Escaping Local Optima using Crossover with Emergent or Reinforced Diversity

Duc-Cuong Dang\textsuperscript{1}, Tobias Friedrich\textsuperscript{2}, Timo Kötzing\textsuperscript{2}, Martin S. Krejca\textsuperscript{2}, Per Kristian Lehre\textsuperscript{1}, Pietro S. Oliveto\textsuperscript{3}, Dirk Sudholt\textsuperscript{3}, and Andrew M. Sutton\textsuperscript{2}

\textsuperscript{1}University of Nottingham, United Kingdom
\textsuperscript{2}Hasso Plattner Institute, Potsdam, Germany
\textsuperscript{3}University of Sheffield, United Kingdom

11th August 2016

Abstract

Population diversity is essential for avoiding premature convergence in Genetic Algorithms (GAs) and for the effective use of crossover. Yet the dynamics of how diversity emerges in populations are not well understood. We use rigorous run time analysis to gain insight into population dynamics and GA performance for the ($\mu+1$) GA and the Jump\textsubscript{k} test function. We show that the interplay of crossover followed by mutation may serve as a catalyst leading to a sudden burst of diversity. This leads to improvements of the expected optimisation time of order $\Omega(\frac{n}{\log n})$ compared to mutation-only algorithms like the (1+1) EA. Moreover, increasing the mutation rate by an arbitrarily small constant factor can facilitate the generation of diversity, leading to speedups of order $\Omega(n)$. We also compare seven commonly used diversity mechanisms and evaluate their impact on run time bounds for the ($\mu+1$) GA. All previous results in this context only hold for unrealistically low crossover probability $p_c = O(k/n)$, while we give analyses for the setting of constant $p_c < 1$ in all but one case. For the typical case of constant $k > 2$ and constant $p_c$, we can compare the resulting expected optimisation times for different diversity mechanisms assuming an optimal choice of $\mu$:

\begin{itemize}
  \item $O(n^{k-1})$ for duplicate elimination/minimisation,
  \item $O(n^2 \log n)$ for maximising the convex hull,
  \item $O(n \log n)$ for deterministic crowding (assuming $p_c = k/n$),
  \item $O(n \log n)$ for maximising the Hamming distance,
  \item $O(n \log n)$ for fitness sharing,
  \item $O(n \log n)$ for the single-receiver island model.
\end{itemize}

This proves a sizeable advantage of all variants of the ($\mu+1$) GA compared to the (1+1) EA, which requires time $\Theta(n^k)$. Experiments complement our theoretical findings and further highlight the benefits of crossover and diversity on Jump\textsubscript{k}. 

1 Introduction

Genetic Algorithms (GAs) are powerful general-purpose optimisers that perform surprisingly well in many applications, including those where the problem is not well understood to apply a tailored algorithm. Their wide-spread success is based on a number of factors: using populations to diversify search, using mutation to generate novel solutions, and using crossover to combine features of good solutions.

Pru¨ gel-Bennett [30] gives several reasons for the success of populations and crossover. Crossover can combine building blocks of good solutions and help to focus search on bits where parents disagree [30]. For both tasks, the population needs to be diverse enough; without sufficient diversity in the population, crossover is not effective. A common problem in the application of GAs is the loss of diversity when the population converges to copies of the same search point, often called premature convergence. Understanding how populations gain and lose diversity during the course of the optimisation is vital for understanding the working principles of GAs and for tuning the design of GAs to get the best possible performance.

Rigorous run time analysis has emerged as a powerful theory that has provided many insights into the performance of GAs [1, 4, 17, 24, 27, 28], including the benefit of crossover [9, 18, 20, 21, 25, 31]. It has guided algorithm design, including the discovery of new variants of GAs such as the (1+(λ,λ)) GA [7], which has shown very good performance across a range of hard problems [15].

However, understanding population diversity and crossover has proved elusive. The first example function where crossover was proven to be beneficial is called Jumpk. In this problem, GAs have to overcome a fitness valley such that all local optima have Hamming distance k to the global optimum. Jansen and Wegener [18] showed that, while mutation-only algorithms such as the (1+1) EA require expected time $\Theta(n^k)$, a simple ($\mu$+1) GA with crossover only needs time $O(\mu n^2 k^3 + 4^k/p_c)$. This time is $O(4^k/p_c)$ for large $k$, and hence significantly faster than mutation-only GAs. However, their analysis requires an unrealistically small crossover probability $p_c \leq 1/(ckn)$ for a large constant $c > 0$.

