# A Timing Analysis of Convergence to Fitness Sharing Equilibrium

Jeffrey Horn[1] and David E. Goldberg[2*]

[1] Northern Michigan University, Marquette, MI, 49855, USA
**jhorn@nmu.edu** (http://aki.nmu.edu)
[2] Illinois Genetic Algorithms Laboratory, University of Illinois at Urbana-Champaign, IL, 61801, USA
**deg@uiuc.edu** (http://www-illigal.ge.uiuc.edu)

**Abstract.** Fitness sharing has been shown to be an effective niching mechanism in genetic algorithms (GAs). Sharing allows GAs to maintain multiple, cooperating "species" in a single population for many generations under severe selective pressure. While recent studies have shown that the *maintenance* time for *niching equilibrium* is long, it has never been shown that the time it takes to reach equilibrium is sufficiently fast. While experiments indicate that selection under fitness sharing drives the population to equilibrium just as fast and as effectively as selection *alone* drives the simple GA to a uniform population, we can now show analytically that this is the case.

## 1 Introduction and Background

Fitness sharing is only one type of niching mechanism, but it has gained acceptance as a well-tested, successful nicher with a growing body of analysis. Before attempting to contribute to fitness sharing theory, we provide some motivation for niching and a brief description of the algorithm itself. We review earlier analyses of fitness sharing equilibrium and niche maintenance times, then give our analysis of convergence under fitness sharing.

### 1.1 The Need For Niching

In a GA, selection drives the evolving population toward a uniform distribution of $N$ copies of the most highly fit individual. Mutation and non-stationary

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fitness functions might stave off 100% convergence, but it is unarguable that the first-order effect of the first-order operator, selection, is the loss of diversity. In many applications of the GA, uniform convergence is undesirable. In multi-objective GA problems, for example, we might want to find a number of solutions with different tradeoffs among the multiple objectives [11]. Even with single objective (scalar fitness function) GAs, we might want to avoid premature convergence, or discover alternative "runner-up" solutions, by maintaining high quality diversity [7]. And in classifier systems [16, 10, 9], we ask the GA to search through the space of all possible rules to find and maintain a diverse, cooperative subpopulation.

To prevent the best individual in the population from replacing all copies of competing rivals, some kind of *niching* (a.k.a. *speciation*) is necessary. Niching induces *restorative pressure* to balance the *convergence pressure* of selection [9].

### 1.2 Fitness Sharing

Fitness sharing [7] accomplishes niching by degrading the *objective* fitness (i.e., the unshared fitness) of an individual according to the presence of nearby (similar) individuals. Thus this type of niching requires a distance metric on the phenotype or genotype of the individuals. In this study we use the Hamming distance between the binary encodings (genotypes) of individuals. We degrade the objective fitness $f_i$ of an individual $i$ by first summing all of the *share values* $Sh(d)$ of individuals within a fixed radius $\sigma_{sh}$ of that individual, and then dividing $f_i$ by this sum, which is known as the *niche count* $m_i = \sum Sh(d)$ for that individual. More specifically, if two individuals, $i$ and $j$, are separated by Hamming distance $d_{i,j}$, then we add a share value

$$Sh(d_{i,j}) = \begin{cases} 1 - (\frac{d_{i,j}}{\sigma_{sh}})^{\alpha_{sh}} & \text{if } d_{i,j} < \sigma_{sh} \\ 0 & \text{otherwise} \end{cases} \tag{1}$$

to both of their niche counts, $m_i$ and $m_j$. Here, $\sigma_{sh}$ is the fixed radius of our *estimated niches*. Individuals separated by $\sigma_{sh}$, or more, do not degrade each other's fitness. The parameters $\alpha_{sh}$ and $\sigma_{sh}$ are chosen by the user of the niched GA based on some *a priori* knowledge of the fitness landscape or a specific user objective (e.g., minimum separation $\sigma_{sh}$ of alternative solutions). The effect of varying $\alpha_{sh}$ has not been studied to the same extent as has been the effect of changing $\sigma_{sh}$. For this reason, $\alpha_{sh}$ is often set to one, yielding the *triangular sharing function*. The contribution to the niche count, $Sh(d)$, always decreases monotonically from one to zero as the distance $d$ between the pair of individuals goes from zero to $\sigma_{sh}$.

