite haploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.1$. Those graphs indicate oscillating behavior of haploid population given violation. Both finite and infinite populations oscillate given violation, and oscillations amplitudes decreases with time. However, for $\epsilon = 0.1$, oscillations in infinite populations die out quickly, but oscillations in finite populations does not die out completely. Rate of damping of ripples with $\epsilon = 0.1$ is larger than with $\epsilon = 0.01$. The all zero mask created in mutation distribution with $\epsilon = 0.1$ have small probability of being used during mutation making it unlikely for oscillation in finite populations to die out quickly.

The left column of figures 4.5 through 4.8 shows distance of finite and infinite haploid populations to limit \mathbf{z}^* (limit with violation in mutation distribution $\boldsymbol{\mu}$) when $\epsilon = 0.1$. The distance between finite population and limit \mathbf{z}^* (limit with violation in $\boldsymbol{\mu}$ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for haploid population in case of violation in $\boldsymbol{\mu}$ distribution with $\epsilon = 0.1$ for different finite population size N is tabulated in table 4.2.

Table 4.2: Distance measured for violation in $\boldsymbol{\mu}$ with $\epsilon = 0.1$ for haploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0158 | 0.0054 | 0.0041 |
| 10 | 0.0158 | 0.0053 | 0.0039 |
| 12 | 0.0157 | 0.0051 | 0.0036 |
| 14 | 0.0156 | 0.0050 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

The results in Table 4.2 show average distance between finite population and limit \mathbf{z}^* approach the expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance decreased as genome length ℓ increased for all sizes of finite haploid populations with $\epsilon = 0.1$.

4.1.3 Haploid Population $\sim \epsilon : 0.5$

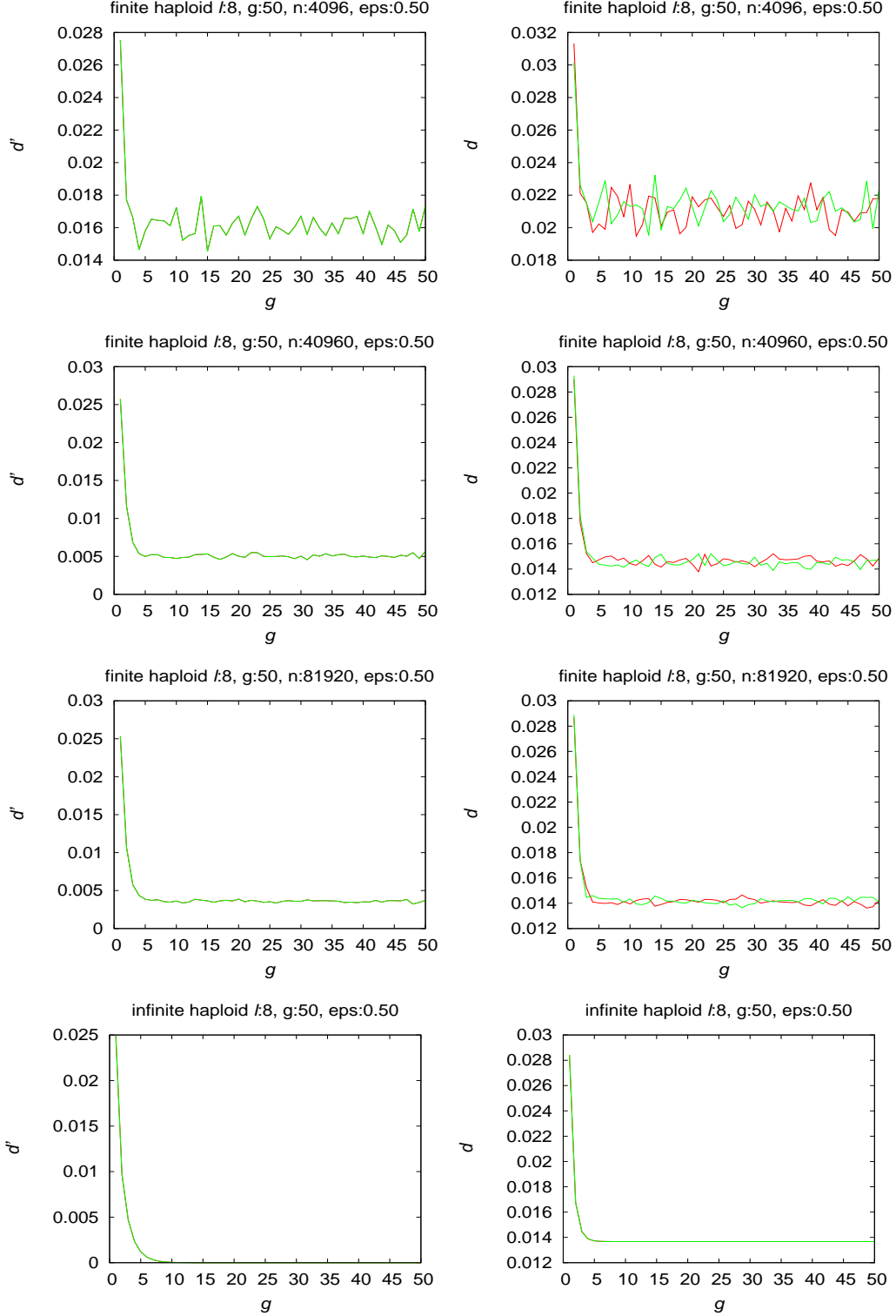


Figure 4.9: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 8$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 67

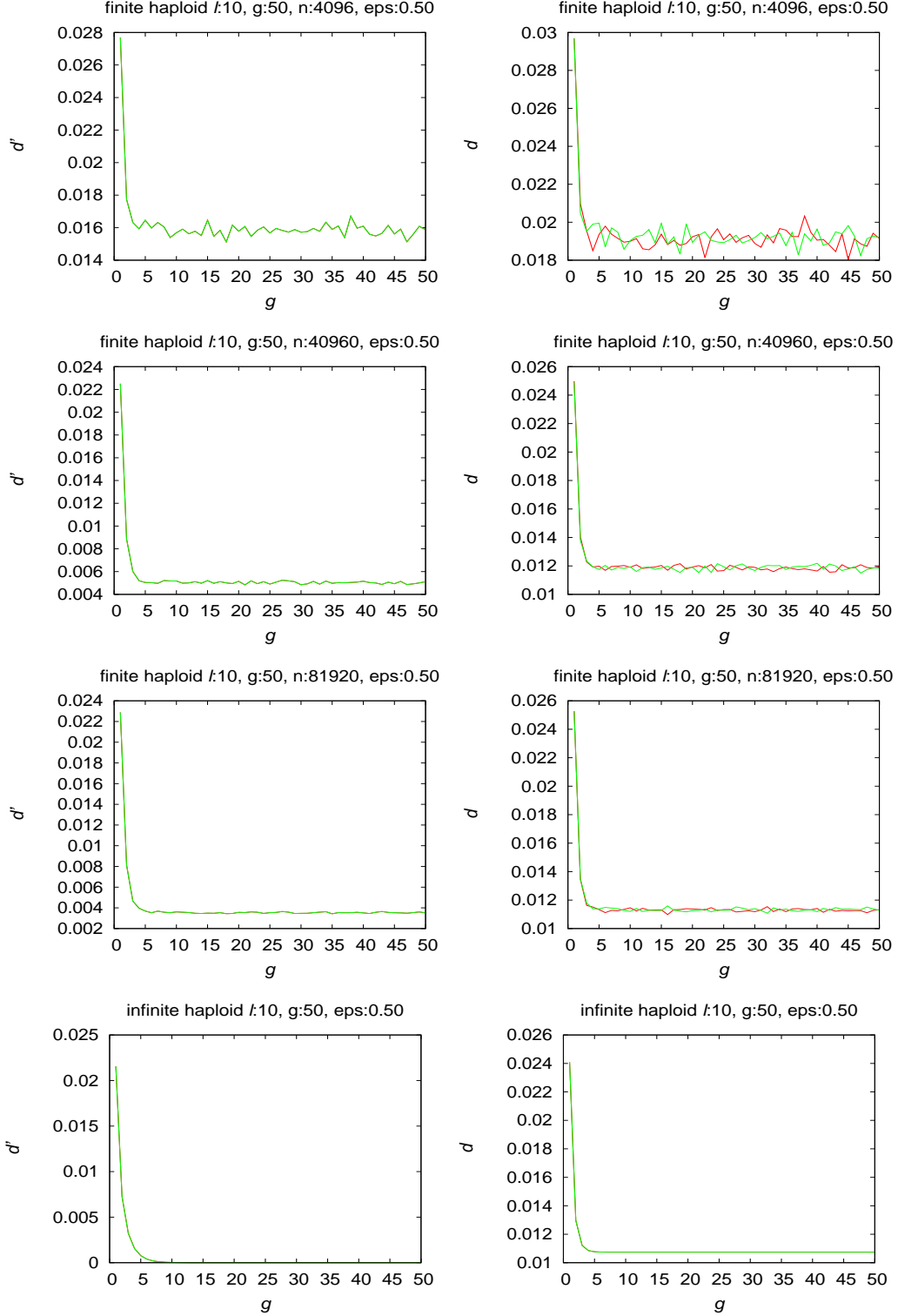


Figure 4.10: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 10$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 68

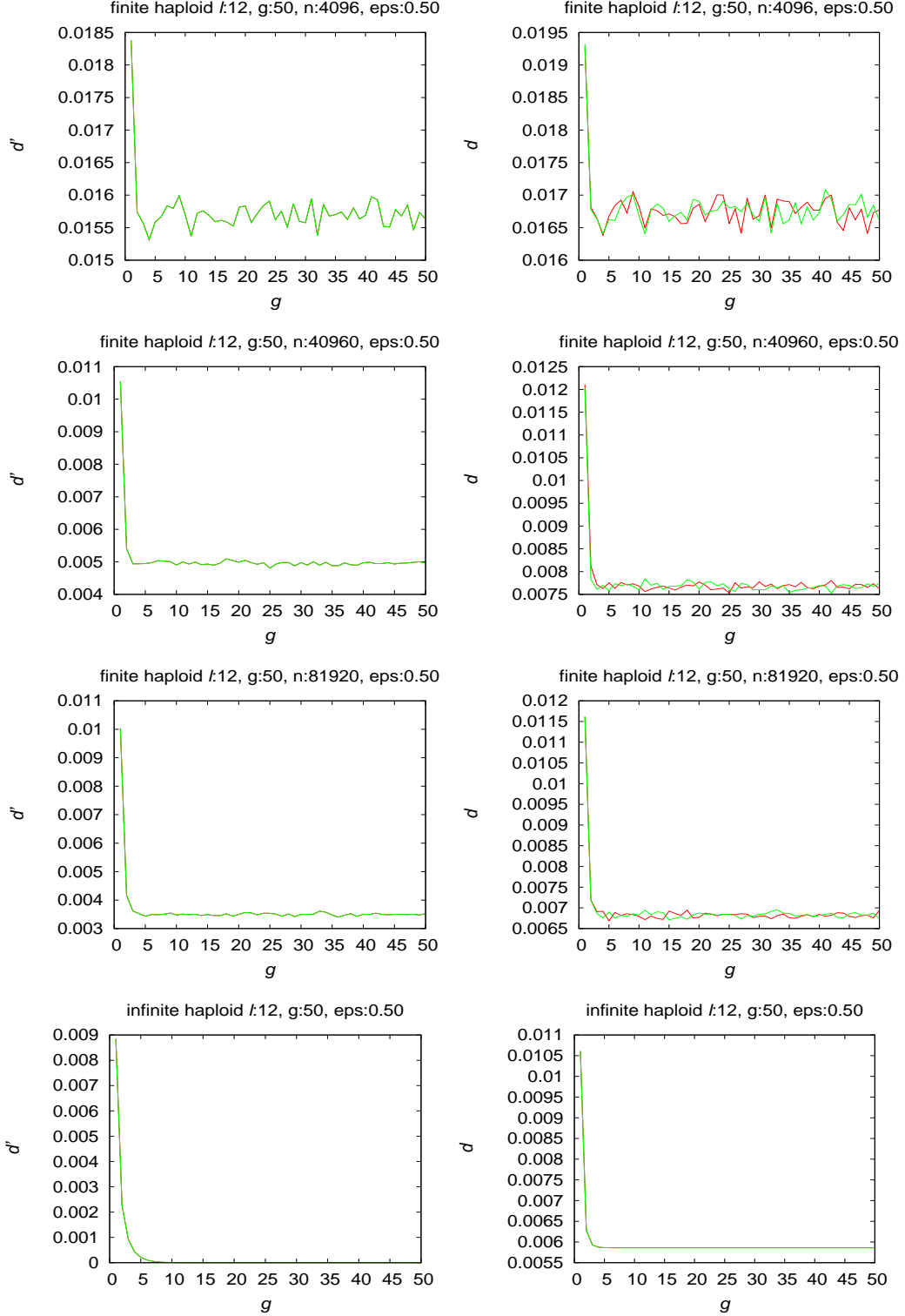


Figure 4.11: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 12$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 69

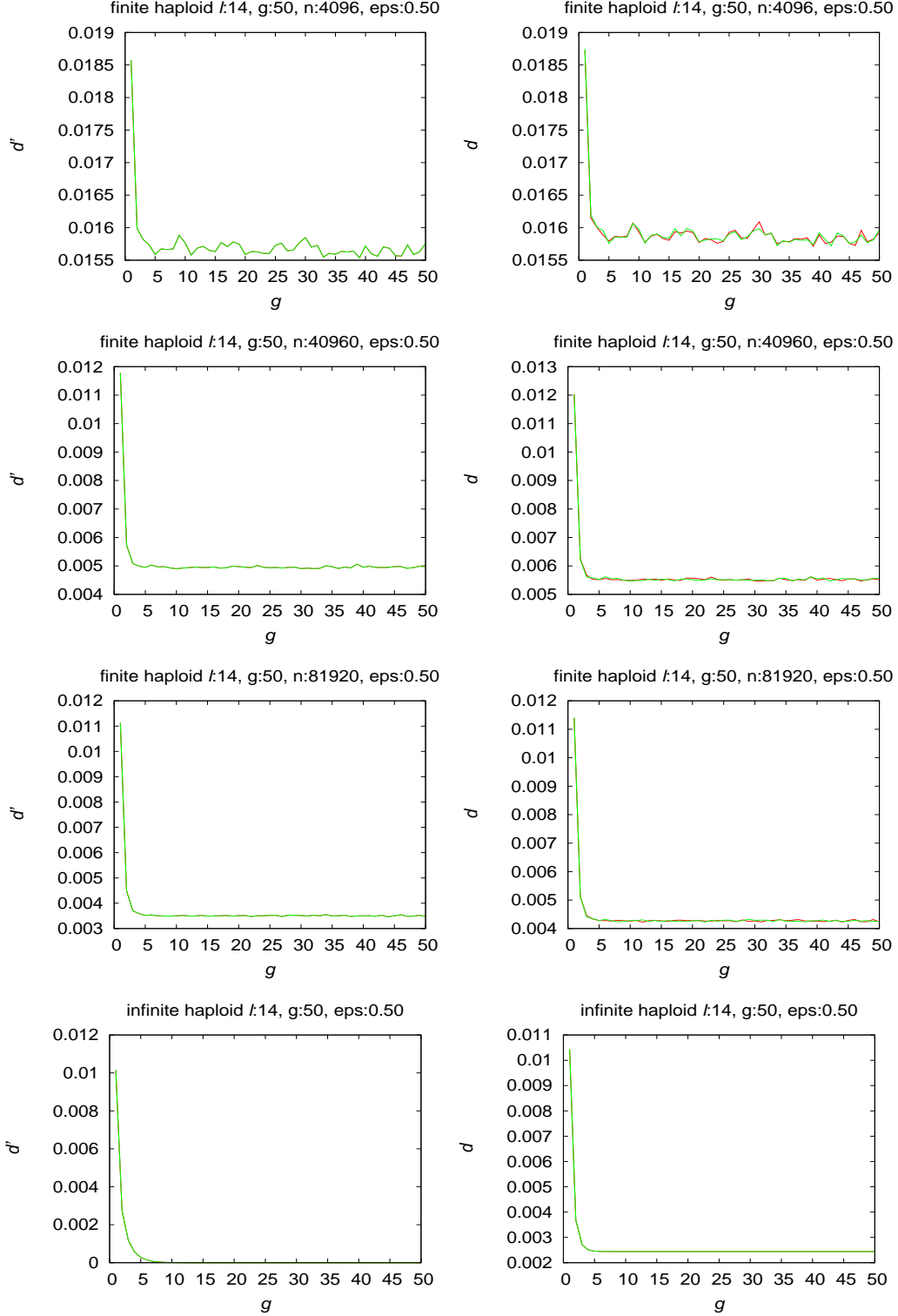


Figure 4.12: Infinite and finite haploid population oscillation behavior in case of violation in μ for genome length $\ell = 14$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 70

The right column in figures 4.9 through 4.12 shows distance of finite and infinite haploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.5$. The graphs indicate oscillating behavior of haploid population given violation. Neither finite nor infinite populations show noticable oscillation given violation. The all zeros mask created in mutation distribution with $\epsilon = 0.5$ has large probability of being used during mutation, so oscillation does not occur.

The left column of figures 4.9 through 4.12 shows distance of finite and infinite haploid populations to limit \mathbf{z}^* (limit with violation in mutation distribution $\boldsymbol{\mu}$) when $\epsilon = 0.5$. The distance between finite population and limit \mathbf{z}^* (limit with violation in $\boldsymbol{\mu}$ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for haploid population in case of violation in $\boldsymbol{\mu}$ distribution with $\epsilon = 0.5$ for different finite population size N are tabulated in table 4.3.

Table 4.3: Distance measured for violation in $\boldsymbol{\mu}$ with $\epsilon = 0.5$ for haploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0161 | 0.0056 | 0.0042 |
| 10 | 0.0161 | 0.0055 | 0.0040 |
| 12 | 0.0157 | 0.0051 | 0.0036 |
| 14 | 0.0157 | 0.0051 | 0.0036 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

The results in Table 4.3 show average distance between finite population and limit \mathbf{z}^* approach expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance decreased as genome length ℓ increased for all sizes of finite haploid populations with $\epsilon = 0.5$.

4.1.4 Diploid Population $\sim \epsilon : 0.01$

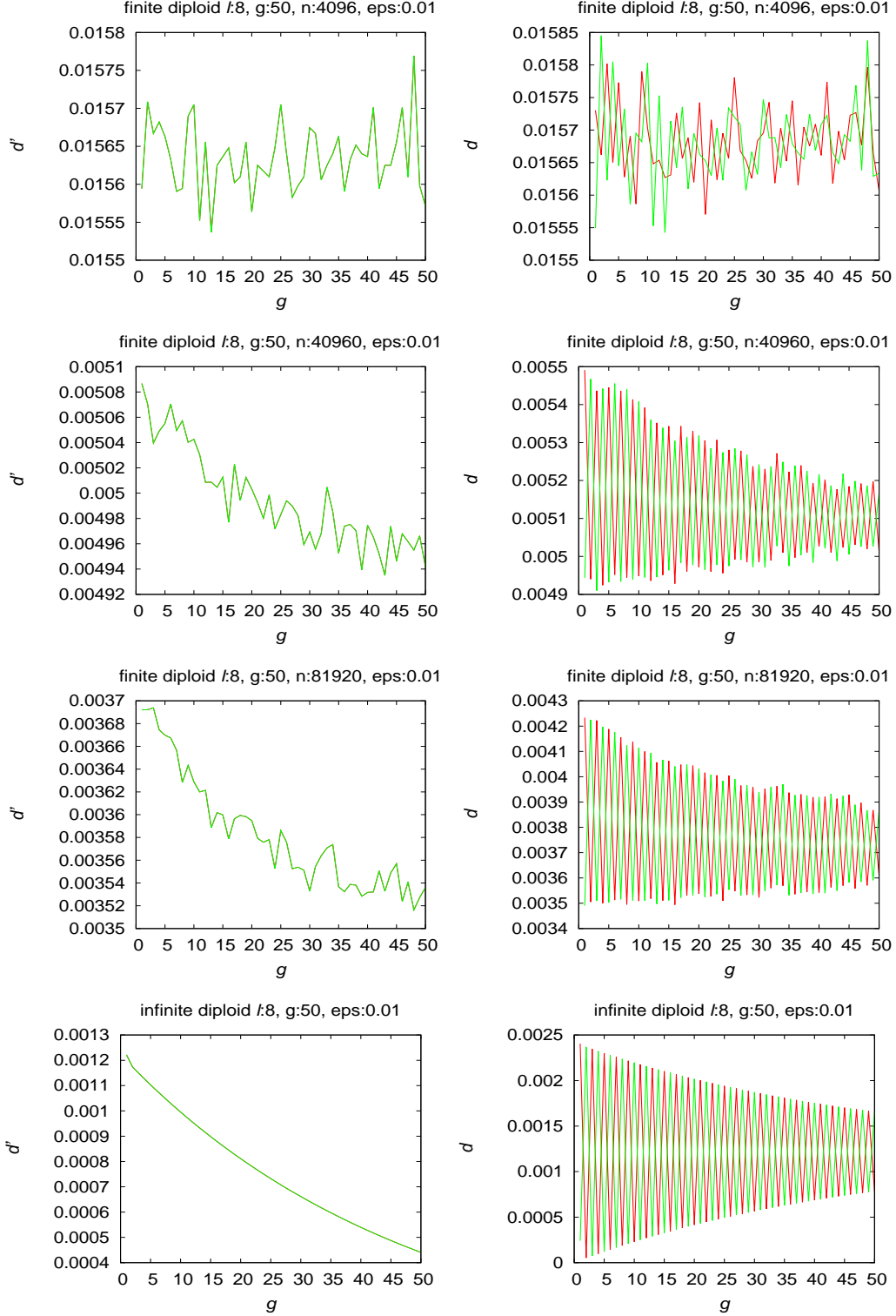


Figure 4.13: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 8$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