Kötzing, Sudholt, and Theile [20] later refined these results towards a crossover probability $p_c \leq k/n$, which is still unrealistically small. Both approaches focus on creating diversity through a sequence of lucky mutations, relying on crossover to create the optimum, once sufficient diversity has been created. Their arguments break down if crossover is applied frequently. Hence, these analyses do not reflect the typical behaviour in GA populations with constant crossover probabilities $p_c = \Theta(1)$ as used in practice.

Lehre and Yao analysed the run time of the ($\mu$+1) GA with deterministic crowding for arbitrary crossover rates $p_c > 0$, showing exponential run time gaps between the case $p_c = 0$ and $p_c > 0$ [21]. The gain in performance in that analysis stems from the ability of a diverse population to optimise multiple, separated paths in parallel using a diversity-preservation mechanism. Similar results have been also shown for instances of the vertex cover problem by generating diversity either through deterministic crowding [25] or through island models [23]. Here, we will consider a different effect.

We provide a novel approach loosely inspired from population genetics: we show that diversity can also be created by crossover, followed by mutation. Note that the perspective of crossover creating diversity is common in population
genetics \[19, 33\]. A frequent assumption is that crossover mixes all alleles in a population, leading to a situation called linkage equilibrium, where the state of a population is described by the frequency of alleles \[3\].

For the maximum crossover probability \(p_c = 1\), we show that on Jump\(_k\) diversity emerges naturally in a population: the interplay of crossover, followed by mutation, can serve as a catalyst for creating a diverse range of search points out of few different individuals. This naturally emerging diversity allows to prove a speedup of order \(n/\log n\) for \(k \geq 3\) and standard mutation rate \(p_m = 1/n\) compared to mutation-only algorithms such as the (1+1) EA. Increasing the mutation rate to \(p_m = (1 + \delta)/n\) for an arbitrarily small constant \(\delta > 0\), leads to a speedup of order \(n\).

Both operators are proven to be vital: mutation requires \(\Theta(n^k)\) expected iterations to hit the optimum from a local optimum. Also using crossover on its own does not help much. As shown in \[20\] Theorem 8, using only crossover with \(p_c = \Omega(1)\) but no mutation following crossover, diversity reduces quickly, leading to inefficient running times for small population sizes \((\mu = O(\log n))\).

In this paper, we also rigorously study varieties of diversity mechanisms of the \((\mu+1)\) GA on the Jump\(_k\) function. We consider three varieties of diversity-preserving mechanisms: (1) methods that encourage genotypic uniqueness, (2) methods that increase genotypic distance, and (3) methods that employ parallelism. Our results are summarised in Table 1. The definition of the mechanisms with their variety are detailed in Section 2. The table presents the run time bound for a best-possible population size \(\mu\) for each diversity mechanism.

We observe on the Jump\(_k\) function how a diverse population spreads on local optima and eventually manages to escape them. Our results show that already small changes in the tie-breaking rule of the \((\mu+1)\) GA can make a big difference. We rigorously prove asymptotic run time upper bounds for different diversity mechanisms. The respective proofs themselves give insight into how the diversity mechanisms help escaping local optima.

All our analyses are based on observing the dynamic behaviour of the size of the largest species, referring to a collection of identical genotypes as species. A population contains no diversity when only one species is present. However, mutation can create further species, and then the combination of crossover and mutation is able to rapidly create further species in a highly stochastic process. This diversity can then be exploited to find the global optimum on Jump\(_k\) efficiently. A higher mutation rate facilitates the generation of new species and leads to better performance, with respect to rigorous upper run time bounds and empirical performance.