For an individual $i$, the niche count $m_i$ is calculated as $m_i = \sum_{j=1}^{N} Sh(d_{i,j})$, where $N$ is the size of the population. The *shared fitness* of individual $i$ is then given by $f_{sh,i} = \frac{f_i}{m_i}$ . In the case of no niche overlap (a.k.a., *perfect sharing* [8]) the niche count for individual $i$ reduces to the number of copies of $i$ ($m_i = n_i$), and $i$'s shared fitness becomes independent of other niches: $f_{sh,i} = \frac{f_i}{n_i}$.

Fitness sharing tends to spread the population out over multiple peaks (niches) in proportion to the height of the peaks. GAs with proportionate selection and fitness sharing have been successfully used to solve a variety of multimodal functions [3].

### 1.3 Stable Niching Equilibrium

Deb and Goldberg [3] calculate equilibrium for the more general fitness sharing case (i.e., niche overlap) by setting shared fitnesses equal to each other:

$$\frac{f_A}{m_A} = \frac{f_B}{m_B}. \tag{2}$$

Recall the calculation of niche counts $m_i$ in Equation 1. (We simplify our calculations by assuming $\alpha_{sh} = 1$.) For our two niches **A** and **B**, we normalize the inter-niche distance, $d(A,B) = 1$, without loss of generality. Since $n_A + n_B = N$ (population size), the niche count of **A** becomes $m_A = n_A * Sh(A,A) + n_B * Sh(A,B)$. Now since $d(A,A) = 0$, then $Sh(A,A) = 1$, while $Sh(A,B) = 1 - \frac{1}{\sigma_{sh}}$. Thus the niche count becomes $m_A = n_A + (N - n_A)(1 - \frac{1}{\sigma_{sh}})$. Similarly for **B**, $m_B = (N - n_A) + n_A(1 - \frac{1}{\sigma_{sh}})$. Substituting $m_A$ and $m_B$ into Equation 2 above, yields

$$\frac{f_A}{n_A + (N - n_A)(1 - \frac{1}{\sigma_{sh}})} = \frac{f_B}{(N - n_A) + n_A(1 - \frac{1}{\sigma_{sh}})}. \tag{3}$$

Solving for $n_A$ and calling it $n_{A,eq}$ for "$n_A$ at equilibrium", and also defining the ratio of fitness $r_f \equiv \frac{f_A}{f_B}$, results in

$$n_{A,eq} = \frac{r_f \sigma_{sh} - \sigma_{sh} + 1}{1 + r_f} N. \tag{4}$$

We recast our equations in terms of proportions of **A** at time $t$, by defining $P_{A,t} \equiv \frac{n_{A,t}}{N}$. At equilibrium, the expected proportion of **A**s is $P_{A,eq} \equiv \frac{n_{A,eq}}{N}$. Thus we rewrite Equation 4 as

$$P_{A,eq} = \frac{r_f \sigma_{sh} - \sigma_{sh} + 1}{1 + r_f}. \tag{5}$$

### 1.4 Exponential Niche Maintenance Times

Fitness sharing tends to *maintain* multiple high-quality niches for long periods of time. Expected times to loss of one or more niches have been shown to grow exponentially with increasing population size $N$ [8, 12]. Mahfoud [12], and Horn, Goldberg, and Deb [10] developed a closed-form expression for the case of non-overlapping niches (perfect sharing):

$$E[t_{abs}] = \frac{(r_f + 1)^N}{r_f^N + 1}. \tag{6}$$

The expected absorption time above grows exponentially in $N$ for any $r_f > 0$.

## 2 Fast Convergence to Niching Equilibrium

Now that we have an upper bound on the (very long) expected lifetimes of niches, we turn to the question of how such steady-states are reached, and in particular, how quickly they are reached. Under normal selection (e.g., in a simple GA) it has been shown that convergence to the "equilibrium point" of a uniform population takes place very quickly [6]. In the case of selective preference (i.e., $r_f \neq 1$) the convergence time grows logarithmically in population size $N$, while under genetic drift (i.e., $r_f = 1$), the expected convergence time grows linearly in $N$. Can we expect similarly quick convergence to "niching equilibrium"?