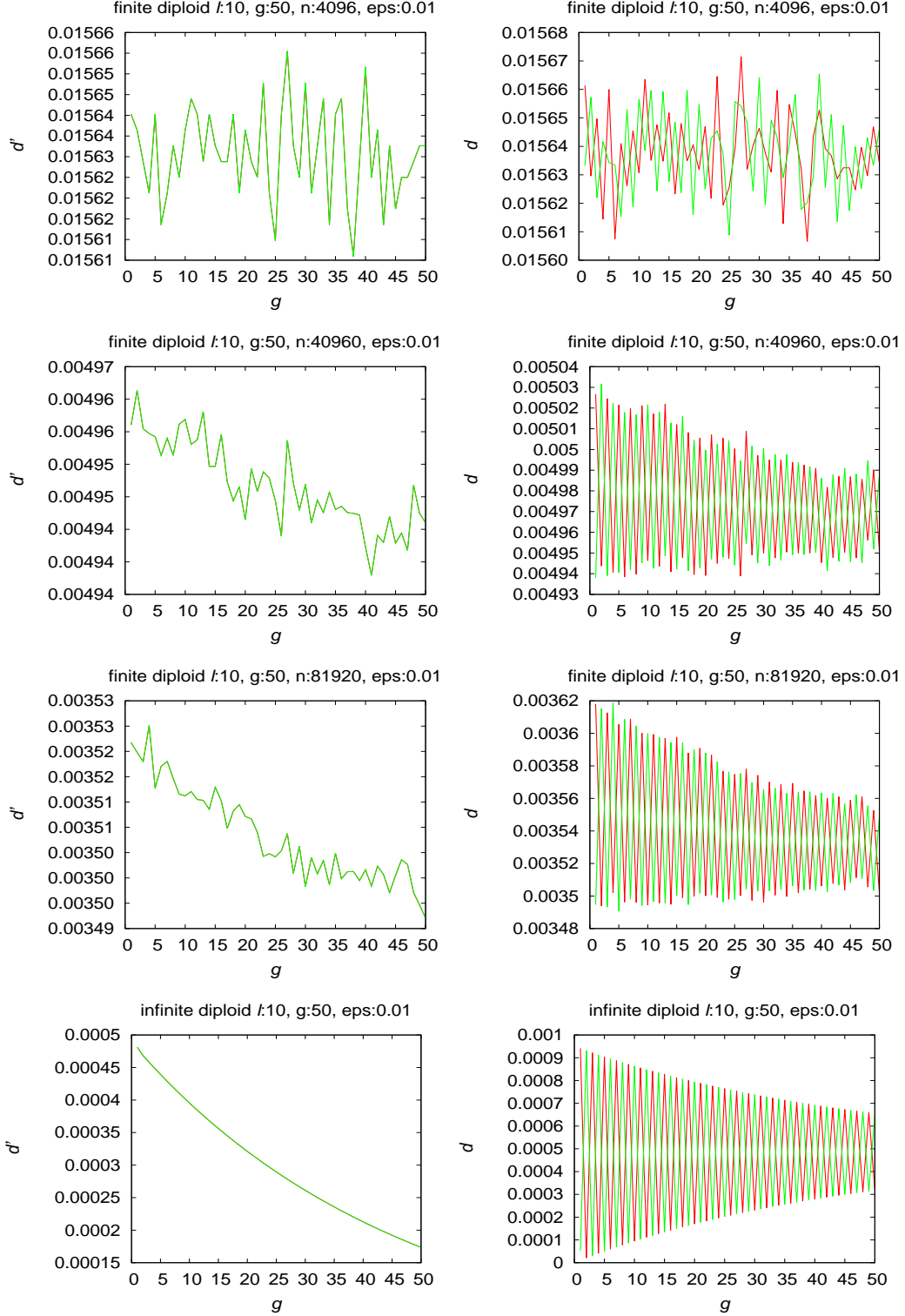


Figure 4.14: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 10$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

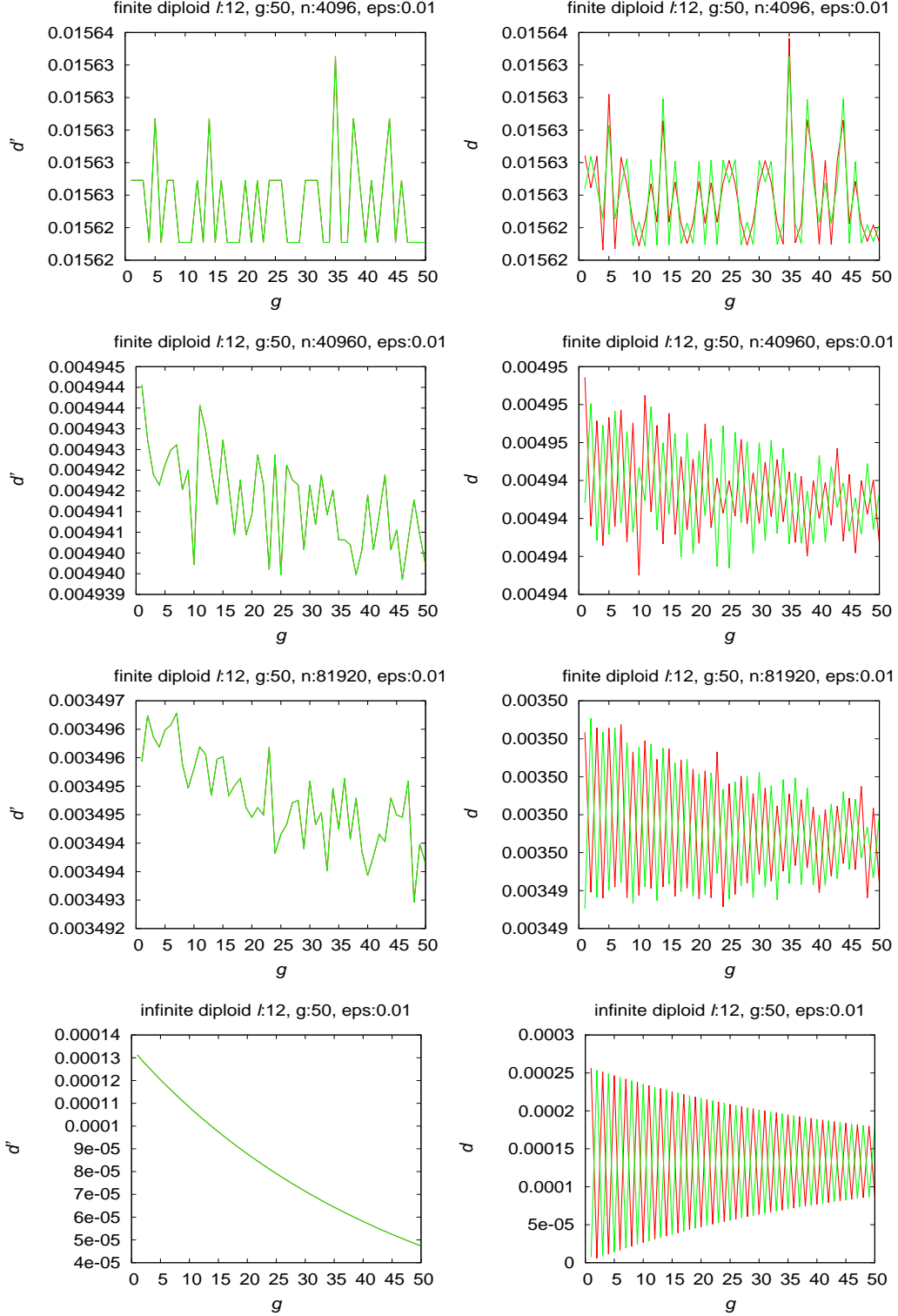


Figure 4.15: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 12$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

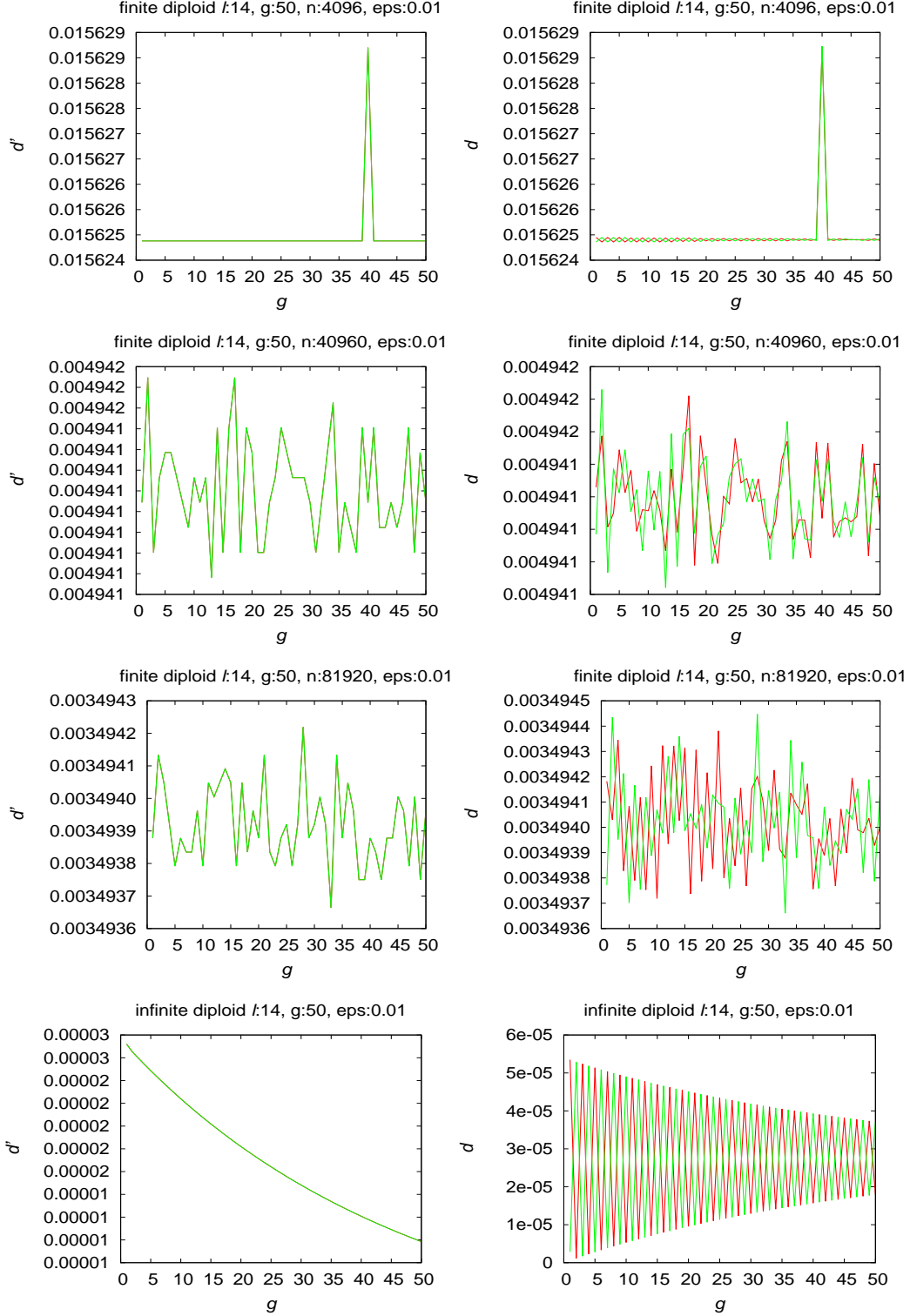


Figure 4.16: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 14$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 75

The right column in figures 4.13 through 4.16 shows distance of finite and infinite diploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.01$. Those graphs indicate oscillating behavior of diploid population given violation. Both finite and infinite populations oscillate given violation. Like in haploid case, oscillations are sharper. Since value of ϵ is very small, damping of ripples is slow. The all zeros mask created in mutation distribution with $\epsilon = 0.01$ has small probability of being used during mutation. Infinite population oscillation does not die out in 50 generations.

The left column of figures 4.13 through 4.16 shows distance of finite and infinite diploid populations to limit \mathbf{z}^* (limit with violation in mutation distribution $\boldsymbol{\mu}$) when $\epsilon = 0.01$. The distance between finite population and limit \mathbf{z}^* (limit with violation in $\boldsymbol{\mu}$ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for diploid population in case of violation in $\boldsymbol{\mu}$ distribution with $\epsilon = 0.01$ for different finite population size N are tabulated in table 4.4.

Table 4.4: Distance measured for violation in $\boldsymbol{\mu}$ with $\epsilon = 0.01$ for diploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0050 | 0.0035 |
| 10 | 0.0156 | 0.0049 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

From table 4.4, average distance calculated for finite population size 4096 is 0.0156, for size 40960 is 0.0049 and for size 81920 is 0.0035. The results in Table 4.4 show average distance between finite population and limit \mathbf{z}^* approach expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance is smaller in diploid populations than in haploid populations with $\epsilon = 0.01$.

4.1.5 Diploid Population $\sim \epsilon : 0.1$

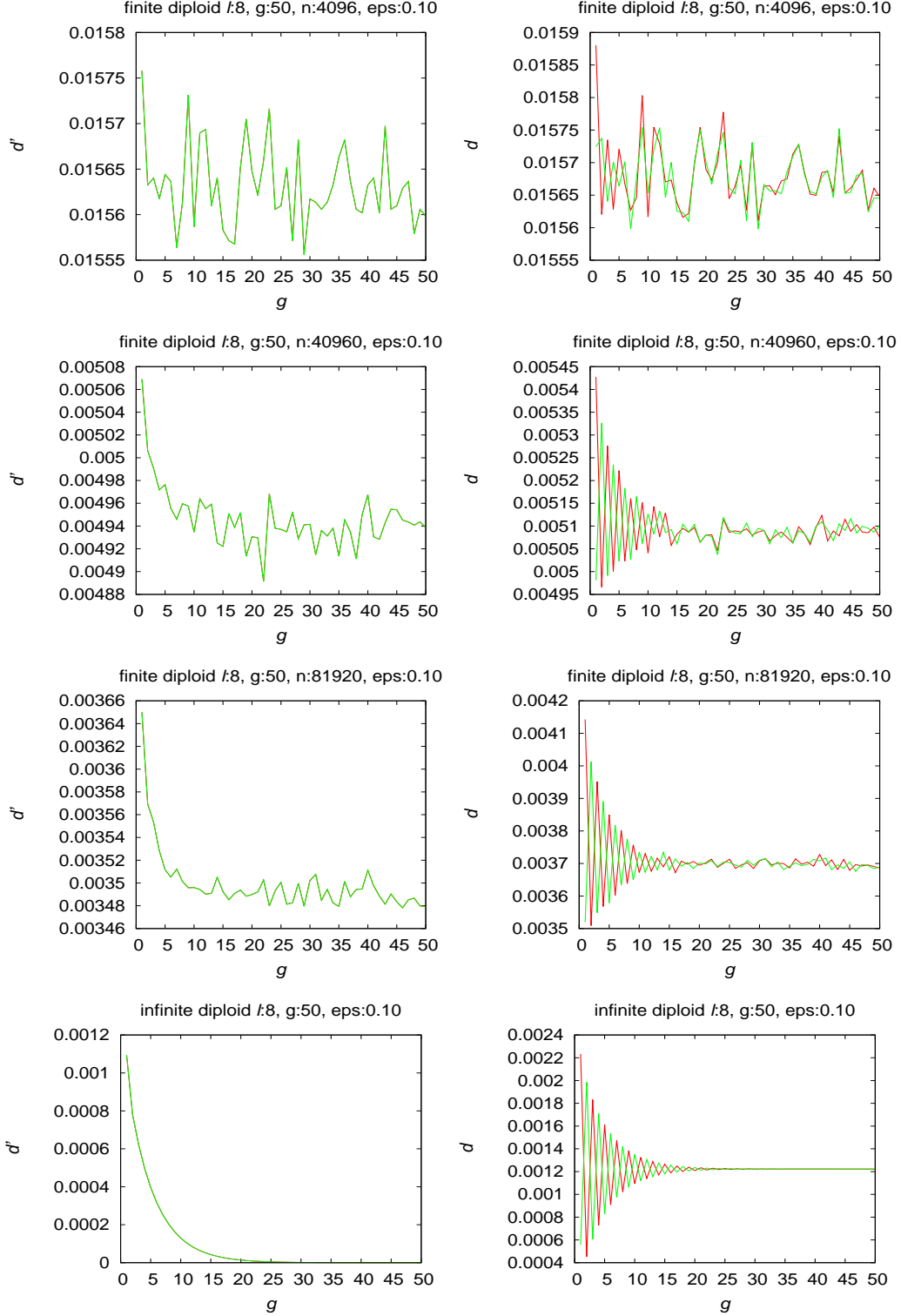


Figure 4.17: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 8$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 78

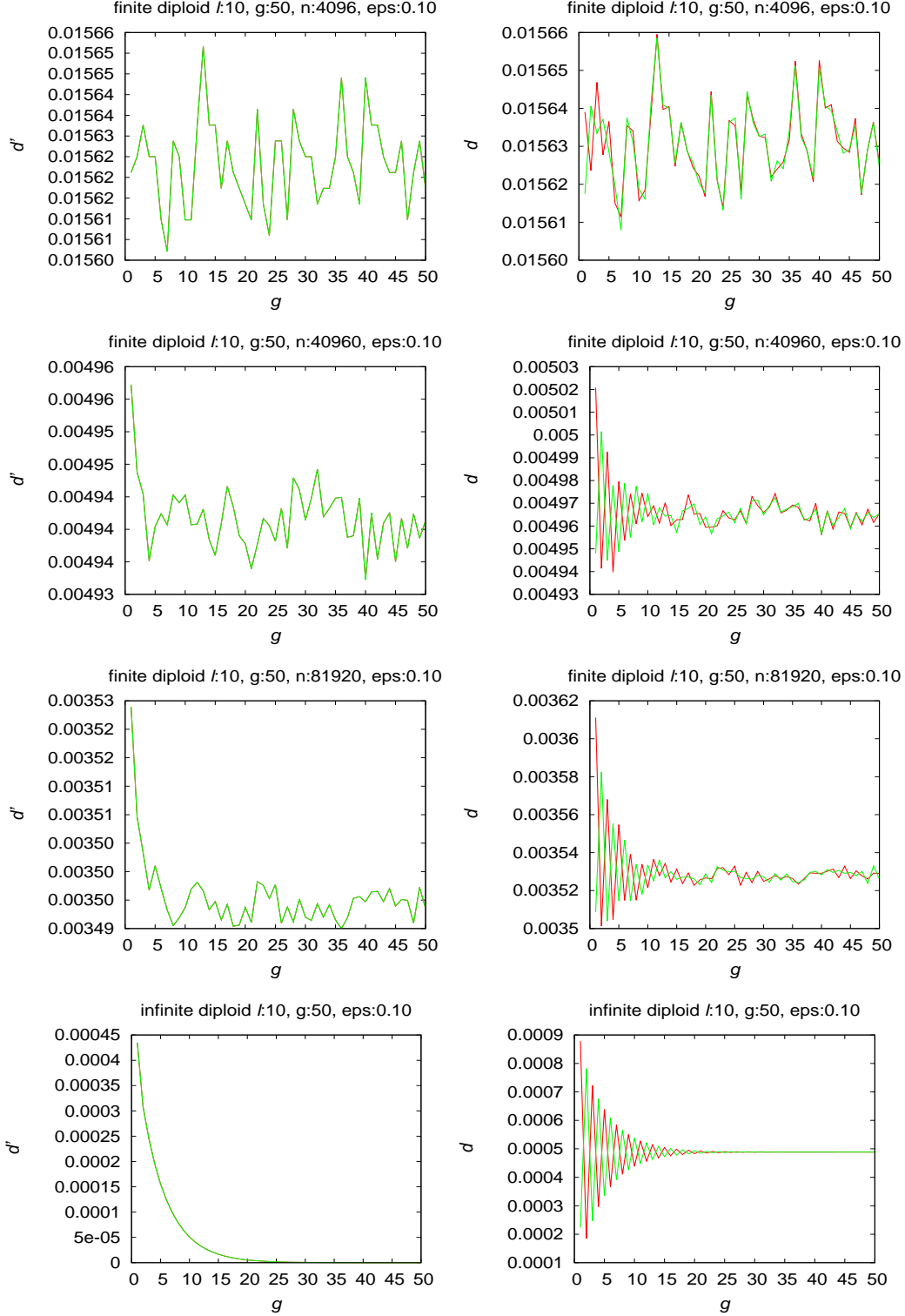


Figure 4.18: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 10$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 79



Figure 4.19: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 12$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 80

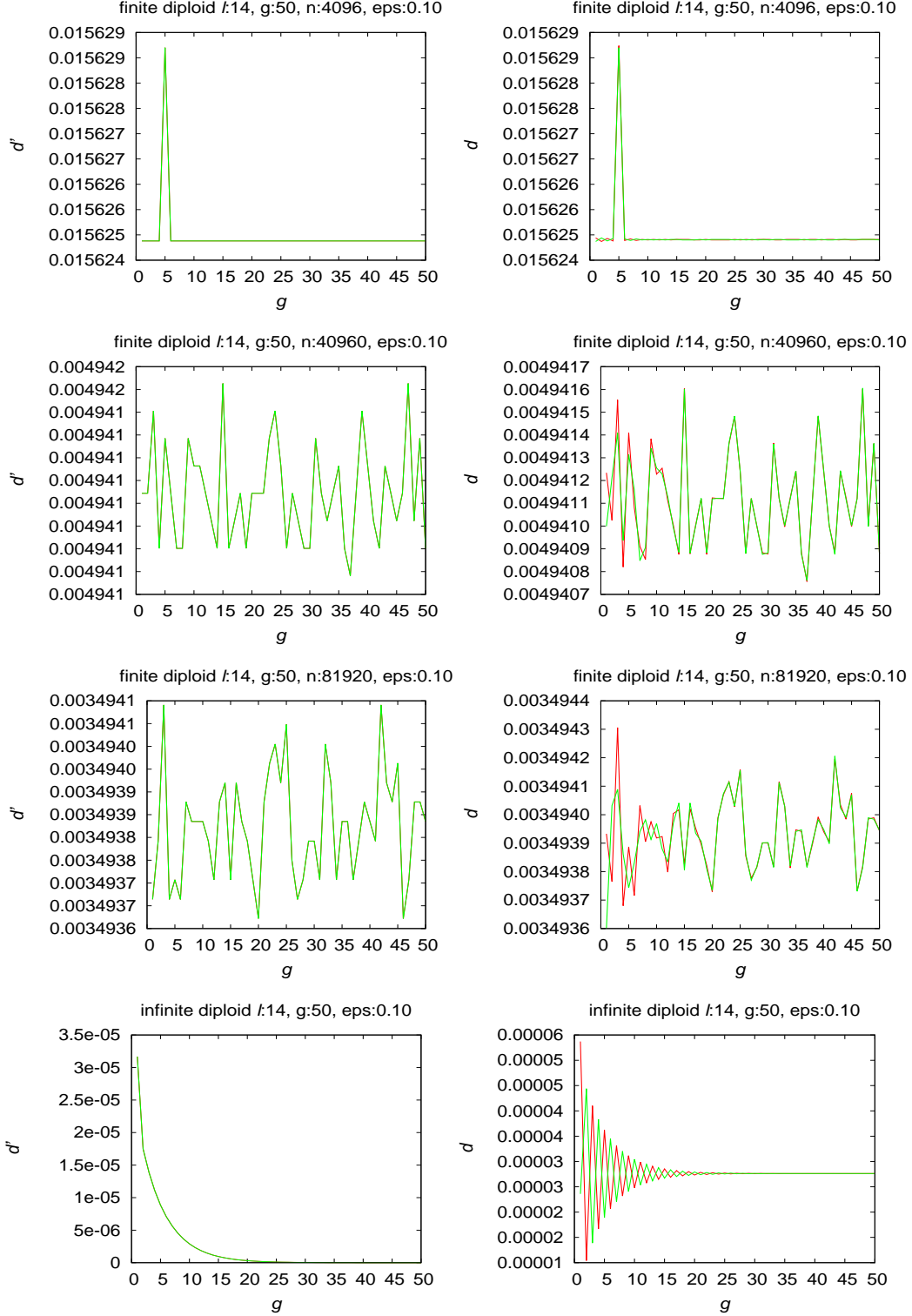


Figure 4.20: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 14$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 81

The right column in figures 4.17 through 4.20 shows distance of finite and infinite diploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.1$. Those graphs indicate oscillating behavior of diploid population given violation. Both finite and infinite populations oscillate given violation, and oscillation amplitudes decreases with time. Like in haploid case, for $\epsilon = 0.1$, oscillations in infinite populations die out quickly, but oscillations in finite populations does not die out completely. Rate of damping of ripples with $\epsilon = 0.1$ is larger than with $\epsilon = 0.01$. The all zeros mask created in mutation distribution with $\epsilon = 0.1$ has small probability of being used during mutation making it unlikely for oscillation in finite populations to die out completely. More random wiggling of finite population are noticed than in case of $\epsilon = 0.01$, and as value of ℓ increases, random wiggling is more prevalent for smaller population size.