### 2.1 Background: Expected Proportions Analysis

To answer such questions, we use the simple, well-known method of *expected proportion equations* to model niche convergence. This method of tracking the expected next generation *population* only (rather than tracking the entire *distribution* over all possible populations) has been put to good use many times in the GA literature (e.g., [14, 6, 13]). The methodology has acquired several names: the *infinite population model* [15], the *virtual average population* [13], or the *local expected path*[3] [4].

### 2.2 Example: Simple GA Convergence

To illustrate the expected proportions analysis, and to provide a basis for comparison with our niching results later, we review some of the work done on convergence time in simple GAs (i.e., no niching). The technique has been applied to a simple GA under proportionate selection by several authors in the literature, including Goldberg [5], Ankenbrandt [1], and Goldberg and Deb [6]. Here we follow our own derivation, to arrive at the same kind of result: a closed-form expression for the expected proportion at generation $t$, with a logarithmic growth in convergence time with increasing population size $N$.

Under proportionate selection, the expected proportion of the next generation's population given to an individual is *equal* to the probability of selecting that individual for reproduction in the current generation's population. Thus if $P_{A,t}$ is the proportion of the current population, at time $t$, consisting of copies of rule **A**, then $E[P_{A,t+1}] = p_A$, where $p_A$ is calculated at time (generation) $t$. That is, $p_A$ is the probability of selecting a single individual copy of rule **A** for reproduction from a particular population with $n_A = NP_{A,t}$ copies of rule **A** and $n_B = N(1 - P_{A,t})$ copies of rule **B**. So in general

$$E[P_{A,t+1}] = p_A = \frac{n_A f_A}{n_A f_A + (N - n_A) f_B}. \tag{7}$$

[3] See [4], Appendix 1, or [15], for in-depth consideration of the accuracy of these models for finite populations.

Dividing numerator and denominator by population size $N$, and by $f_B$, and then substituting $r_f \equiv \frac{f_A}{f_B}$, yields

$$E[P_{A,t+1}] = \frac{P_{A,t}\, r_f}{P_{A,t}(r_f - 1) + 1}. \tag{8}$$

Now we make the major assumption that is key to this type of analysis: we assume that $E[P_{A,t+1}] \approx P_{A,t+1}$. That is, we allow ourselves to plug the expected proportion for the next generation back into our Equation 8 to get the expected proportion for the $t+2$ generation, and so on[4]. Substituting $E[P_{A,t+1}]$ for $P_{A,t+1}$, we derive a simple linear recurrence relation on $P_{A,t}$:

$$P_{A,t+1} = \frac{P_{A,t}\, r_f}{P_{A,t}(r_f - 1) + 1}. \tag{9}$$

**The Convergence Equation.** Solving the recurrence relation in Equation 9 results in

$$P_{A,t} = \frac{P_{A,0} r_f^t}{P_{A,0} r_f^t - P_{A,0} + 1}, \tag{10}$$

which is equivalent to Equation 7 of [6] with only $k = 2$ types of individuals (i.e., niches). In Figure 1 we plot an example expected convergence using Equation 10 with a fitness ratio of $r_f = 2$ so that the population quickly converges to all **A**s. The initial proportion is $P_{A,0} = \frac{1}{100}$ (e.g., for a population size $N = 100$ and only a single copy of **A** in the initial population).

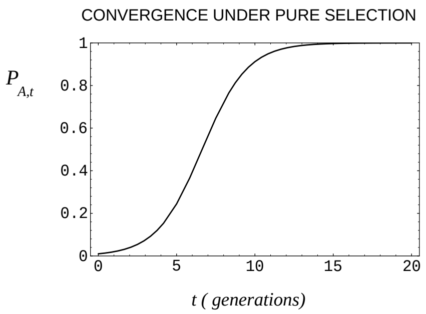


**Fig. 1.** Expected proportion of **A**s in a simple GA under proportionate selection.

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[4] Of course, $E[P_{A,t+1}] \approx P_{A,t+1}$ is a strict equality only for deterministic selection operators or for infinite populations [15]. But we use it to model our finite population, stochastic selection GA here.

**Convergence Times.** We can solve Equation 10 for time (generations) $t$:

$$t = \frac{1}{\ln r_f}(\ln \frac{P_{A,t}}{P_{A,0}} + \ln \frac{1 - P_{A,0}}{1 - P_{A,t}}). \tag{11}$$

We can see from this equation that increasing fitness difference speeds up convergence time, in agreement with our intuition.

Equation 11 is written in terms of proportions, and so is general to all population sizes, including infinite $N$. To add in the effects of finite populations, let's assume population size $N$ and look for the time to go from a single copy of **A**, which is the worst case (i.e., longest time), to *almost* (one less than) full convergence[5]. In other words, we set $P_{A,0} = \frac{1}{N}$ and $P_{A,t_{conv}} = \frac{N-1}{N} = 1 - \frac{1}{N}$. Plugging these into Equation 11, and simplifying, we find that

$$t_{conv} = \frac{2}{\ln r_f} \ln(N-1). \tag{12}$$

Clearly then convergence time in the simple GA grows logarithmically in population size. But convergence time here in the "selective case" of the simple GA is the time for a single species to take over the entire population. Will convergence time for niching, to arrive at some non-uniform population equilibrium, be different?

### 2.3 Perfect Sharing Convergence (no overlap)

We already know that the case of perfect sharing is special under proportionate selection [9]. Sharing (with no overlap) allocates objective fitness to individuals in proportion to the numbers of individuals, while proportionate selection allocates numbers of individuals in proportion to their objective fitnesses. The result is an "instantaneous" (one generation) transition to the niching equilibrium, in expectation. Using Equation 7 above, but substituting the shared fitnesses $f_{A,sh} = \frac{f_A}{n_A}$ and $f_{B,sh} = \frac{f_B}{N-n_A}$ for the objective fitnesses $f_A$ and $f_B$, results in

$$E[P_{A,t+1}] = p_A = \frac{n_A \frac{f_A}{n_A}}{n_A \frac{f_A}{n_A} + (N - n_A)\frac{f_B}{N-n_A}} = \frac{f_A}{f_A + f_B} = \frac{r_f}{r_f + 1} = P_{A,eq}.$$

Thus we expect to get to equilibrium in one time step, no matter in what state $P_{A,0}$ we begin. So $t_{conv} = 1$ for perfect sharing ($\sigma_{sh} = 1$).

### 2.4 Fitness Sharing Convergence (with niche overlap)

Next we examine convergence time for fitness sharing with two overlapping niches ($1 < \sigma_{sh}$).

[5] Note that even our finite model will approach $N$ only asymptotically. So we consider convergence to be $N - 1$ to allow us to compute a finite convergence time $t$.

**The Convergence Equation.** We start with the probability of selecting an **A** under fitness sharing,

$$p_A = \frac{n_A f_{A,sh}}{n_A f_{A,sh} + n_B f_{B,sh}}. \tag{13}$$

We recall that **A**'s shared fitness $f_{A,sh}$ is its objective fitness $f_A$ divided by its niche count. Since we only have two types of individuals, **A** and **B**, we only have two possible contributions to the niche count: 1 for each **A** and $(1 - \frac{1}{\sigma_{sh}})$ for each **B**:

$$f_{A,sh} = \frac{f_A}{n_A + n_B(1 - \frac{1}{\sigma_{sh}})}.$$

Let's define $\mathcal{S} \equiv (1 - \frac{1}{\sigma_{sh}})$ (that is, the sharing function $Sh$). Now we can rewrite the probability of selecting an **A** under fitness sharing:

$$p_A = \frac{n_A \frac{f_A}{n_A + n_B \mathcal{S}}}{n_A \frac{f_A}{n_A + (N - n_A)\mathcal{S}} + n_B \frac{f_B}{n_B + n_A \mathcal{S}}}. \tag{14}$$