The left column of figures 4.17 through 4.20 shows distance of finite and infinite diploid populations to limit \mathbf{z}^* (limit with violation in mutation distribution $\boldsymbol{\mu}$) when $\epsilon = 0.1$. The distance between finite population and limit \mathbf{z}^* (limit with violation in $\boldsymbol{\mu}$ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for diploid population in case of violation in $\boldsymbol{\mu}$ distribution with $\epsilon = 0.1$ for different finite population size N are tabulated in table 4.5.

Table 4.5: Distance measured for violation in $\boldsymbol{\mu}$ with $\epsilon = 0.1$ for diploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0049 | 0.0035 |
| 10 | 0.0156 | 0.0049 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

The results from Table 4.5 show average distance between finite population and limit z^* approaches the expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance is smaller in diploid populations than in haploid populations with $\epsilon = 0.1$.

4.1.6 Diploid Population $\sim \epsilon : 0.5$

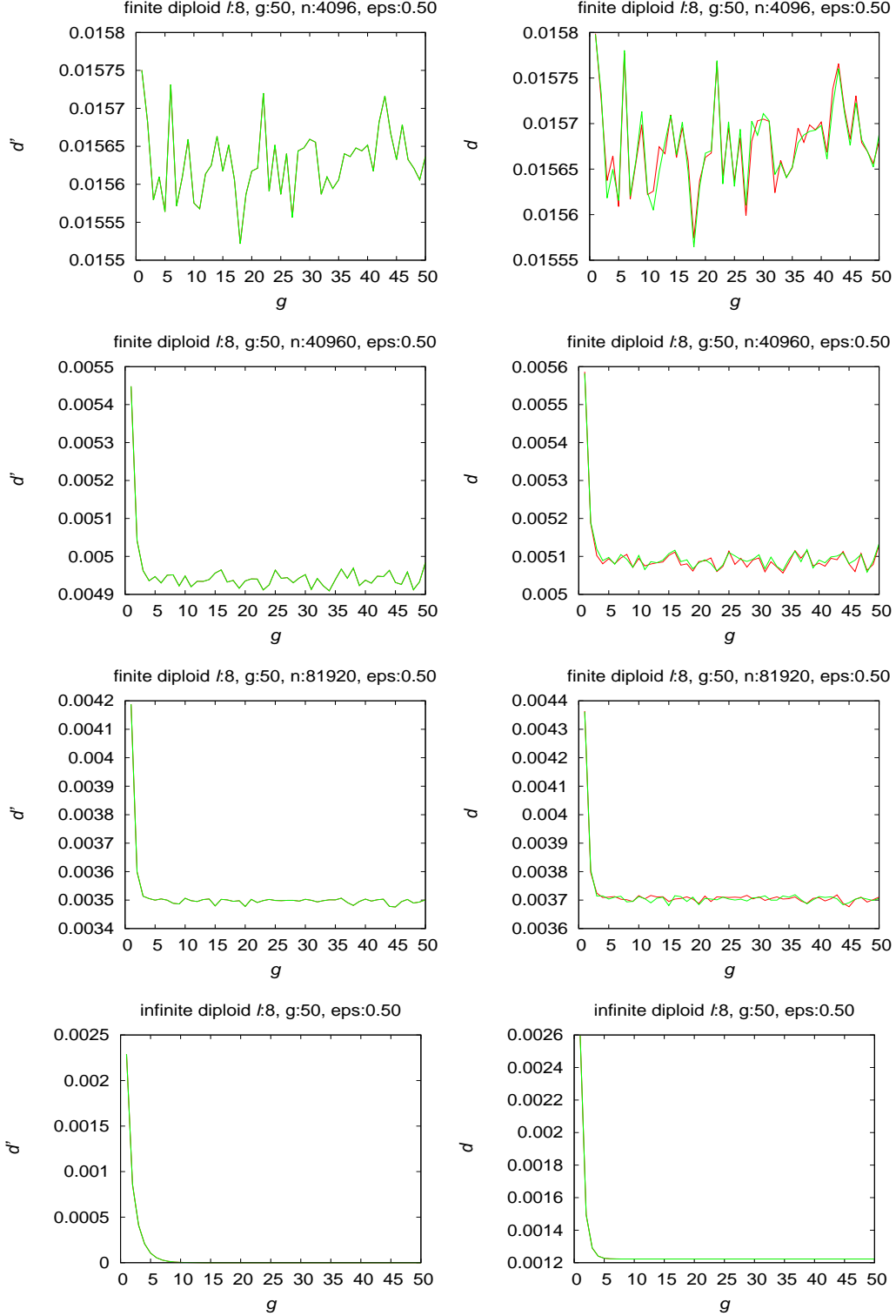


Figure 4.21: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 8$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 84

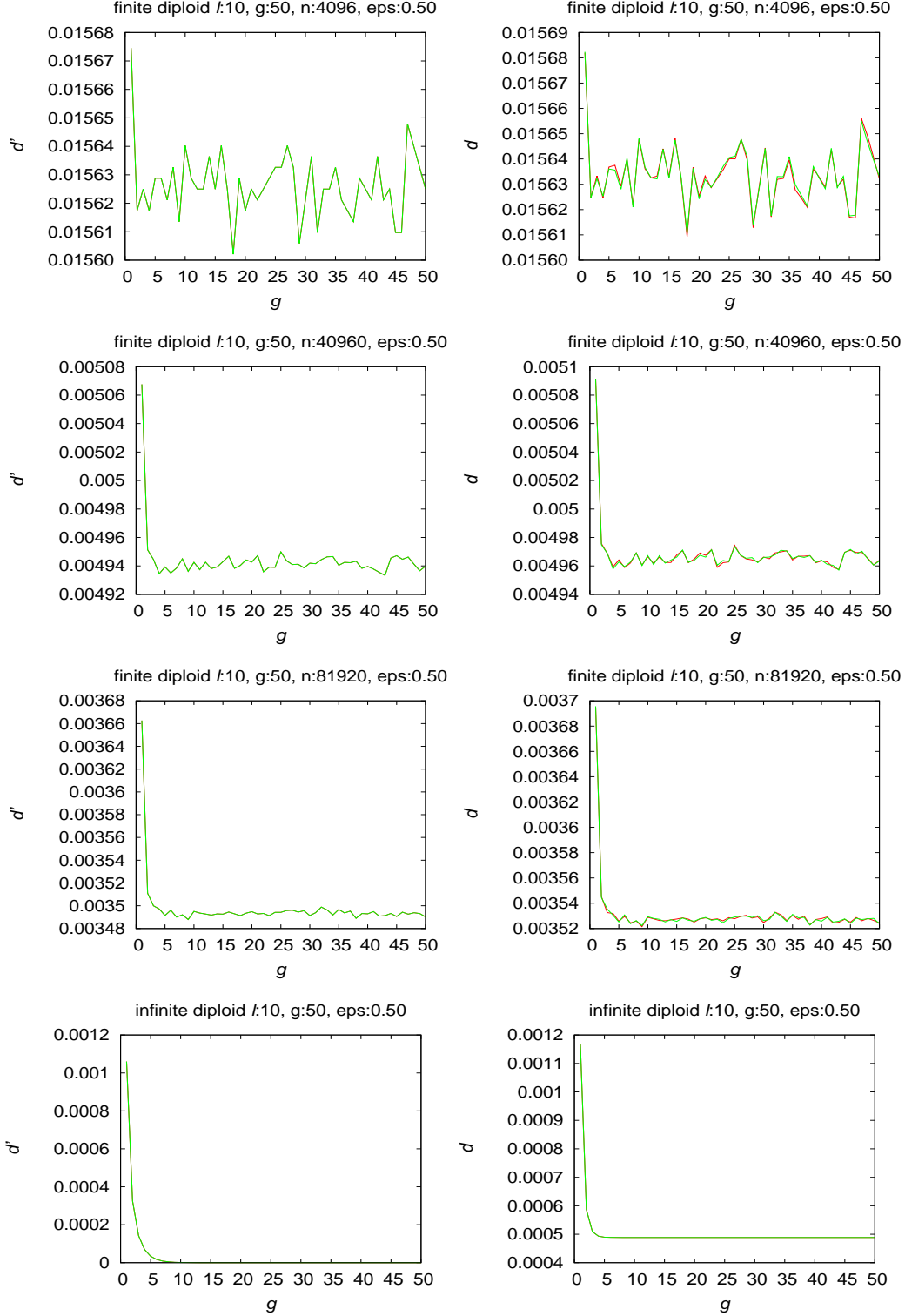


Figure 4.22: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 10$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 85

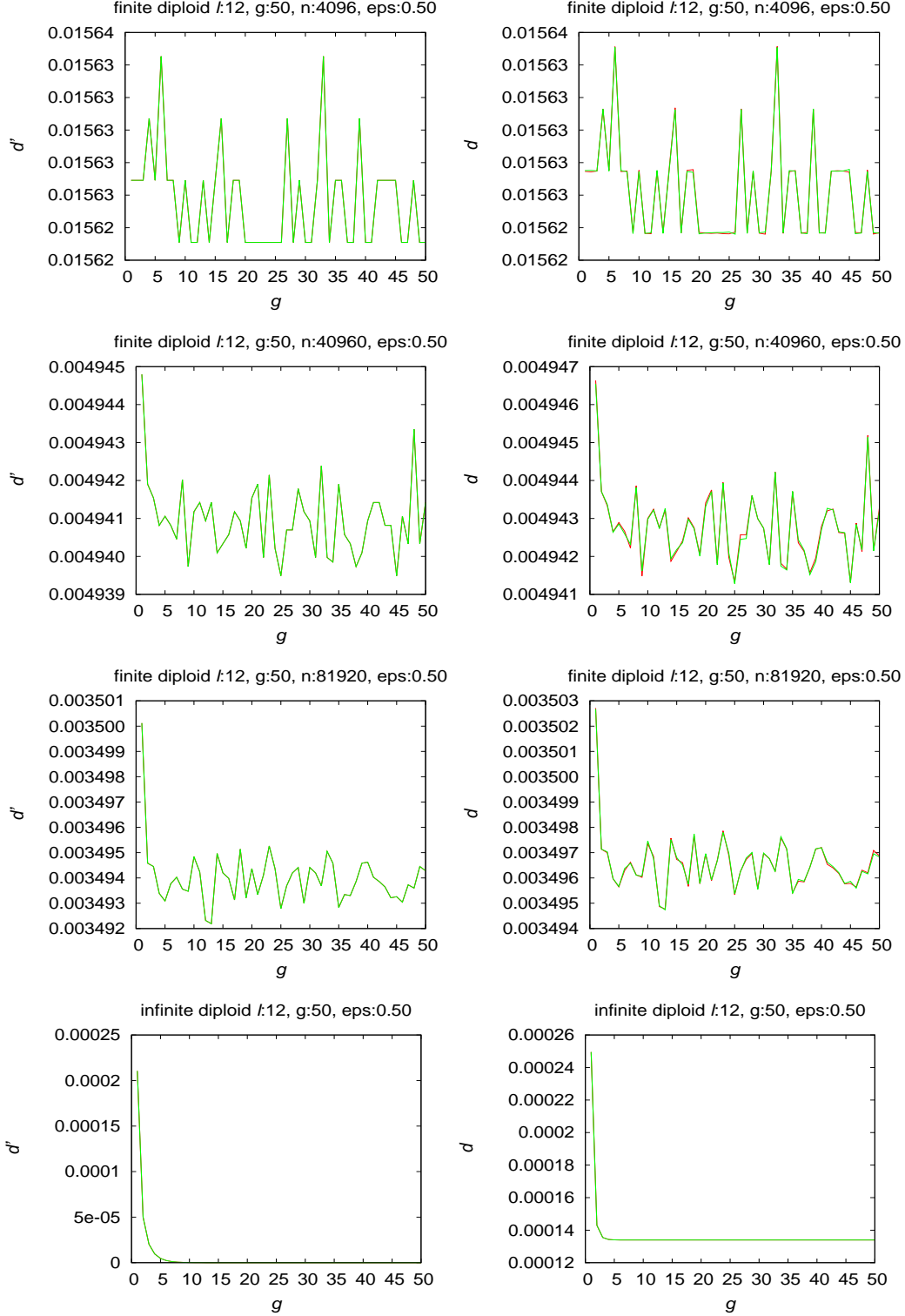


Figure 4.23: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 12$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 86

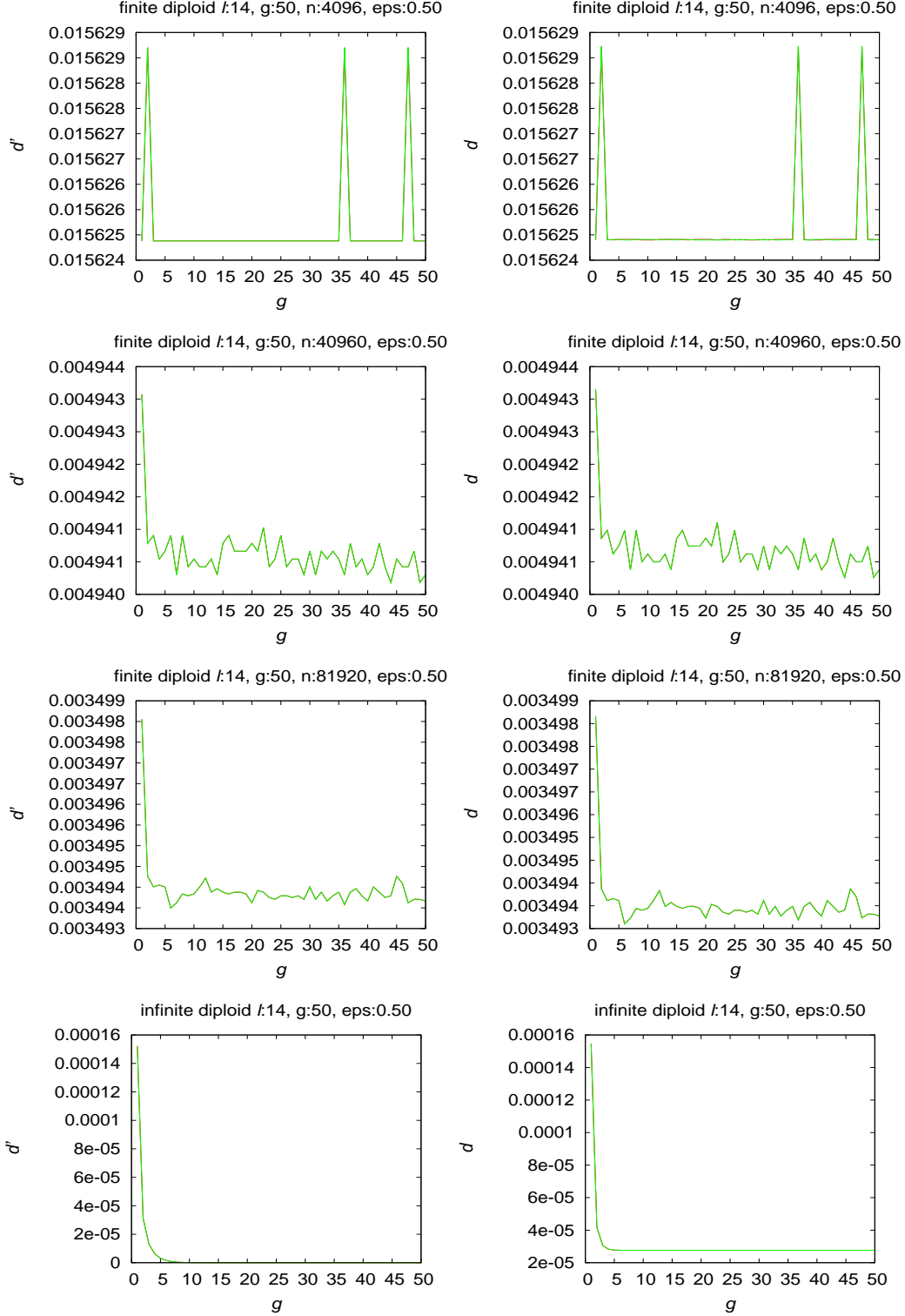


Figure 4.24: Infinite and finite diploid population oscillation behavior in case of violation in μ for genome length $\ell = 14$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 87

The right column in figures 4.21 through 4.24 shows distance of finite and infinite diploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.5$. Those graphs indicate oscillating behavior of diploid population given violation. Neither finite nor infinite populations show noticable oscillation given violation. The all zeros mask created in mutation distribution with $\epsilon = 0.5$ has large probability of being used during mutation, so oscillation does not occur.

The left column of figures 4.21 through 4.24 shows distance of finite and infinite diploid populations to limit \mathbf{z}^* (limit with violation in mutation distribution $\boldsymbol{\mu}$) when $\epsilon = 0.5$. The distance between finite population and limit \mathbf{z}^* (limit with violation in $\boldsymbol{\mu}$ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for diploid population in case of violation in $\boldsymbol{\mu}$ distribution with $\epsilon = 0.5$ for different finite population size N are tabulated in table 4.6.

Table 4.6: Distance measured for violation in $\boldsymbol{\mu}$ with $\epsilon = 0.5$ for diploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0049 | 0.0035 |
| 10 | 0.0156 | 0.0049 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

From table 4.6, average distance calculated for finite population size 4096 is 0.0156, for size 40960 is 0.0049 and for size 81920 is 0.0035. The results from Table 4.6 show average distance between finite population and limit \mathbf{z}^* approaches the expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance is smaller in diploid populations than in haploid populations with $\epsilon = 0.5$.

4.2 Discussion

In oscillation of population in presence of violation in μ , as value of ℓ increases, amplitude of oscillation decreases. Populations with larger population size, show better oscillations. Since diploid population consists of string length twice the size of string length of haploid population, diploid population needs larger population size than haploid population to exhibit good oscillations. For diploid population, increasing string length ℓ degrades convergence (as finite population size increases) to infinite population behavior. The behavior is noticeable in figures 4.13 through 4.20 for violation in μ . The behavior is less noticeable in haploid population.

With increase in value of ϵ , oscillation in population diminishes, and oscillation completely ceases after certain threshold value for ϵ . Like in oscillations in non-violation case in chapter 3, diploid populations hopping to other levels are observed for string length values 12 and 14 for population size of 4096 in figures 4.15, 4.16, 4.19, 4.20, 4.23 and 4.24, and the behavior is absent when population size is larger.

Figure 4.25 summarizes the distance data from tables 4.1 \cdots 4.6. Distance of infinite population from finite population of three finite population sizes 4096, 40960, 81920 are plotted for different ℓ . Plots for different violation levels ϵ are arranged in columns. Plots for haploid and diploid populations are arranged in two rows. With increase in ℓ , distance moves closer to the single step distance. So, since diploid population string length is twice of haploid population, distance in diploid case moves closer to the single step distance than in haploid case. It is also noticeable in haploid population case that as ϵ increases, the distance moves closer to the single step distance.