Dividing numerator and denominator by $N$ to get proportions and by $f_B$ to get the fitness ratio $r_f$, then substituting $p_A$ into Equation 7,

$$E[P_{A,t+1}] = p_A = \frac{\frac{P_{A,t} r_f}{P_{A,t} + (1 - P_{A,t})\mathcal{S}}}{\frac{P_{A,t} r_f}{P_{A,t} + (1 - P_{A,t})\mathcal{S}} + \frac{1 - P_{A,t}}{1 - P_{A,t} + P_{A,t}\mathcal{S}}}. \tag{15}$$

This is a rather messy equation that can't be simplified much nor can it be solved (as a recurrence relation) directly for $P_{A,t}$. However, we can solve for something just as useful, the ratio of **A**s to **B**s: $\frac{n_A}{n_B}$. Note that the ratio of numbers is the same as the ratio of proportions: $\frac{P_{A,t}}{P_{B,t}} = \frac{n_A}{n_B}$. We'll name the proportion ratio $P_{r,t} \equiv \frac{P_{A,t}}{P_{B,t}}$ for short. Now since $P_{r,t+1} = \frac{P_{A,t+1}}{P_{B,t+1}} = \frac{P_{A,t+1}}{1 - P_{A,t+1}}$, we can just divide both sides of Equation 15 above by $(1 - P_{A,t+1})$. On the left hand side this gives us:

$$\frac{E[P_{A,t+1}]}{1 - P_{A,t+1}} \Rightarrow \frac{P_{A,t+1}}{1 - P_{A,t+1}} \Rightarrow P_{r,t+1} \Rightarrow E[P_{r,t+1}].$$

Dividing the right hand side of Equation 15 by $(1 - P_{A,t+1})$, and simplifying, we now have

$$E[P_{r,t+1}] = \frac{P_{A,t}\, r_f}{P_{A,t} + (1 - P_{A,t})\mathcal{S}} \frac{1 - P_{A,t} + P_{A,t}\mathcal{S}}{1 - P_{A,t}}. \tag{16}$$

Making our key assumption that $E[P_{r,t+1}] \approx P_{r,t+1}$ for the right hand side, and substituting our defined ratio of proportions $P_{r,t} \equiv \frac{P_{A,t}}{1 - P_{A,t}}$ on the left hand side, we derive

$$P_{r,t+1} = r_f \frac{1 + P_{r,t}\,\mathcal{S}}{1 + \frac{\mathcal{S}}{P_{r,t}}}. \tag{17}$$

Equation 17 appears simple in form, but unfortunately it is difficult to solve exactly. To obtain a closed-form, we use the continuous approximation method.

That is, we set up a differential equation approximating the difference equation 17 and then integrate the differential equation. Subtracting $P_{r,t}$ from both sides of Equation 17 above, we obtain

$$P_{r,t+1} - P_{r,t} = r_f \frac{1 + P_{r,t}\,\mathcal{S}}{1 + \frac{\mathcal{S}}{P_{r,t}}} - P_{r,t},$$

which we can then approximate by the differential equation

$$\frac{dP_{r,t}}{dt} = r_f \frac{1 + P_{r,t}\mathcal{S}}{1 + \frac{\mathcal{S}}{P_{r,t}}} - P_{r,t},$$

which upon integration yields

$$t + \frac{\mathcal{S} \ln P_{r,t}}{\mathcal{S} - r_f} + \frac{(\mathcal{S}^2 r_f - r_f) \ln(\mathcal{S} - r_f + P_{r,t} - \mathcal{S} r_f P_{r,t})}{\mathcal{S} - r_f - \mathcal{S}^2 r_f + \mathcal{S} r_f^2} = C. \tag{18}$$

We can solve for the constant $C$ if we substitute the initial proportion ratio $P_{r,0}$ for the first generation ($t = 0$):

$$C = 0 + \frac{\mathcal{S} \ln P_{r,t}}{\mathcal{S} - r_f} + \frac{(\mathcal{S}^2 r_f - r_f) \ln(\mathcal{S} - r_f + P_{r,t} - \mathcal{S} r_f P_{r,t})}{\mathcal{S} - r_f - \mathcal{S}^2 r_f + \mathcal{S} r_f^2}.$$

Plugging this $C$ back into Equation 18, we can solve for $t$ as a function of proportion ratio "desired", $P_{r,t}$, (as well as of the initial proportion ratio $P_{r,0}$):

$$t[P_{r,t}] = \frac{\ln(\frac{P_{r,0}}{P_{r,t}})}{1 - \frac{r_f}{\mathcal{S}}} + \frac{(\mathcal{S} - \frac{1}{\mathcal{S}}) \ln(\frac{\mathcal{S} - r_f + P_{r,0} - \mathcal{S} r_f P_{r,0}}{\mathcal{S} - r_f + P_{r,t} - \mathcal{S} r_f P_{r,t}})}{1 + r_f - \mathcal{S} - \frac{1}{\mathcal{S}}}. \tag{19}$$

So now we have in Equation 19 a closed-form equation relating time (generations) to proportion ratio ($P_{r,t} = \frac{P_A}{P_B}$). Unfortunately, we cannot solve this equation generally for $P_{r,t}$ in terms of $t$, but we can always solve it numerically for any particular values of $t$, $r_f$, and $P_{r,0}$. For now we compare our continuous approximation, Equation 19, to our more accurate discrete model, Equation 17, in Figure 2. We assume equal fitness $r_f = 1$, and an overlap ($\sigma_{sh} = 2$ so that $\mathcal{S} = 1 - \frac{d}{\sigma_{sh}} = 0.5$). Note how the population asymptotically approaches the niching equilibrium proportion ratio ($\frac{n_A}{n_B} = P_{r,eq} = 1$). Note also how the curve of this plot is similar in form to the curve for simple GA convergence (Figure 1).

**Convergence Times.** Equation 19 is already solved for time $t$ (in generations), but since it is uses only proportions (as in Equation 11 for simple GA convergence times), it implicitly models infinite population sizes. We now introduce into Equation 19 the discrete nature of a finite population size $N$ by re-defining the two proportion ratios $P_{r,0}$ (the initial proportions) and $P_{r,t}$ (the proportions at time $t$). We model the bounding case of growing from a single copy of species **A** to within one copy of the niching equilibrium.

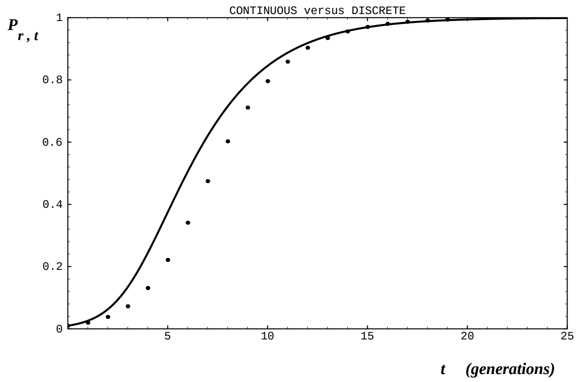


**Fig. 2.** Expected convergence under fitness sharing. The predictions of the discrete model are the solid dots, while the continuous model predicts the solid line.

With $n_{A,0} = 1$, the initial proportion of **A**s is $P_{A,0} = \frac{1}{N}$, and $P_{B,t} = \frac{N-1}{N}$. It follows that the initial proportion *ratio* $P_{r,0} = \frac{P_{A,0}}{P_{B,0}} = \frac{1}{N} / \frac{N-1}{N} = \frac{1}{N-1}$. For equilibrium, we rewrite Equation 5, substituting our sharing function $\mathcal{S} = 1 - \frac{1}{\sigma_{sh}}$ for $\sigma_{sh}$ (by using $\sigma_{sh} = \frac{1}{1-\mathcal{S}}$):

$$P_{A,eq} = \frac{\frac{r_f - 1}{1-\mathcal{S}} + 1}{r_f + 1}.$$

When we are just one (copy of **A**) less than the equilibrium:

$$P'_{r,eq} = \frac{P_{A,eq} - \frac{1}{N}}{P_{B,eq} + \frac{1}{N}} = \frac{P_{A,eq} - \frac{1}{N}}{1 - P_{A,eq} + \frac{1}{N}},$$

where $P'_{r,eq}$ is our symbol for *near* (within one of) equilibrium. Now we can substitute in $P_{A,eq}$ from Equation 5 and simplify:

$$P'_{r,eq} = \frac{N\frac{r_f - 1}{1-\mathcal{S}} + N - r_f - 1}{(N+1)(r_f+1) + N\frac{1-r_f}{1-\mathcal{S}} - N}. \tag{20}$$