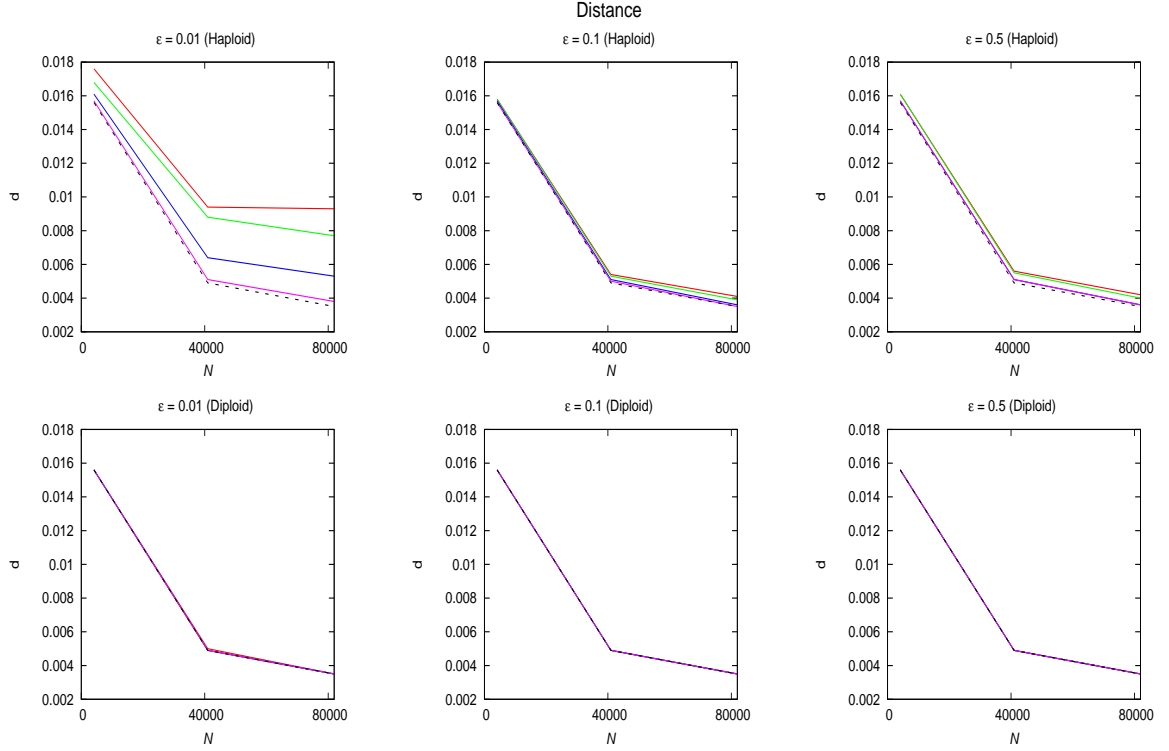


Figure 4.25: Distance of finite population to infinite population in case of violation in μ : d is distance; N is finite population size; ϵ is level of violation; red line represents distance for $\ell = 8$, green line for $\ell = 10$, blue line for $\ell = 12$, pink line for $\ell = 14$ and black dotted line for expected single step distance.

4.3 Summary

In this chapter, we violated the condition 3.3 through violation in mutation making the Markov chain representing finite population regular and infinite population trajectories have no periodic orbit, and studied infinite and finite populations oscillation behavior with the violation through experiments. Infinite population ceases to oscillate when the condition 3.3 for convergence to periodic orbits is violated, but finite population is robust enough to continue to approximately oscillate for small values of ϵ . For smaller values of ϵ , finite population does not get aware of violation because the probability of using new mask created in the mutation distribution μ due to violation is very low, and if no new mask is used, finite population follows behavior of infinite population without violation in the condition for convergence to periodic orbits.

Chapter 5

Violation in Crossover Distribution

This chapter explores the robustness of finite population oscillation when condition 3.3 for the crossover distribution is violated and infinite population trajectories have no periodic orbit.

Error ϵ is introduced into the crossover distribution χ so as to violate condition 3.3; this guarantees that infinite population trajectories have no periodic orbit. Consequently, $\mathbf{p}^* = \mathbf{q}^* = \mathbf{z}^*$. The initial population is computed using same procedure as described in section 3.3. To explore the effects of the degree of violation of condition 3.3 in χ , different values of ϵ are used in experiments. String length $\ell \in \{8, 10, 12, 14\}$ are considered for simulation. Going forward, we use ‘limit \mathbf{z}^* ’ to denote evolutionary limit when crossover distribution χ violates condition 3.3, and ‘non-violation limits \mathbf{p}^* and \mathbf{q}^* ’ to denote limits without violation.

5.1 Violation

The crossover distribution χ was modified as

$$\chi_i = (1 - \epsilon)\chi_i; \quad i = \{1, 2, \dots, 2^\ell - 1\}$$

So that

$$\chi_i + \chi_{i+g} = 1 - \epsilon; \quad g \text{ is defined in section } \textcolor{blue}{3.1}$$

Then j is chosen where $\chi_j = 0$ and set $\chi_j = \epsilon$.

Violation in crossover distribution χ is different from violation in mutation distribution μ . Markov chain formed by transition matrix Q is regular under violation in μ but that is not the case under violation in χ . Markov chain formed under violation in χ might not be regular.

Simulations are repeated with violation levels ϵ as above. The distances of both infinite and finite populations to limit z^* are plotted. The distances of both infinite and finite populations to non-violation limits p^* and q^* are also plotted.

5.1.1 Haploid Population $\sim \epsilon : 0.01$

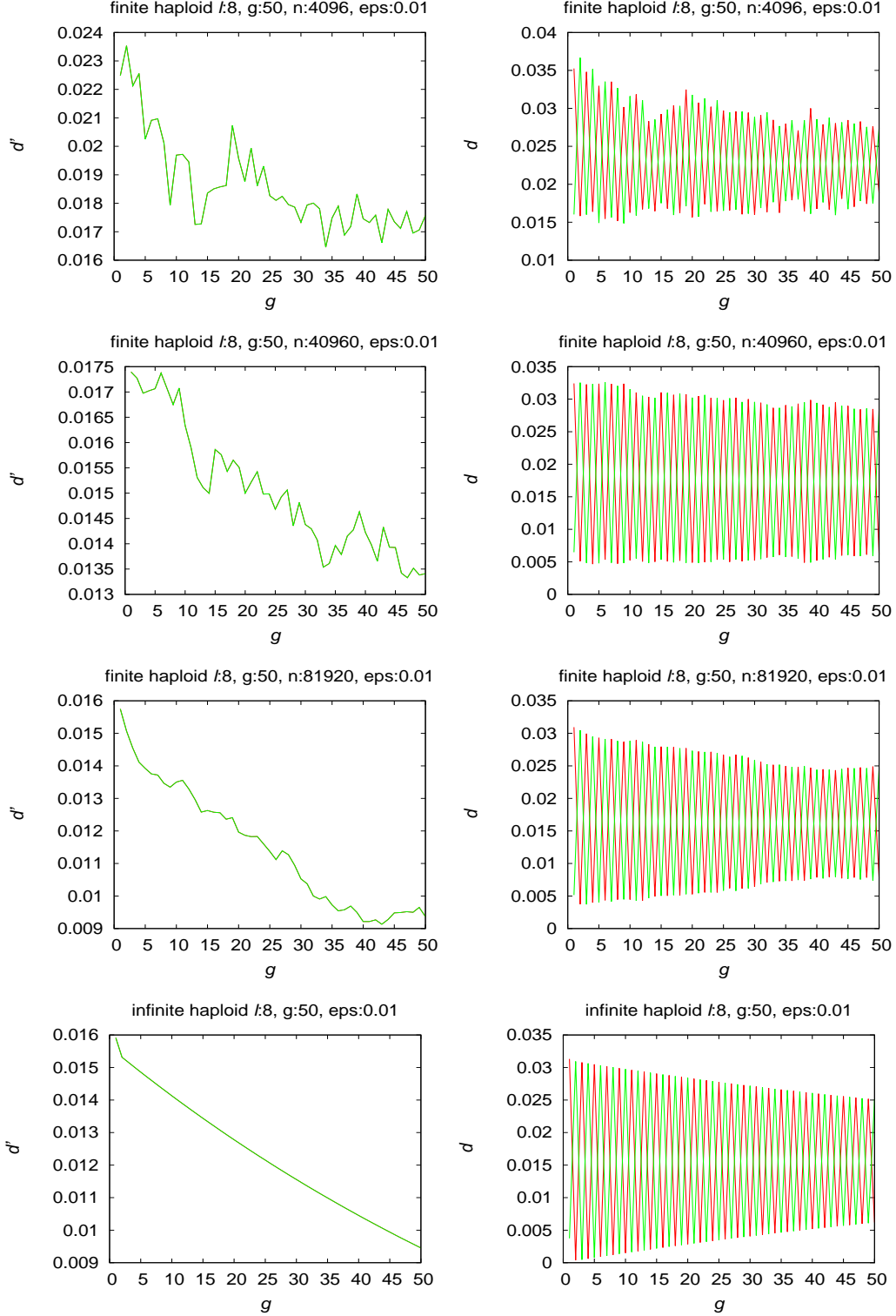


Figure 5.1: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 8$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 94

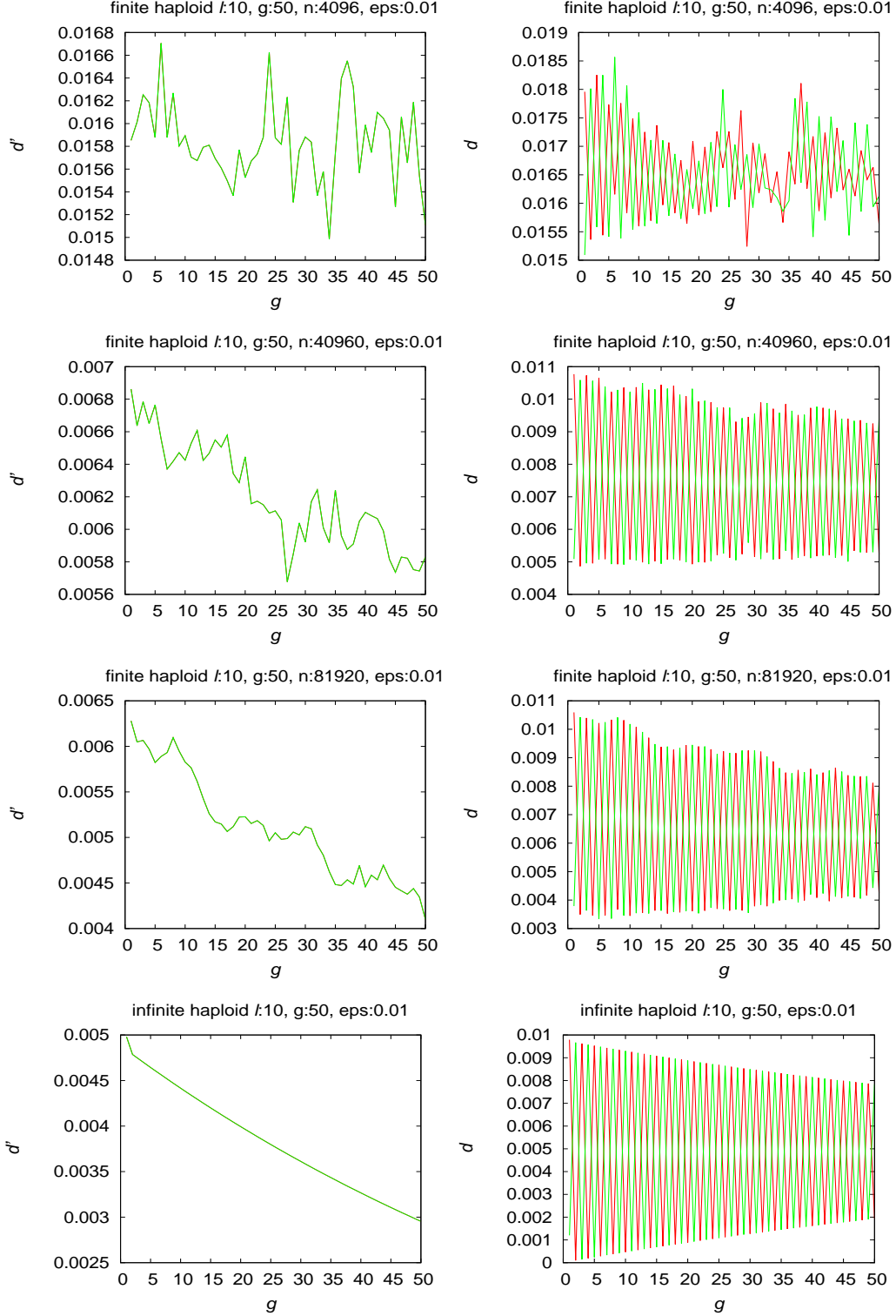


Figure 5.2: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 10$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 95

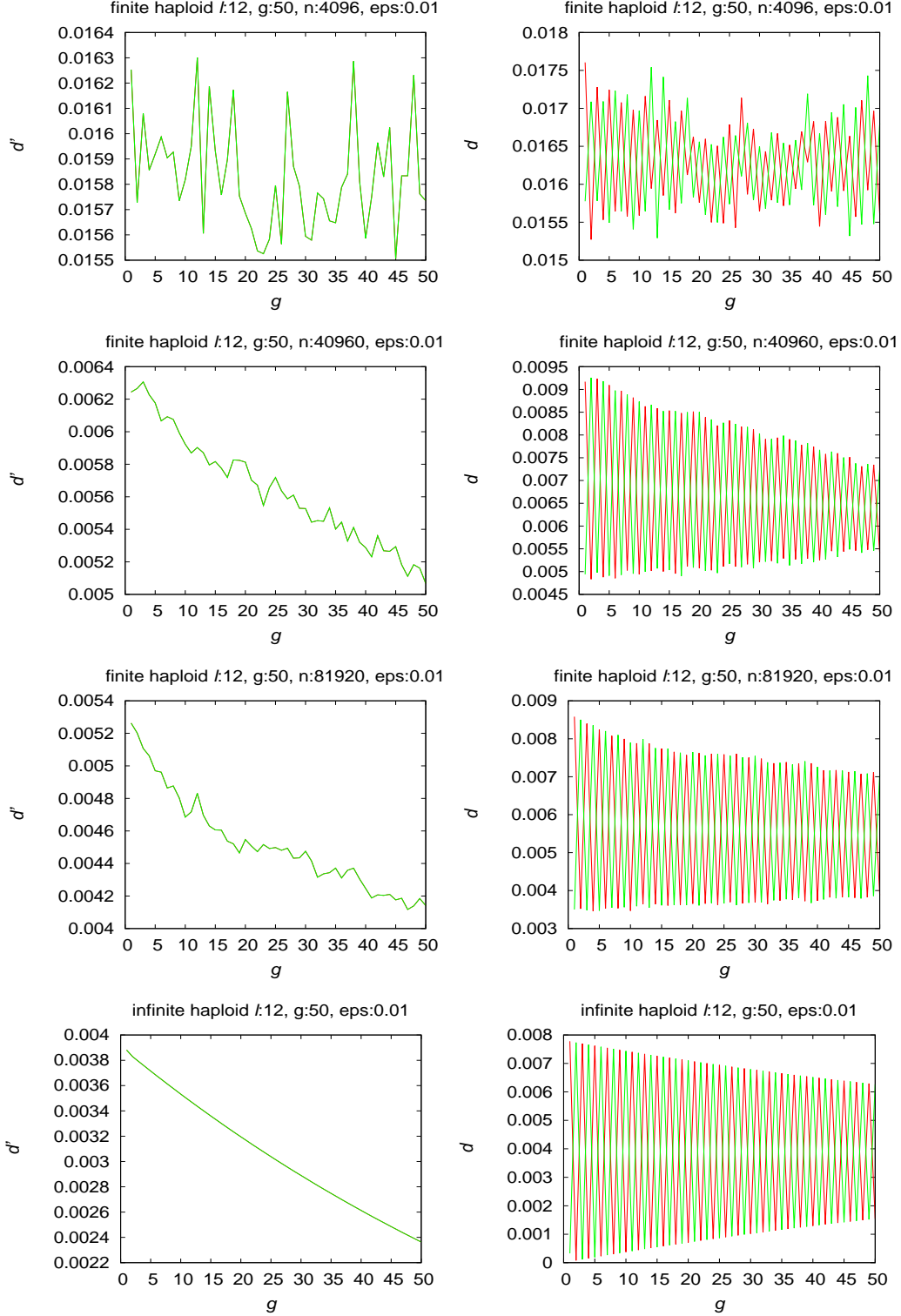


Figure 5.3: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 12$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 96

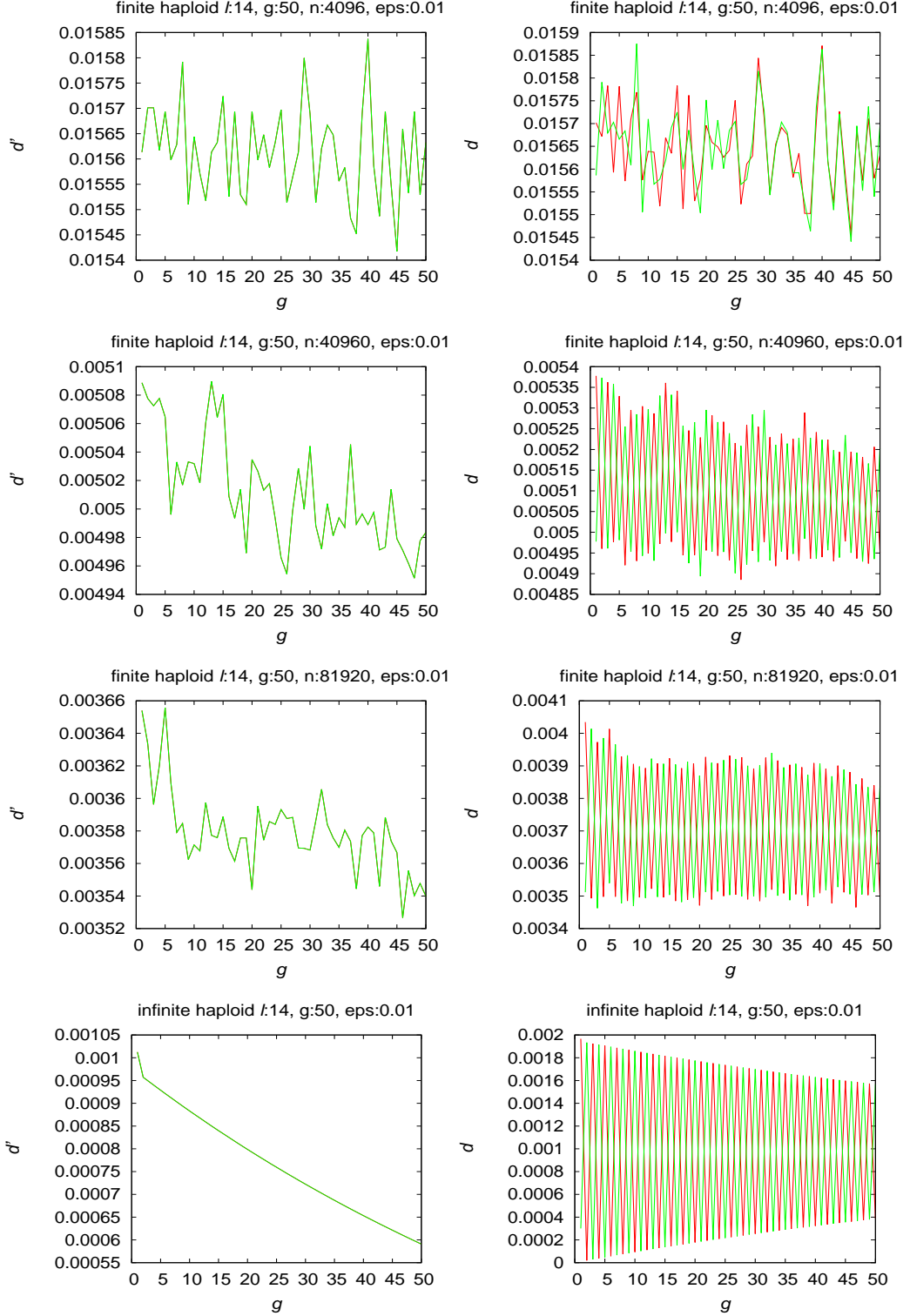


Figure 5.4: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 14$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 97

The right column in figures 5.1 through 5.4 shows distance of finite and infinite haploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.01$. Those graphs indicate oscillating behavior of haploid populations given violation. Both finite and infinite populations oscillate given violation. Since the value of ϵ is small, damping of ripples is slow. A new mask created in crossover distribution with $\epsilon = 0.01$ has small probability of being used during crossover and when they are not used, behavior should be consistent with the behavior without violation in the distribution. Moreover, $\epsilon = 0.01$ is so small that infinite population oscillation does not die out in 50 generations.

The left column of figures 5.1 through 5.4 shows distance of finite and infinite haploid populations to limit \mathbf{z}^* (limit with violation in crossover distribution χ) when $\epsilon = 0.01$. The distance between finite population and limit \mathbf{z}^* (limit with violation in χ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for haploid population in case of violation in χ distribution with $\epsilon = 0.01$ for different finite population size N are tabulated in table 5.1.

Table 5.1: Distance measured for violation in χ with $\epsilon = 0.01$ for haploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0186 | 0.0150 | 0.0115 |
| 10 | 0.0158 | 0.0062 | 0.0051 |
| 12 | 0.0158 | 0.0056 | 0.0045 |
| 14 | 0.0156 | 0.0050 | 0.0036 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

The results from Table 5.1 show average distance between finite population and limit \mathbf{z}^* approaches the expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance decreased as genome length ℓ increased for all sizes of finite haploid populations with $\epsilon = 0.01$.

5.1.2 Haploid Population $\sim \epsilon : 0.1$

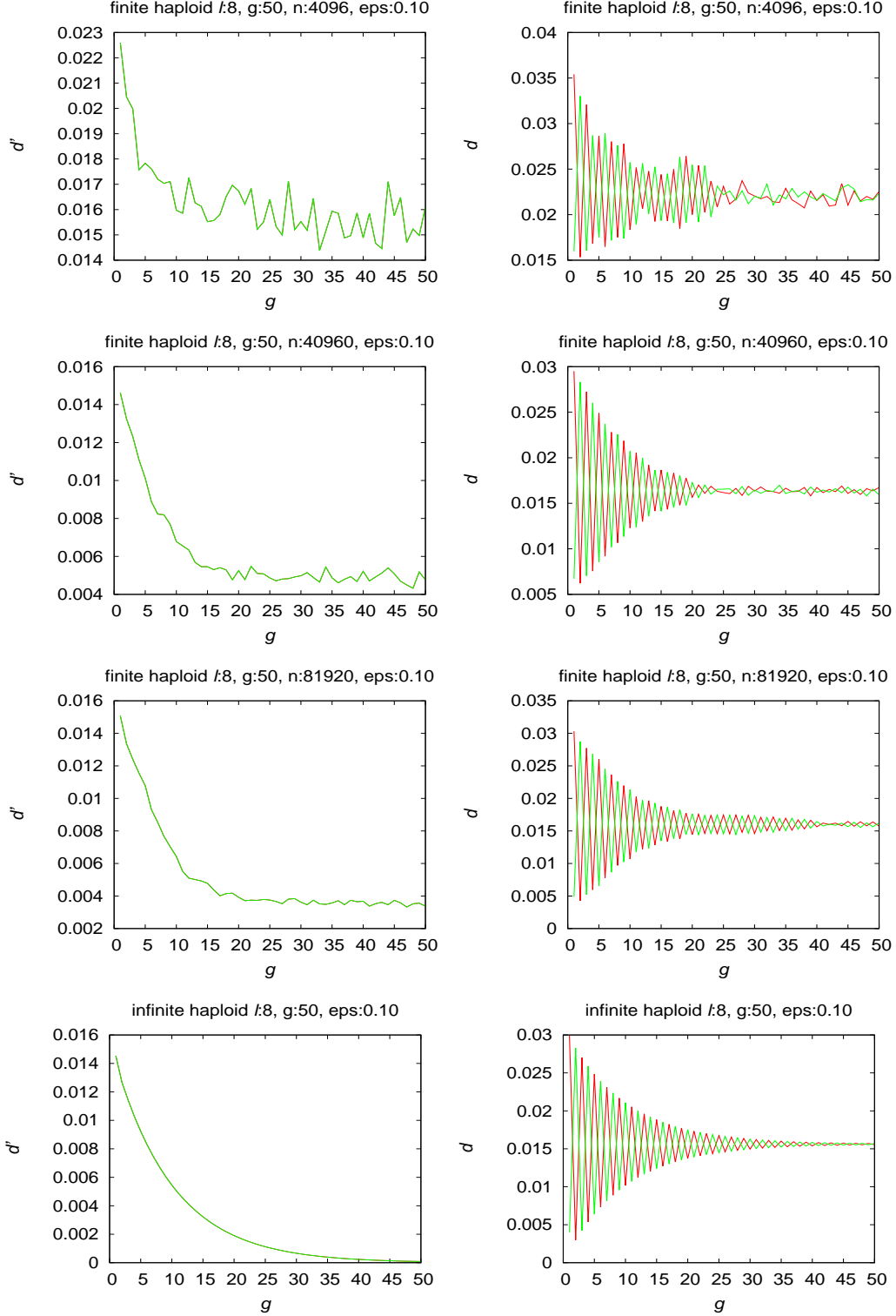


Figure 5.5: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 8$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 100

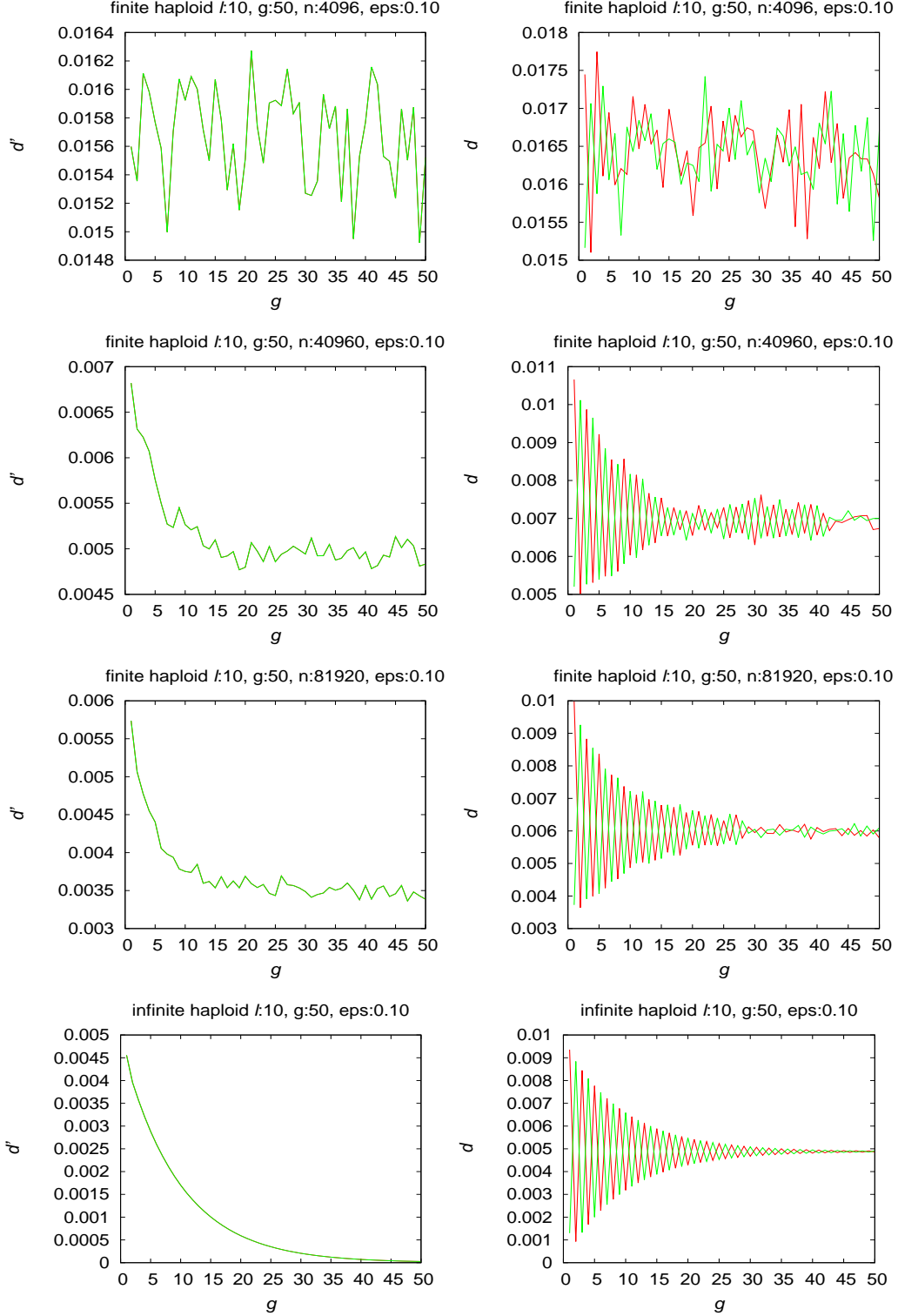


Figure 5.6: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 10$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 101

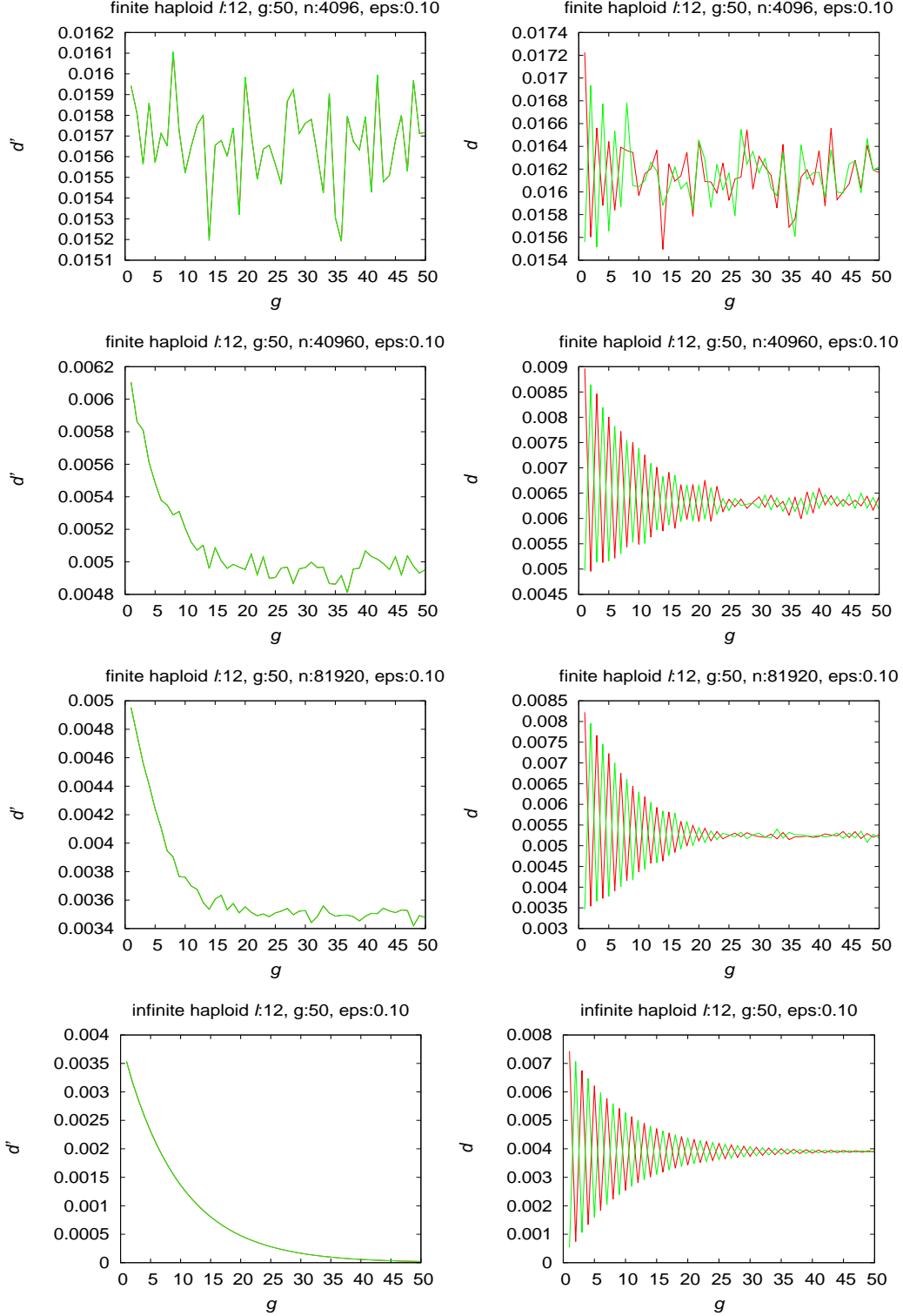


Figure 5.7: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 12$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 102

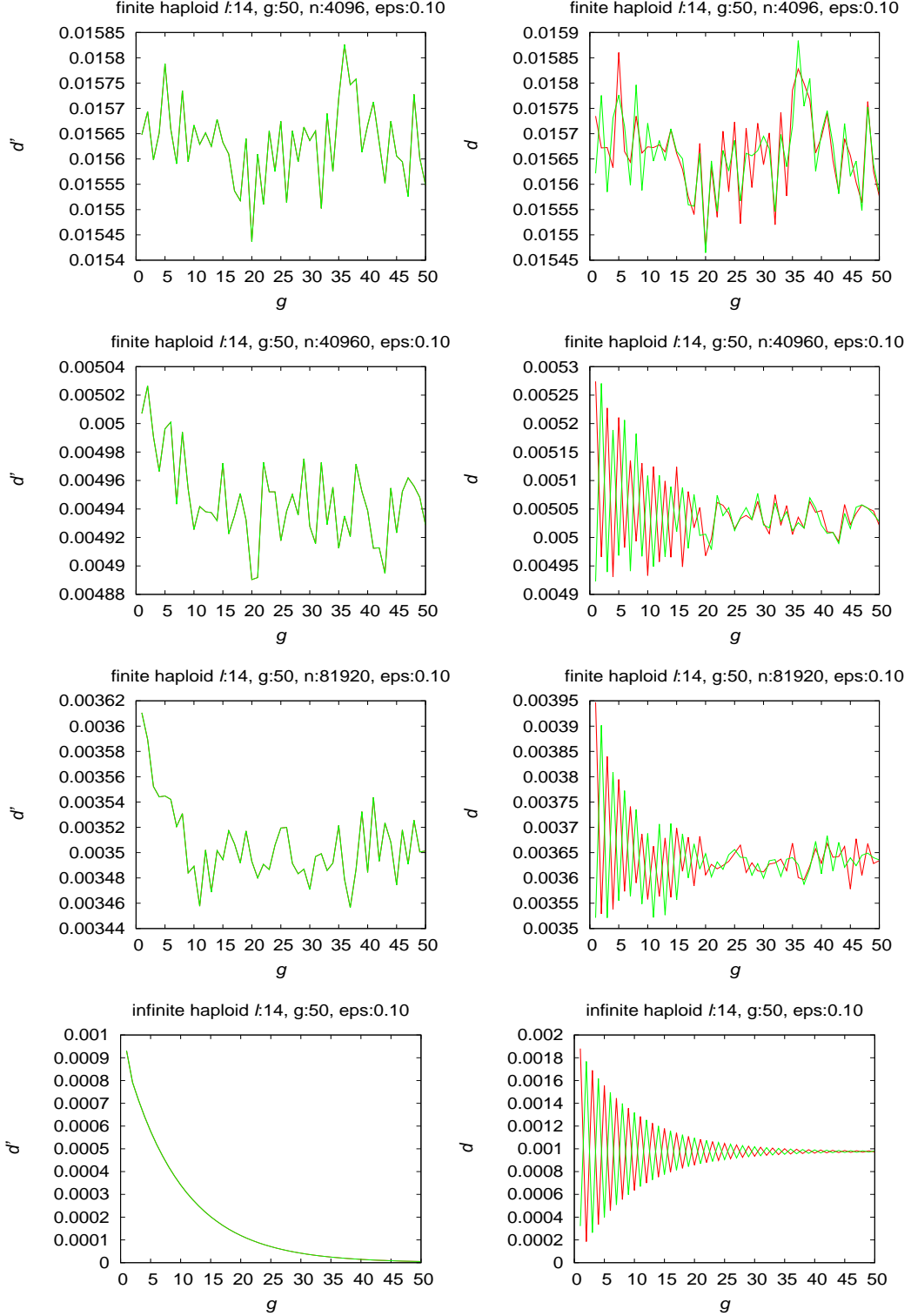


Figure 5.8: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 14$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 103

The right column in figures 5.5 through 5.8 shows distance of finite and infinite haploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.1$. Those graphs indicate oscillating behavior of haploid population given violation. Both finite and infinite populations oscillate given violation, and oscillations amplitudes decreases with time. However, for $\epsilon = 0.1$, oscillations in infinite populations die out quickly, but oscillations in finite populations does not die out completely. Rate of damping of ripples with $\epsilon = 0.1$ is larger than with $\epsilon = 0.01$. A new mask introduced in crossover distribution with $\epsilon = 0.1$ has small probability of being used during crossover for oscillation in finite populations to die out completely.

The left column of figures 5.5 through 5.8 shows distance of finite and infinite haploid populations to limit \mathbf{z}^* (limit with violation in crossover distribution χ) when $\epsilon = 0.1$. The distance between finite population and limit \mathbf{z}^* (limit with violation in χ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for haploid population in case of violation in χ distribution with $\epsilon = 0.1$ for different finite population size N are tabulated in table 5.2.

Table 5.2: Distance measured for violation in χ with $\epsilon = 0.1$ for haploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0163 | 0.0061 | 0.0051 |
| 10 | 0.0157 | 0.0051 | 0.0037 |
| 12 | 0.0157 | 0.0051 | 0.0037 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

From , average distance calculated for finite population size 4096 is 0.0158, for size 40960 is 0.0053 and for size 81920 is 0.0038. The results from Table 5.2 show average distance between finite population and limit \mathbf{z}^* approaches the expected single step distance between finite and infinite population. The distance decreased

as $1/\sqrt{N}$. Also, the distance decreased as genome length ℓ increased for all sizes of finite haploid populations with $\epsilon = 0.1$.

5.1.3 Haploid Population $\sim \epsilon : 0.5$

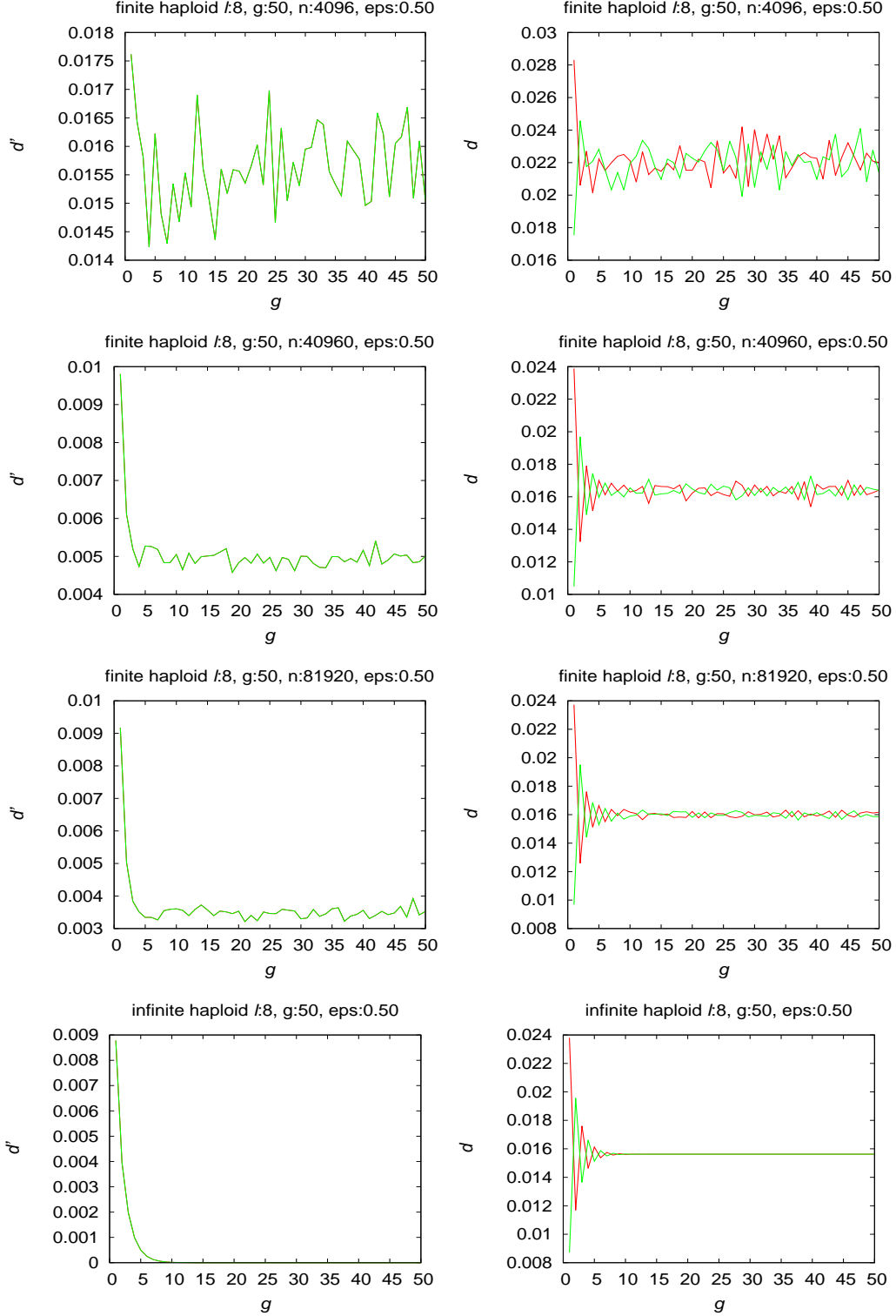


Figure 5.9: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 8$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 106

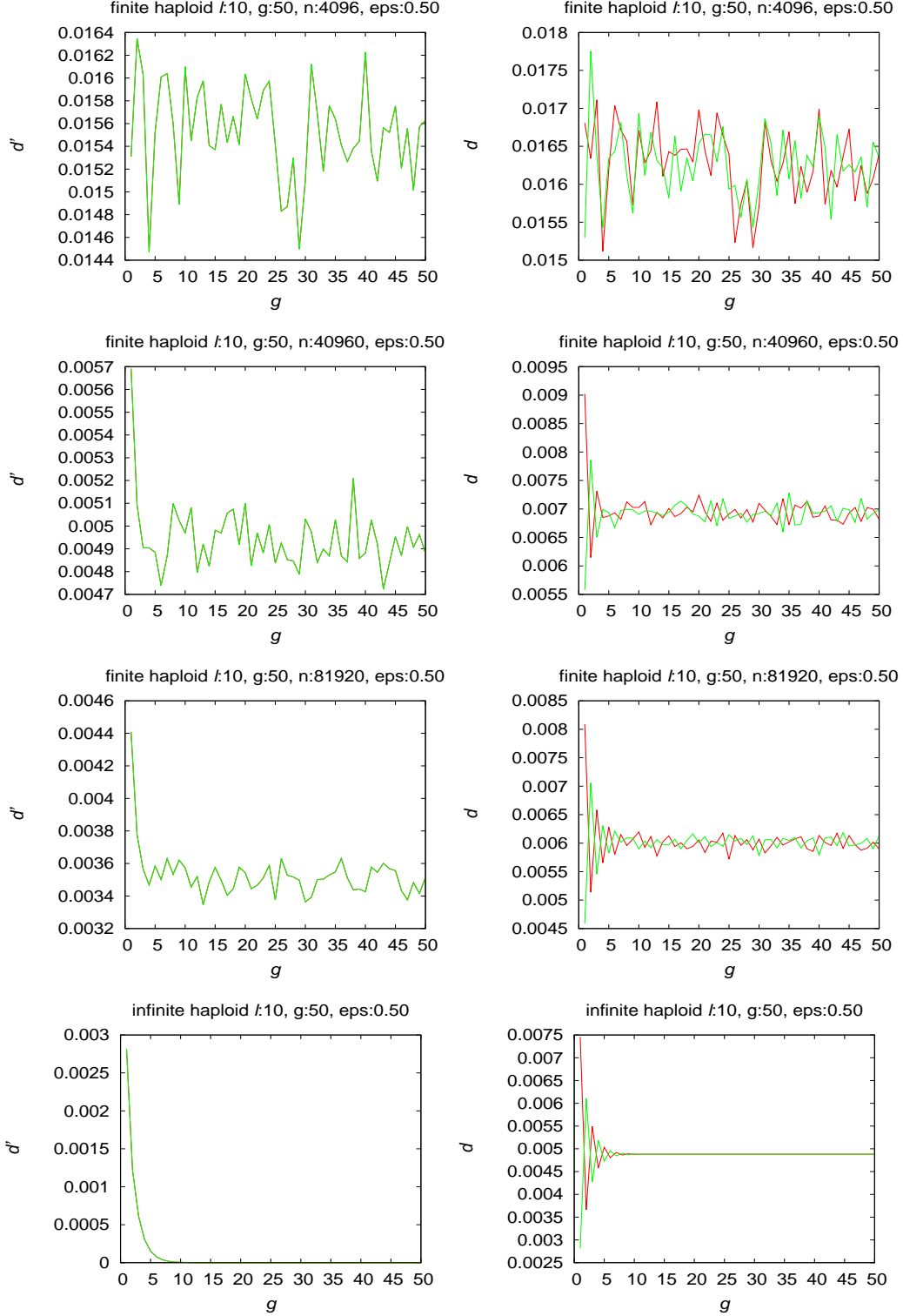


Figure 5.10: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 10$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 107