We want to know the expected time to go from $P_{r,0} = \frac{1}{N-1}$ to $P_{r,t} = P'_{r,eq}$. Plugging these two proportion ratios into Equation 19 above, and solving, yields:

$$\begin{aligned} t_{conv} = {} & \frac{(\mathcal{S}^2-1)}{r_f\mathcal{S}-\mathcal{S}^2+\mathcal{S}-1} \ln\left(\frac{(\frac{1}{N-1} - r_f + \mathcal{S} + \frac{r_f\mathcal{S}}{1-N})(Nr_f\mathcal{S}+r_f\mathcal{S}+\mathcal{S}-r_f-N-1)}{(r_f+1)^2(\mathcal{S}-1)^2}\right) \\ & + \frac{\mathcal{S}}{\mathcal{S}-r_f} \ln\left(\frac{N-Nr_f\mathcal{S}-r_f\mathcal{S}-\mathcal{S}+r_f+1}{(N-1)(r_f\mathcal{S}-N\mathcal{S}+\mathcal{S}+Nr_f-r_f-1)}\right). \end{aligned} \tag{21}$$

Although not a very simple formula, this expression for expected niche convergence time is clearly logarithmic in population size $N$, as predicted. Figure 3 illustrates a typical expected growth in convergence time with increasing $N$ from 1 to 1000. Here we plot Equation 21 with $r_f = 1$ and $\mathcal{S} = \frac{1}{2} \Rightarrow \sigma_{sh} = \frac{1}{2}$. The growth in time does appear to be logarithmic.

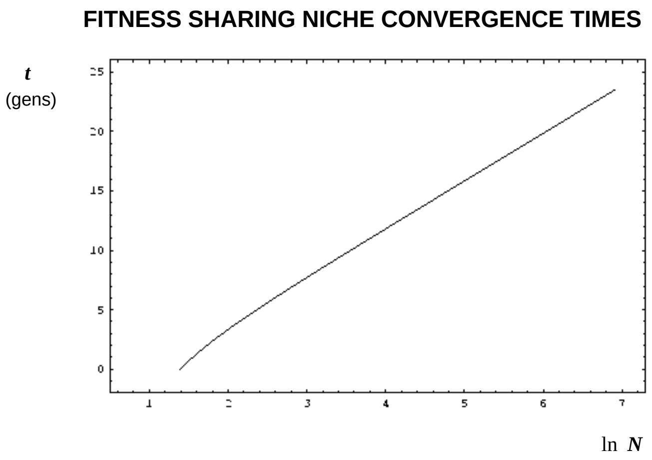


**Fig. 3.** Expected convergence times under fitness sharing grow logarithmically in $N$.

## 3 Summary

In this paper we have shown that convergence to niching equilibrium is fast, as we suspected. It is immediate for perfect sharing, and grows slowly, logarithmically, in population size $N$ for overlapped niches. This fast convergence time means that not only is niching equilibrium reached quickly initially, but that perturbations from equilibrium are quickly compensated for. This fact supports our intuition that the GA will maintain the population at or very near equilibrium most of the time. Contrasting the fast (logarithmic) convergence times with the long (exponential) niche loss times, we can see that niching equilibrium dominates the evolutionary time scale.

We note, however, that increasing fitness difference $r_f$ and increasing overlap $\sigma_{sh}$ slow niche convergence time while also speeding up niche loss. We conjecture that when these two characteristic niching times are similar, perhaps differing only by an order of magnitude, niching fails. Applying this conjecture, and solving for the combinations of fitness difference and overlap that give us these niche failure conditions, we hope to plot the "boundary" between niching failure (i.e., competition) and success (i.e., cooperation), in future work.

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