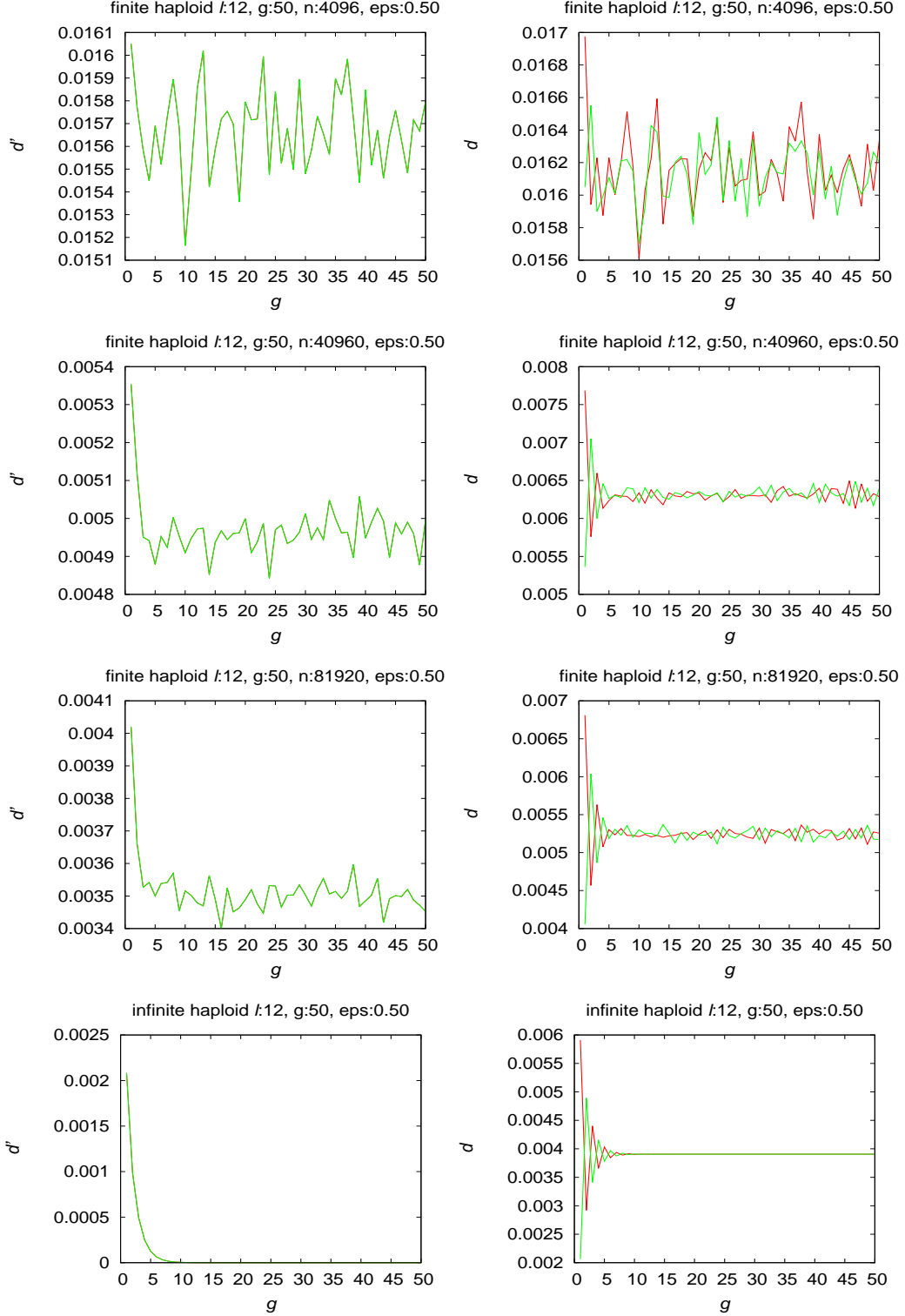


Figure 5.11: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 12$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 108

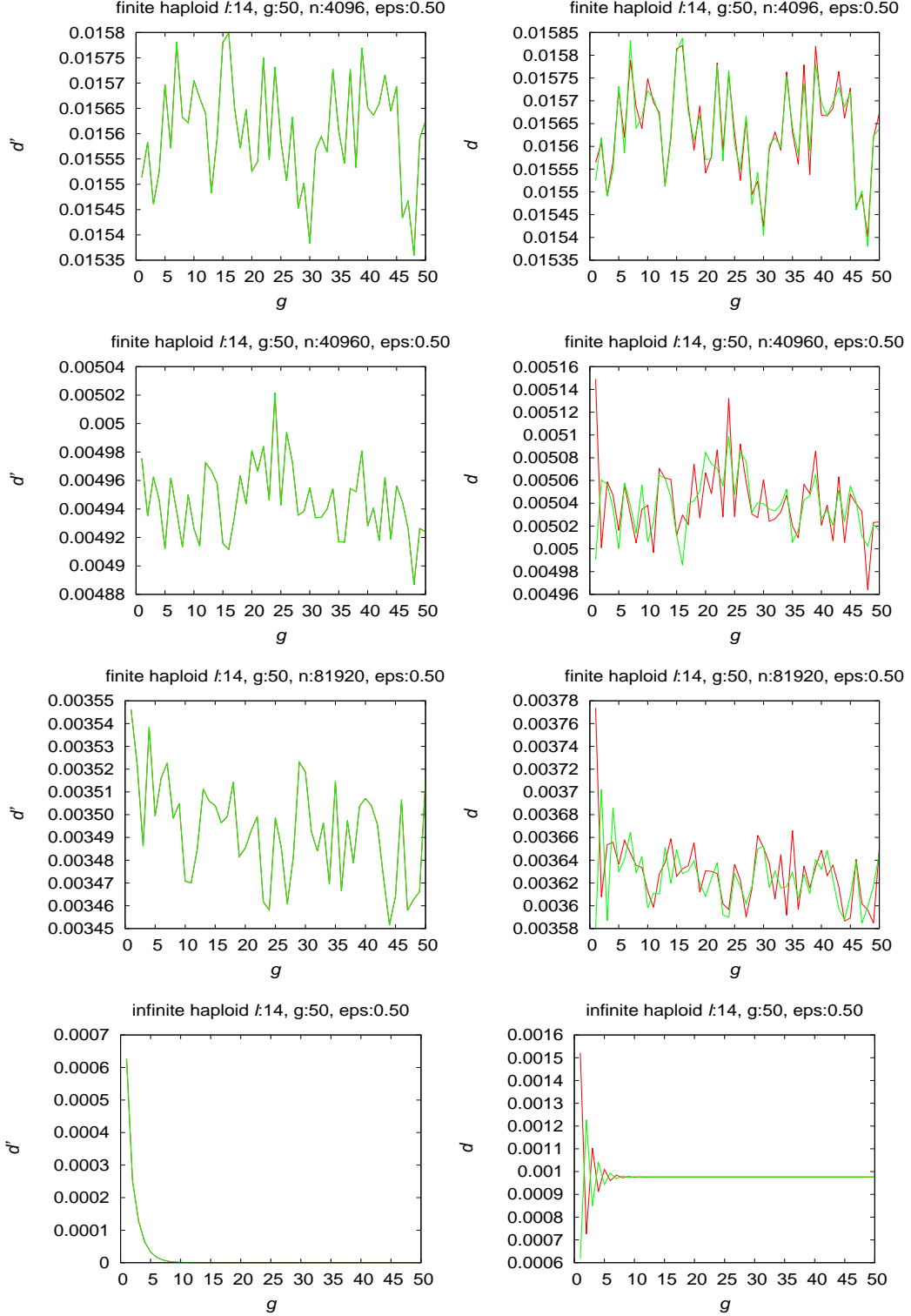


Figure 5.12: Infinite and finite haploid population oscillation behavior in case of violation in χ for genome length $\ell = 14$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 109

The right column in figures 5.9 through 5.12 shows distance of finite and infinite haploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.5$. The graphs indicate oscillating behavior of haploid population given violation. Unlike mutation with violation $\epsilon = 0.5$, absence of oscillation is not observed. Finite populations still show some though not very clear oscillations, and infinite populations also oscillate but the oscillation dies out quickly.

The left column of figures 5.9 through 5.12 shows distance of finite and infinite haploid populations to limit \mathbf{z}^* (limit with violation in crossover distribution χ) when $\epsilon = 0.5$. The distance between finite population and limit \mathbf{z}^* (limit with violation in χ distribution) decreases as finite population size increases, and finite population shows behavior similar to infinite population behavior as finite population size grows. Average distance data for haploid population in case of violation in χ distribution with $\epsilon = 0.5$ for different finite population size N are tabulated in table 5.3.

Table 5.3: Distance measured for violation in χ with $\epsilon = 0.5$ for haploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0051 | 0.0036 |
| 10 | 0.0155 | 0.0049 | 0.0035 |
| 12 | 0.0157 | 0.0050 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

The results from Table 5.3 show average distance between finite population and limit \mathbf{z}^* approaches expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$.

5.1.4 Diploid Population $\sim \epsilon : 0.01$

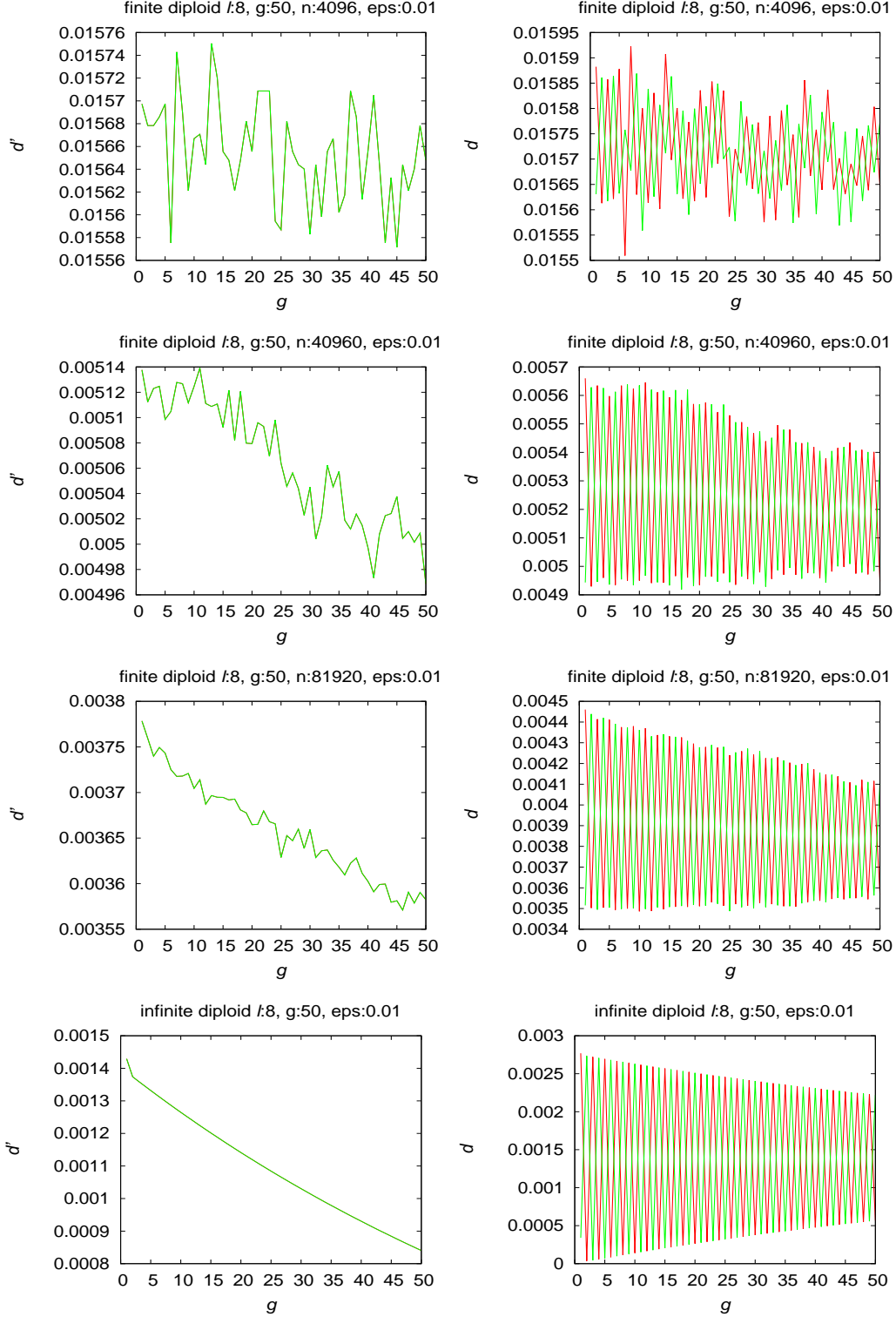


Figure 5.13: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 8$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 111

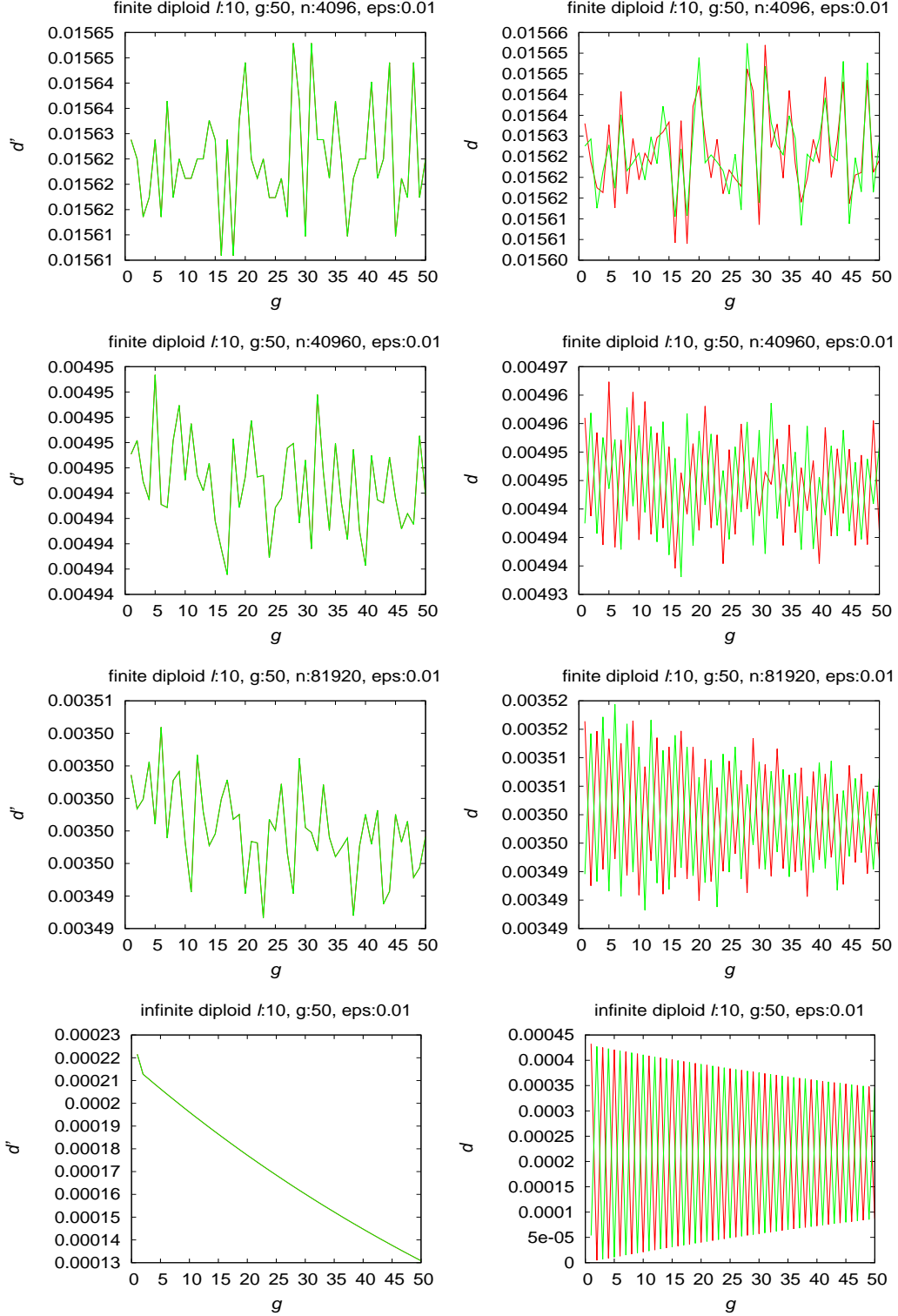


Figure 5.14: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 10$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation.

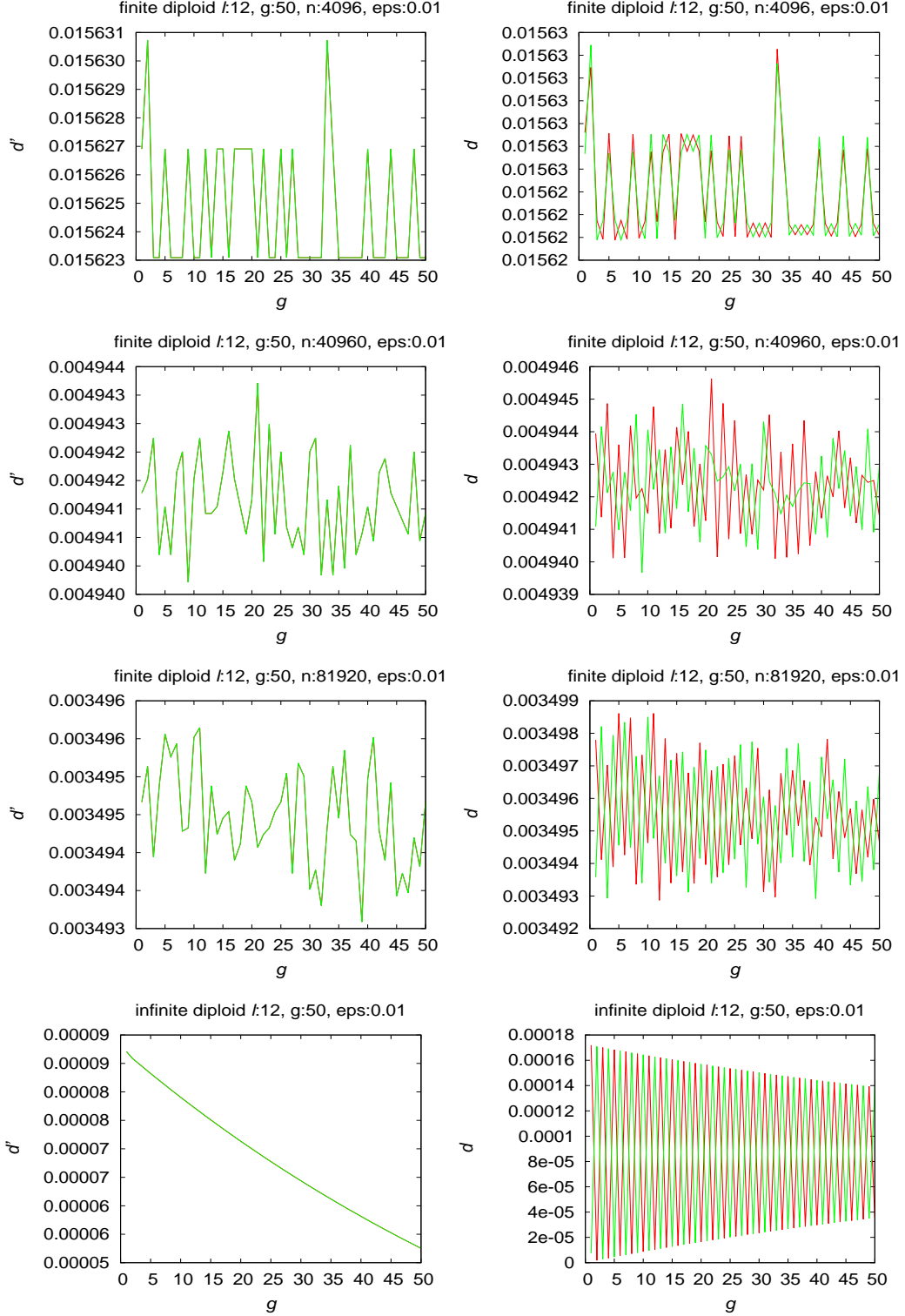


Figure 5.15: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 12$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 113

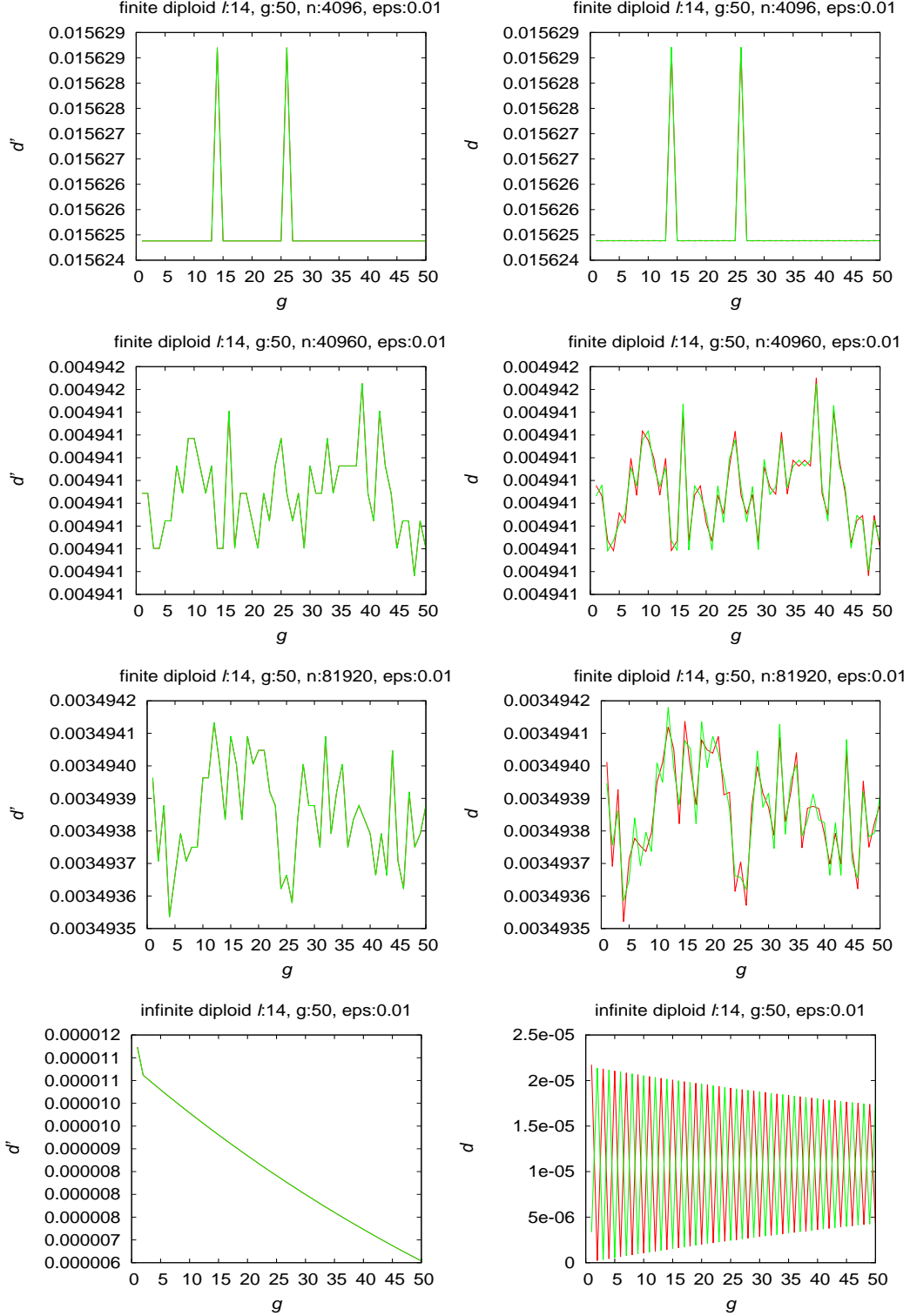


Figure 5.16: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 14$ and $\epsilon = 0.01$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 114

The right column in figures 5.13 through 5.16 shows distance of finite and infinite diploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.01$. Those graphs indicate oscillating behavior of diploid population given violation. Both finite and infinite populations oscillate given violation. Like in haploid case, oscillations are sharper. Since value of ϵ is small, damping of ripples is slow. A new mask introduced in crossover distribution with $\epsilon = 0.01$ has small probability of being used during crossover. Infinite population oscillation does not die out in 50 generations. As value of ℓ increases, random drifting and wiggling of finite population occurs for small population size, and oscillation gets better with increase in population size. These are noticed more clearly in figures 5.15 and 5.16.

The left column of figures 5.13 through 5.16 shows distance of finite and infinite diploid populations to limit \mathbf{z}^* (limit with violation in crossover distribution χ) when $\epsilon = 0.01$. The distance between finite population and limit \mathbf{z}^* (limit with violation in χ distribution) decreases as finite population size increases. Average distance data for diploid population in case of violation in χ distribution with $\epsilon = 0.01$ for different finite population size N are tabulated in table 5.4.

Table 5.4: Distance measured for violation in χ with $\epsilon = 0.01$ diploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0051 | 0.0036 |
| 10 | 0.0156 | 0.0049 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

The results from Table 5.4 show average distance between finite population and limit \mathbf{z}^* approaches the expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance is smaller in diploid populations than in haploid populations with $\epsilon = 0.01$.

5.1.5 Diploid Population $\sim \epsilon : 0.1$

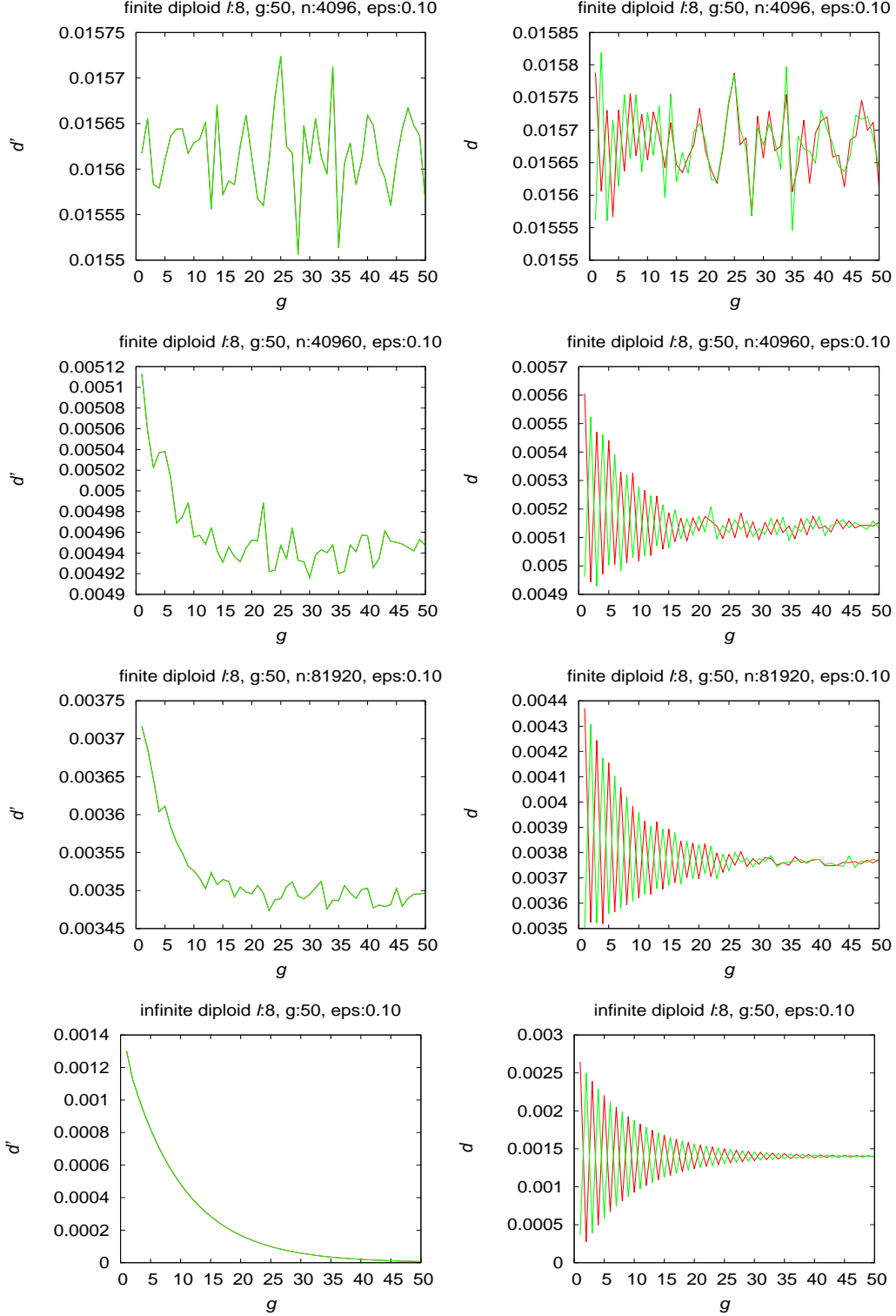


Figure 5.17: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 8$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 117



Figure 5.18: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 10$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 118

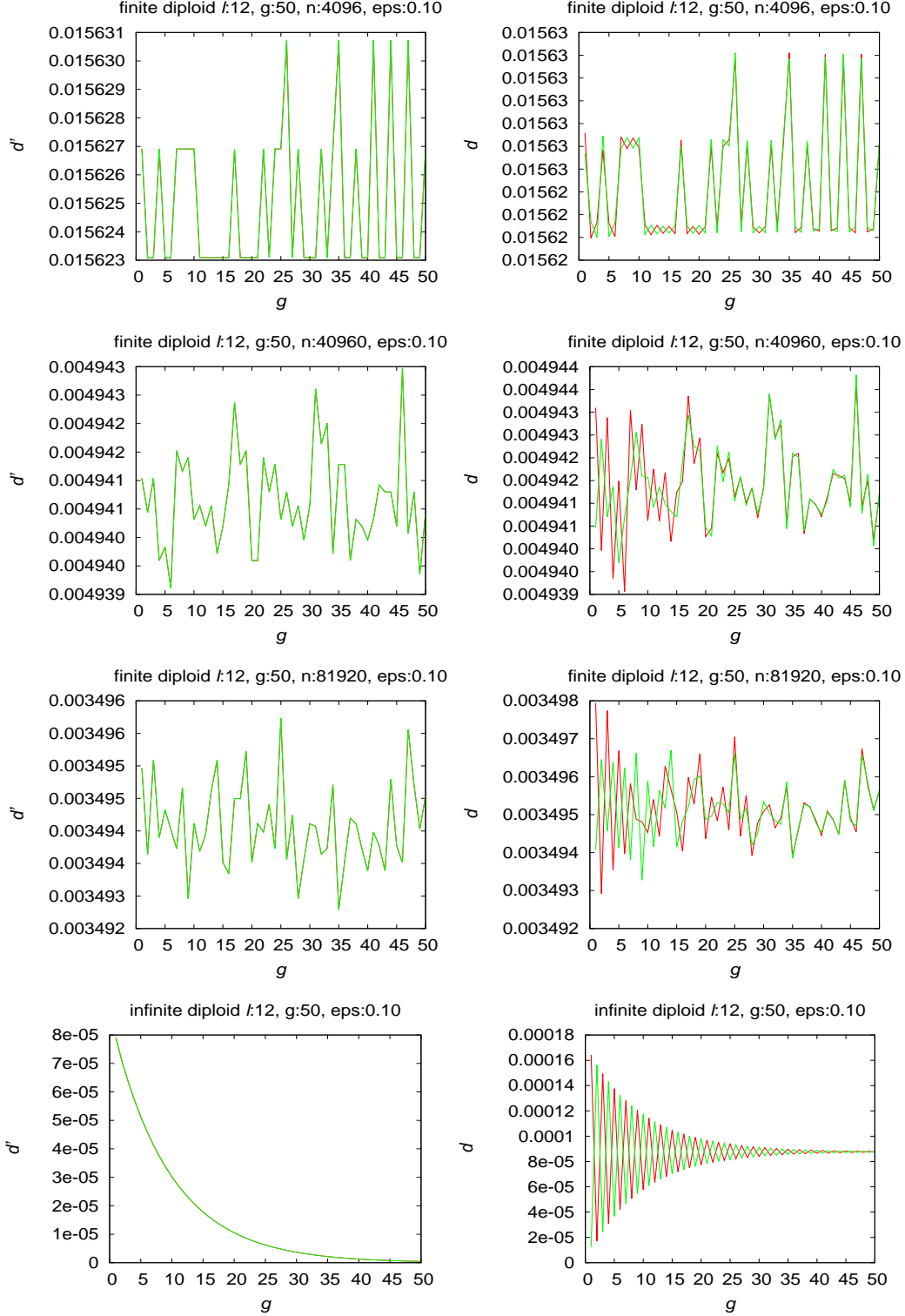


Figure 5.19: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 12$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 119

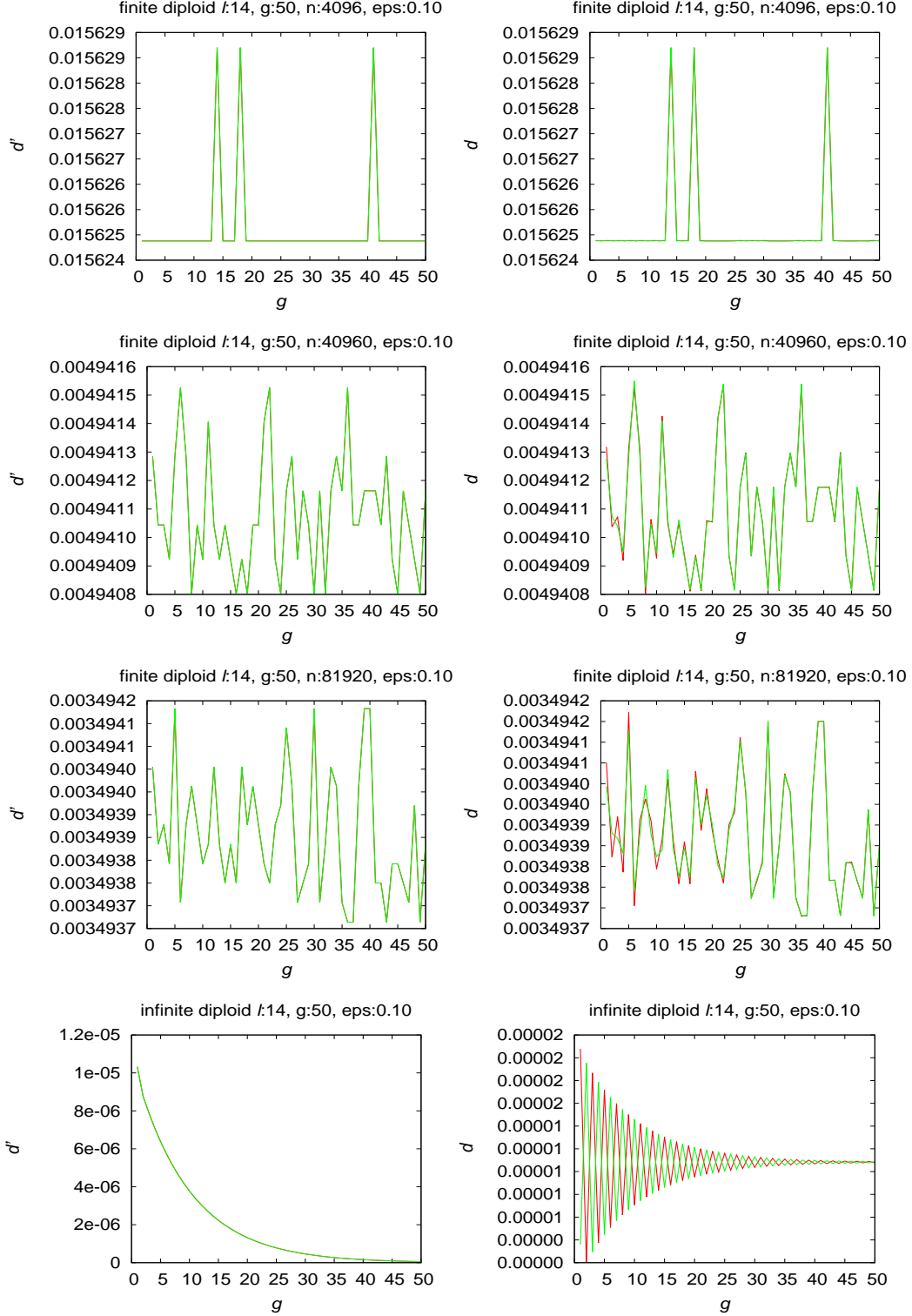


Figure 5.20: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 14$ and $\epsilon = 0.1$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 120

The right column in figures 5.17 through 5.20 shows distance of finite and infinite diploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.1$. Those graphs indicate oscillating behavior of diploid population given violation. Both finite and infinite populations oscillate given violation, and oscillation amplitude decreases with time. Like in haploid case, oscillations in infinite populations die out quickly for $\epsilon = 0.1$ but oscillations in finite populations does not die out completely. Rate of damping of ripples with $\epsilon = 0.1$ is larger than with $\epsilon = 0.01$. A new mask introduced in crossover distribution with $\epsilon = 0.1$ has small probability of being used during crossover for oscillation in finite populations to die out completely. More random wiggling of finite population are noticed than in case of $\epsilon = 0.01$, and as value of ℓ increases, random wiggling increases more for smaller population size.

The left column of figures 5.17 through 5.20 shows distance of finite and infinite diploid populations to limit \mathbf{z}^* (limit with violation in crossover distribution χ) when $\epsilon = 0.1$. The distance between finite population and limit \mathbf{z}^* (limit with violation in χ distribution) decreases as finite population size increases. Average distance data for diploid population in case of violation in χ distribution with $\epsilon = 0.1$ for different finite population size N are tabulated in table 5.5.

Table 5.5: Distance measured for violation in χ with $\epsilon = 0.1$ for diploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0050 | 0.0035 |
| 10 | 0.0156 | 0.0049 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

From table , average distance calculated for finite population size 4096 is 0.0156, for size 40960 is 0.0049 and for size 81920 is 0.0035. The results from Table 5.5 show average distance between finite population and limit \mathbf{z}^* approaches the expected

single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance is smaller in diploid populations than in haploid populations with $\epsilon = 0.1$.

5.1.6 Diploid Population $\sim \epsilon : 0.5$

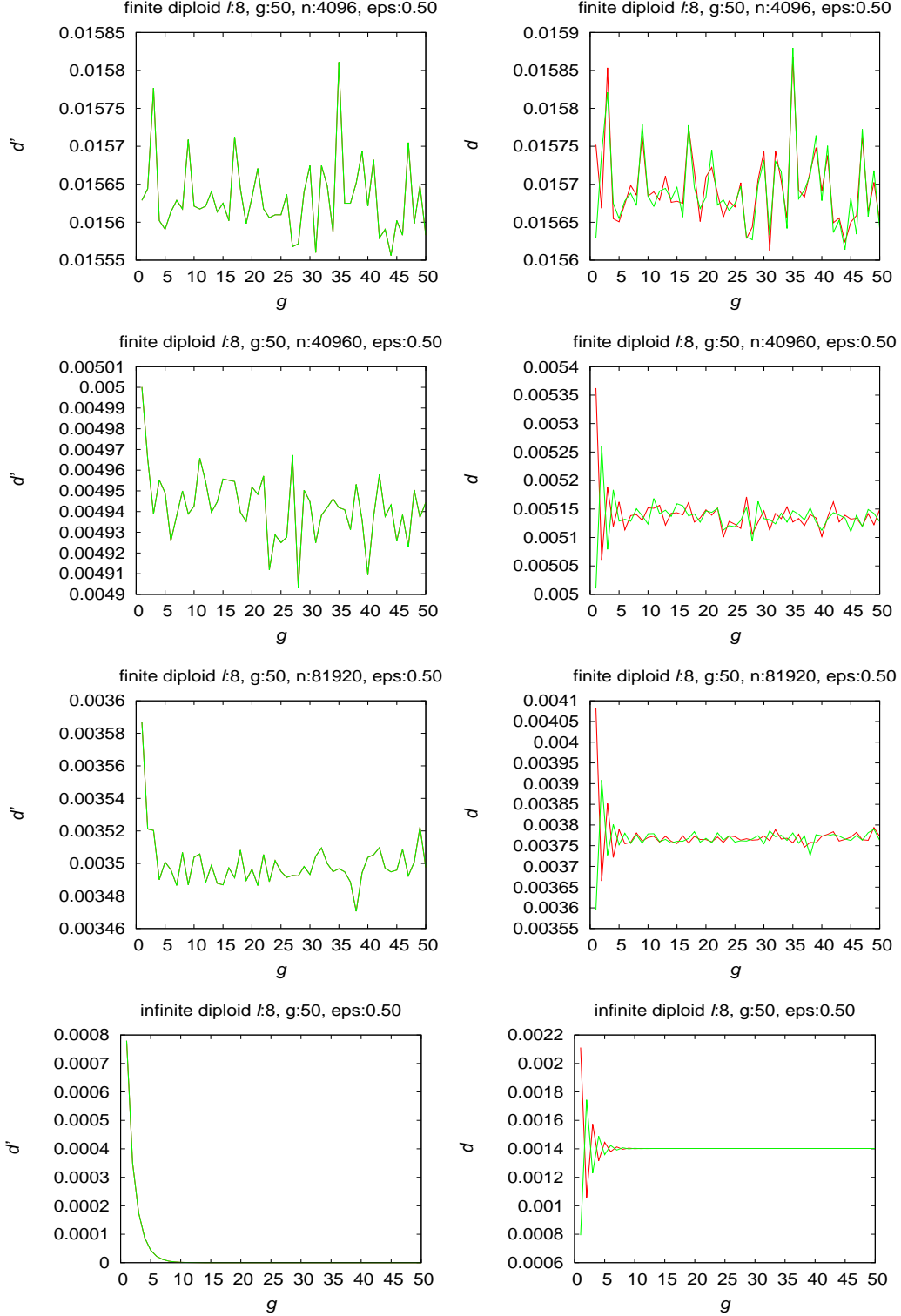


Figure 5.21: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 8$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 123

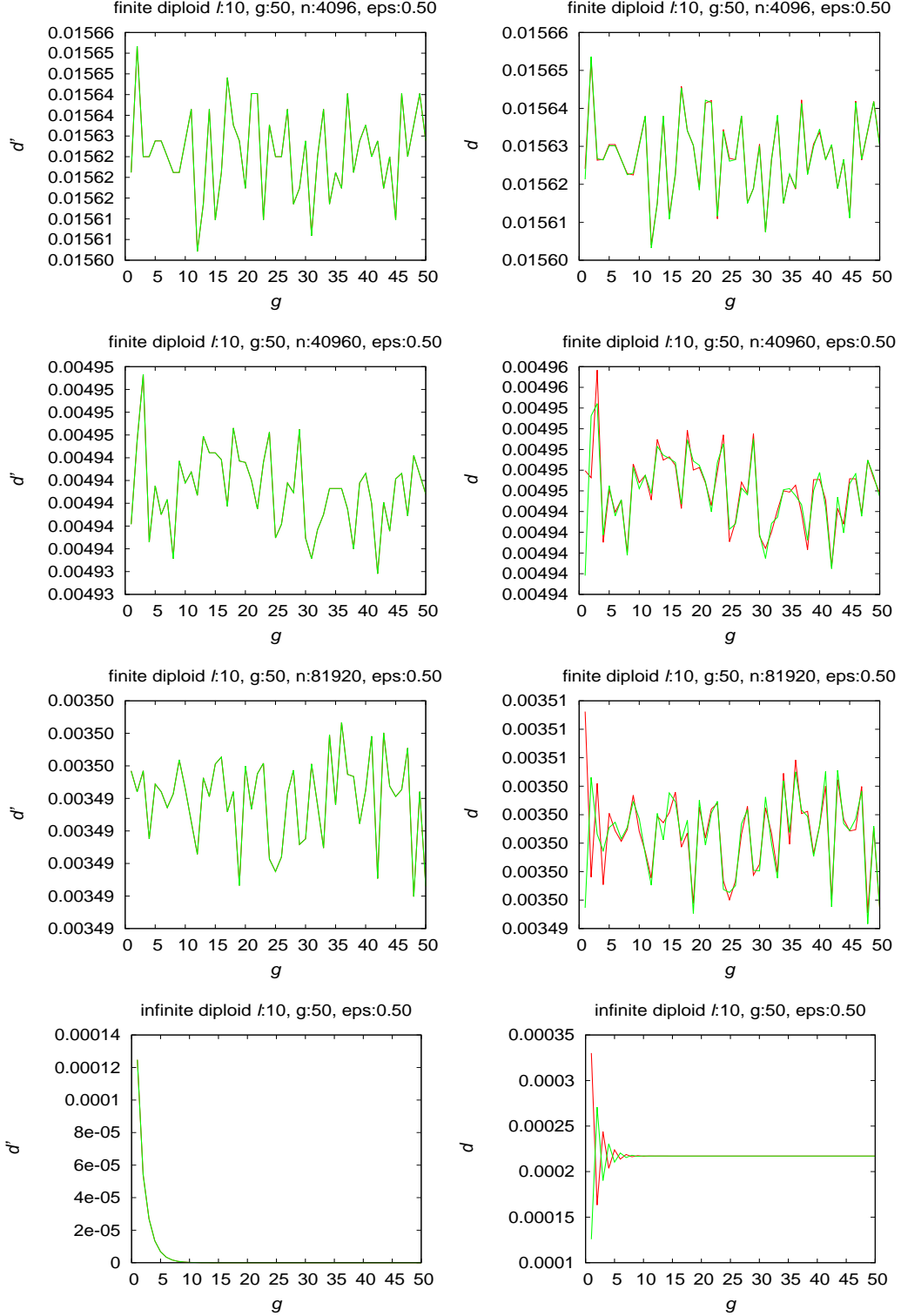


Figure 5.22: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 10$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 124

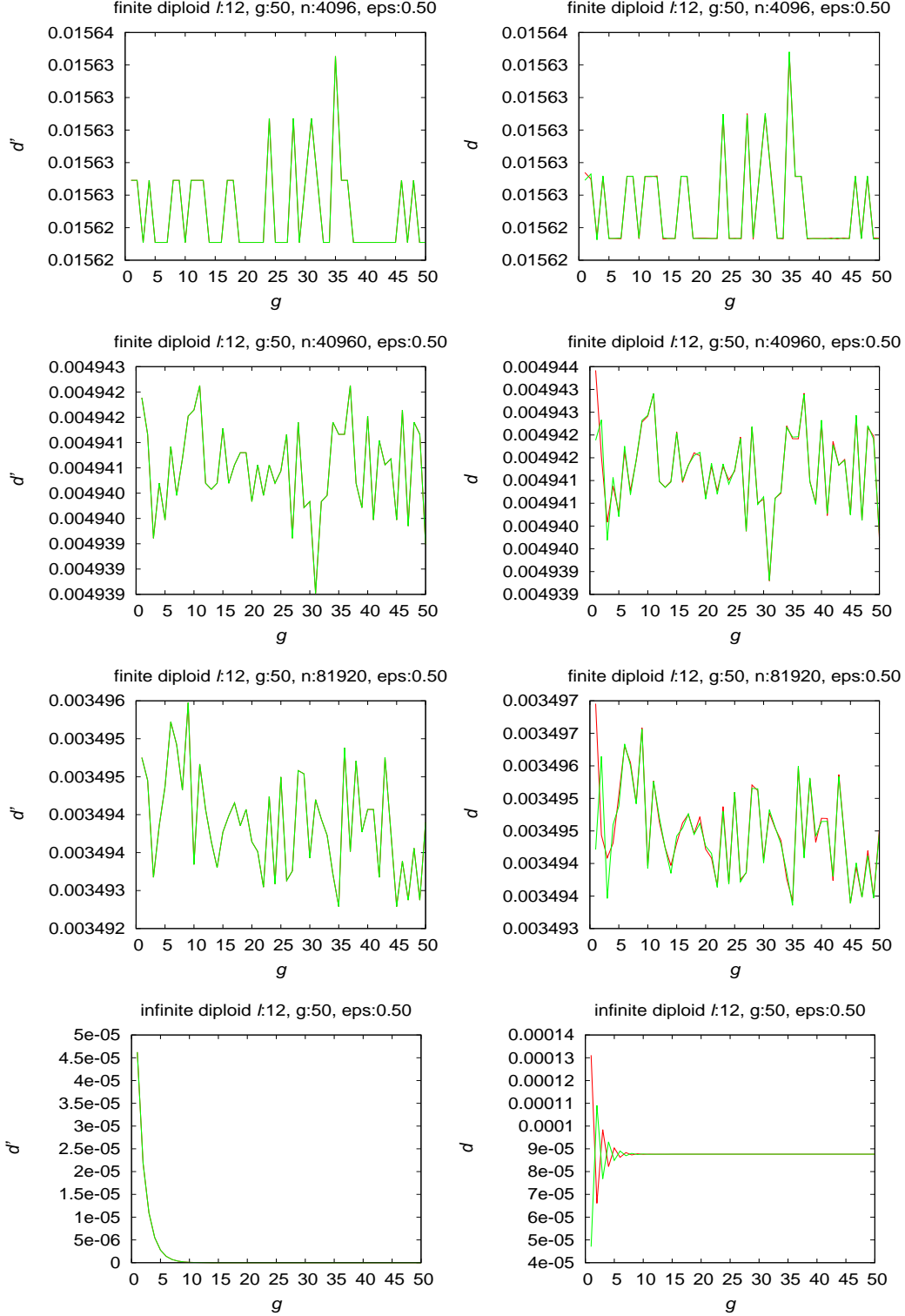


Figure 5.23: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 12$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 125

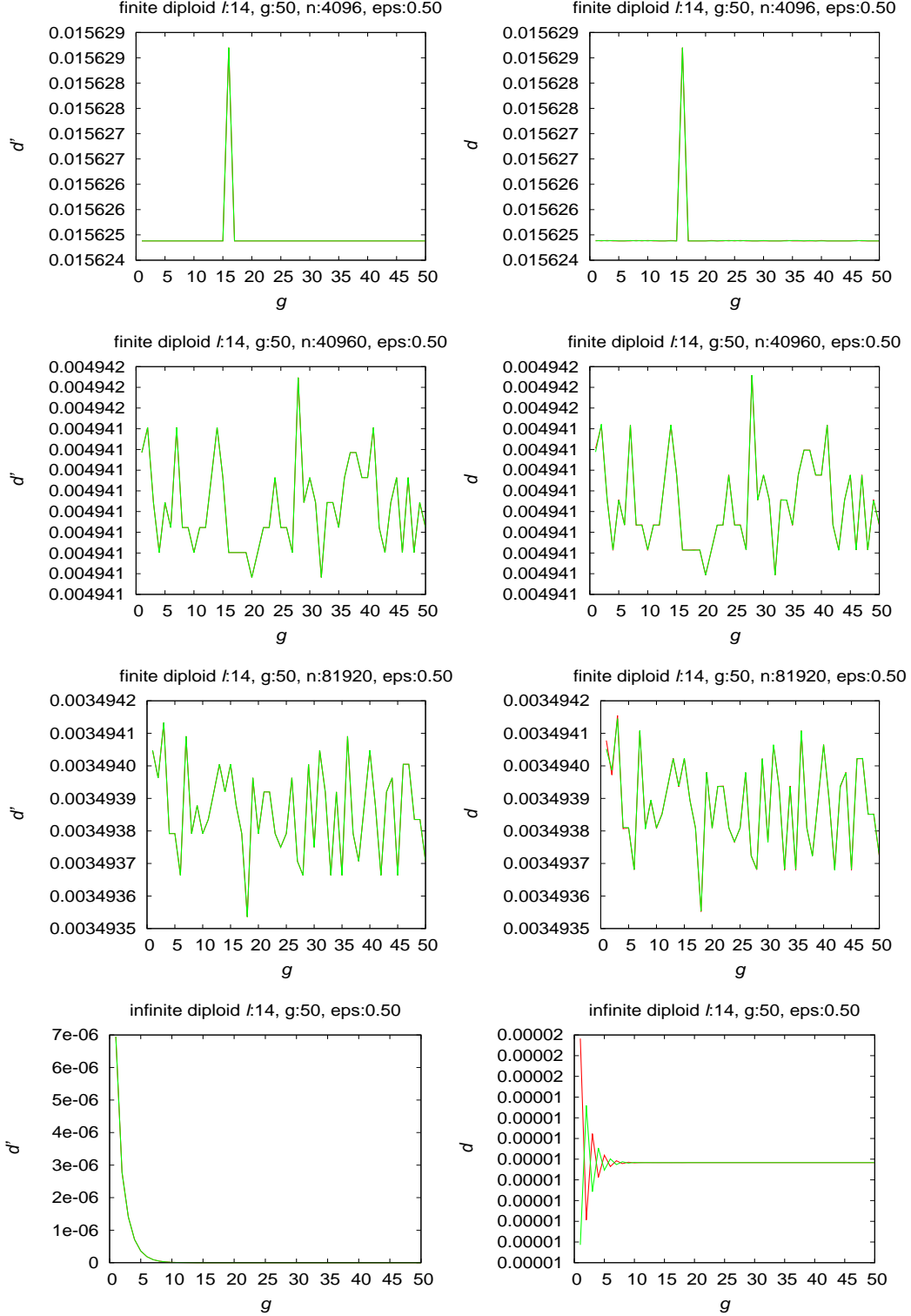


Figure 5.24: Infinite and finite diploid population oscillation behavior in case of violation in χ for genome length $\ell = 14$ and $\epsilon = 0.5$: In left column, d' is distance of finite population of size n or infinite population to limit z^* for g generations. In right column, d is distance of finite population or infinite population to limits p^* and q^* without violation. 126

The right column in figures 5.21 through 5.24 shows distance of finite and infinite diploid populations to non-violation limits \mathbf{p}^* and \mathbf{q}^* with $\epsilon = 0.5$. Those graphs indicate oscillating behavior of diploid population given violation. Infinite populations oscillate for some generations, but the oscillation quickly dies out. Finite populations show some oscillations when $\ell = 8$ for higher population size as in figure 5.21, but for larger ℓ , finite populations show only random wiggles.

The left column of figures 5.21 through 5.24 shows distance of finite and infinite diploid populations to limit \mathbf{z}^* (limit with violation in crossover distribution χ) when $\epsilon = 0.5$. The distance between finite population and limit \mathbf{z}^* (limit with violation in χ distribution) decreases as finite population size increases. Average distance data for diploid population in case of violation in χ distribution with $\epsilon = 0.5$ for different finite population size N are tabulated in table 5.6.

Table 5.6: Distance measured for violation in χ with $\epsilon = 0.5$ for diploids: ℓ is genome length, average distance between finite and infinite population is tabulated in the last three columns, and last row is expected single step distance.

| ℓ | $N = 4096$ | $N = 40960$ | $N = 81920$ |
|--------------|------------|-------------|-------------|
| 8 | 0.0156 | 0.0049 | 0.0035 |
| 10 | 0.0156 | 0.0049 | 0.0035 |
| 12 | 0.0156 | 0.0049 | 0.0035 |
| 14 | 0.0156 | 0.0049 | 0.0035 |
| $1/\sqrt{N}$ | 0.0156 | 0.0049 | 0.0035 |

The results from Table 5.6 show average distance between finite population and limit \mathbf{z}^* approaches expected single step distance between finite and infinite population. The distance decreased as $1/\sqrt{N}$. Also, the distance is smaller in diploid populations than in haploid populations with $\epsilon = 0.5$.

5.2 Discussion

In oscillation of population in presence of violation in μ , as value of ℓ increases, amplitude of oscillation decreases. Populations with larger population size, show better oscillations. Since diploid population consists of string length twice the size of string length of haploid population, diploid population needs larger population size than haploid population to exhibit good oscillations. Like in case of violation in μ , for diploid population, increasing string length ℓ degrades convergence (as finite population size increases) to infinite population behavior. The behavior is noticeable in figures 5.13 through 5.24 for violation in χ . The behavior is less noticeable in haploid population.

With increase in value of ϵ , oscillation in population diminishes, and oscillation completely ceases after certain threshold value for ϵ . Comparing oscillation with violation in μ and χ , rate of dampening of oscillation with violation in χ seems to be slower than with violation in μ , and so we see some oscillation even for $\epsilon = 0.5$ for haploid population in this case. Diploid populations jumping to other levels were observed for string length ℓ of values 12 and 14 for population size of 4096 in figures 5.15, 5.16, 5.19, 5.20, 5.23 and 5.24, but unlike in case of violation in μ , the behavior is not completely absent when population size was larger. Random wiggles are seen in populations with larger population size also for $\ell = 12$ and 14. Jumping to other levels are observed for string length $\ell = 10$ when population size is 4096 in figures 5.14 and 5.14. For $\ell = 10$, random wiggles are noticeable for larger population also when ϵ value is increased to 0.5 (see figure 5.22).

Figure 5.25 summarizes the distance data from tables 5.1 \dots 5.6. Distance of infinite population from finite population of three finite population sizes 4096, 40960, 81920 are plotted for different ℓ . Plots for different violation levels ϵ are arranged in columns. Plots for haploid and diploid populations are arranged in two rows. With increase in ℓ , distance moves closer to the single step distance. So, since diploid population string length is twice of haploid population, distance in diploid case moves

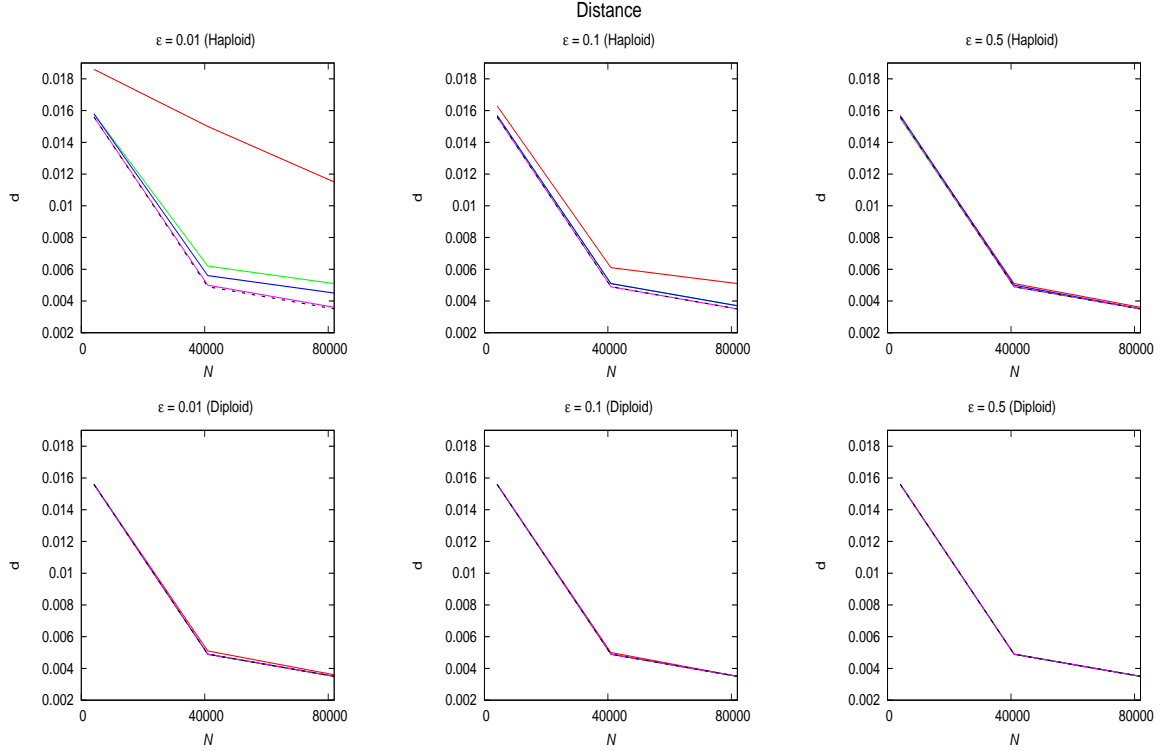


Figure 5.25: Distance of finite population to infinite population in case of violation in χ : d is distance; N is finite population size; ϵ is level of violation; red line represents distance for $\ell = 8$, green line for $\ell = 10$, blue line for $\ell = 12$, pink line for $\ell = 14$ and black dotted line for expected single step distance.

closer to the single step distance than in haploid case. Like in case of μ violation, it is more noticeable in haploid population case that as ϵ increases, the distance moves closer to the single step distance.

5.3 Summary

In this chapter, we violated the condition 3.3 through violation in crossover distribution making infinite population trajectories have no periodic orbit, and studied infinite and finite populations oscillation behavior with the violation through experiments. Like in case of μ violation, infinite population ceases to oscillate when the condition 3.3 for convergence to periodic orbits is violated, but finite population

continued to approximately oscillate for small values of ϵ . For smaller values of ϵ , finite population does not get aware of violation because the probability of using new mask created in the crossover distribution χ due to violation is very low, and if no new mask is used, finite population follows behavior of infinite population without violation in the condition for convergence to periodic orbits. However, rate of dampening of oscillation with violation in χ was observed to be slower than with violation in μ .

Chapter 6

Conclusion

This research shows how Vose's haploid model for Genetic Algorithms extends to the diploid case, improving the computation of infinite population evolutionary trajectories by significantly reducing the time and space used. Efficiency is achieved through decoupling haploid evolution from the evolution of infinite diploid populations and employing Walsh transform methods to compute the effects of mask-based crossover and mutation.

Simulations are thereby made feasible which otherwise would require excessive resources, as illustrated through computations exploring the convergence rate of finite population short-term behavior to infinite population evolutionary trajectories. Results confirm that distance can be inversely proportional to the square root of population size.

Simulations showed that when the necessary condition for oscillation in infinite populations is met, finite populations also exhibit approximate oscillation. Amplitude of oscillation increases with increase in population size, and larger population exhibit better oscillation. Also amplitude of oscillation decreases with increase in genome length.

When the condition for infinite population oscillation is violated for the mutation distribution, we showed that the Markov chain representing finite population evolution is regular, and hence, perfect oscillation should not occur. However, simulation results showed infinite populations ceases to oscillate, but finite populations continue to approximately oscillate if the violation is small.

When the condition is violated for crossover distribution, we could not show that Markov chain formed is regular, but results showed finite populations continue to approximately oscillate when the violation is small, and ceases to oscillate when the violation is larger. As genome length increases oscillation in population degrades. Moreover, larger population shows better oscillation as in the case of oscillation without violation.

In this research, for simplicity we did not consider fitness factor for selection. In future, we plan to extend our work by accommodating fitness factor in our model and investigate the influence of that change upon the results obtained in the absence of selective pressure.

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Appendix

Vita

Mahendra Duwal Shrestha was born in Kathmandu, Nepal, to the parents Krishna Prasad and Laxmi Duwal Shrestha. He is the first of three children: Ambika and Anuka. He attended Panga Secondary School up to tenth grade. Graduating tenth grade in distinction division, he attended NIC Higher Secondary School, where he was also awarded scholarship, taking Physics and Mathematics major. After graduation, he attended Pulchowk Engineering Campus, Institute of Engineering, Tribhuvan University where he was merit listed student for four years. He was introduced to applied mathematics, programming in C and C++, and electronic circuits and communication. He got bachelor's degree of Engineering in Electronics and Communication from Pulchowk Engineering Campus, IOE, Tribhuvan University in March 2011. He worked for two and half years as software engineer at Deerwalk Services Pvt. Ltd, developing health care business applications for clients in US. During the short stint at Deerwalk Services, he learnt and applied knowledge in programming and scripting languages as C#, Java, Groovy and javascript, web frameworks as ASP.NET, ASP.NET MVC, Grails, Ajax and jquery, and databases as MYSQL and MSSQL. He accepted teaching assistantship at The University of Tennessee, Knoxville in Electrical Engineering and Computer Science program. He is continuing his education in Masters of Science in Computer Science working as research assistant at Sergey's lab in Ecology and Evolutionary Biology.