Using Jump\(_k\) as a case study, our analyses shed light on how diversity emerges in populations and how to facilitate the emergence of diversity by tuning the mutation rate or by making use of specific diversity mechanisms.
| Mechanism                        | \(\mu\) | \(p_c\) | \(p_m\) | \(k = 2\)                               | \(k = 4\)                               | any \(k\)                                 |
|----------------------------------|---------|---------|---------|------------------------------------------|------------------------------------------|-------------------------------------------|
| No mechanism, Thm. 7             | \(\Theta\left(\frac{\sqrt{n}}{\sqrt{\log n}}\right)\) | 1       | \(1/n\) | \(O\left(\frac{n^{1.5}}{\sqrt{\log n}}\right)\) | \(O\left(\frac{n^{3.5}}{\sqrt{\log n}}\right)\) | \(O\left(\frac{n^{k-0.5}}{\sqrt{\log n}}\right)\) |
|                                  | \(\Theta(n)\) | 1       | \(1/n\) | \(O(n^2 \log n)\)                       | \(O(n^3 \log n)\)                       | \(O(n^{k-1} \log n)\)                    |
| No mechanism, Thm. 11            | \(\Theta(\log n)\) | 1       | \((1 + \delta)/n\) | \(O(n \log n \log \log n)\) | \(O(n^3)\) | \(O\left(n \sqrt{k \log n \log \log n} + n^{k-1}\right)\) |
| Duplicate elim., Thm. 16          | 2       | \(\Omega(1)\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n^3)\) | \(O\left(n \sqrt{k \log n \log \log n} + n^{k-1}\right)\) |
|                                  | 2       | \(1 - \Omega(1)\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n^3)\) | \(O(n \log n + n^{k-1})\) |
| Duplicate min., Thm. 17           | 2       | \(\Omega(1)\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n^3)\) | \(O\left(n \sqrt{k \log n \log \log n} + n^{k-1}\right)\) |
|                                  | 2       | \(1 - \Omega(1)\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n^3)\) | \(O(n \log n + n^{k-1})\) |
| Det. crowding, Thm. 18            | 2       | \(k/n\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n \log n)\)                         | \(O(n \log n + \log^5 k)\) |
| Convex hull max., Thm. 19         | 2       | \(1 - \Omega(1)\) | \(1/n\) | \(O(n^2 \log n)\)                       | \(O(n^2 \log n)\)                       | \(O(n^2 \log n + 4^k)\) |
| Hamming dist. max., Thm. 20       | 2       | \(1 - \Omega(1)\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n \log n)\)                         | \(O(n \log n + nk \log k + 4^k)\) |
| Fitness sharing, Thm. 22          | 2       | \(1 - \Omega(1)\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n \log n)\)                         | \(O(n \log n + nk \log k + 4^k)\) |
| Island model, Thm. 23             | 2       | \(n/a\) | \(1/n\) | \(O(n \log n)\)                         | \(O(n \log n)\)                         | \(O(n \log n + kn + 4^k)\) |

Table 1: Comparison of the asymptotically best known run time bounds for the \((\mu+1)\) GA with crossover rate \(p_c > 0\) and mutation rate \(p_m\) on Jump\(_k\) with bit string length \(n\). More general results are presented in the respective theorems. Note that some of the results are subject to further conditions, e.g., \(k = o(n)\).
Parts of the results were published in [6] and [5]. Here we extend the analysis of no diversity mechanisms in [5] to higher mutation rates, leading to the surprising conclusion that increasing the mutation rates leads to smaller runtime bounds, compared to the standard mutation rate $1/n$. Furthermore, the analysis of standard mutation rates in [5] was restricted to very short jumps, $k = O(1)$. Here we generalise the results to a much larger class of Jump$_k$ functions, only requiring $k = o(n)$.

2 Preliminaries

The Jump$_k$: \{0, 1\}$^n \rightarrow \mathbb{N}$ class of pseudo-Boolean fitness functions was originally introduced by Jansen and Wegener [18]. The function value increases with the number of 1-bits in the bit string until a plateau of local optima is reached, consisting of all points with $n-k$ 1-bits. However, its only global optimum is the all-ones string $1^n$. Between the plateau and the global optimum, there is a valley of deteriorated fitness, which we call the gap of length $k$, and the algorithm has to jump over this gap to optimise the function.

The function is formally defined as

$$\text{Jump}_k(x) = \begin{cases} 
k + |x|_1 & \text{if } |x|_1 = n \text{ or } |x|_1 \leq n - k, \\ n - |x|_1 & \text{otherwise,} \end{cases}$$

where $|x|_1 = \sum_{i=1}^{n} x_i$ is the number of 1-bits in $x$.

We will analyse the performance of a standard steady-state ($\mu+1$) GA [18] using uniform crossover (i.e., each bit of the offspring is chosen uniformly at random from one of the parents) and standard bit mutation (i.e., each bit is flipped with probability $p_m$). The algorithm uses a population of $\mu$ individuals. In each generation, a new individual is created. With probability $p_c$, it is created by selecting two parents from the population uniformly at random, crossing them over, and then applying mutation to the resulting offspring. With probability $1 - p_c$ instead, one single individual is selected and only mutation is applied. The generation is concluded by removing the worst individual from the population and breaking ties uniformly at random. Algorithm 1 shows the pseudocode for the ($\mu+1$) GA.

Diversity-preserving mechanisms, which are introduced in the tie-breaking rule in line 11 of the algorithm, can be of four varieties: (1) methods that encourage genotypic uniqueness, (2) methods that increase genotypic distance, (3) methods that employ parallelism, and (4) no specific diversity-preserving mechanism, which corresponds to tie-breaking completely uniform at random.

In the first variety, tie-breaking mechanisms are used to promote genotypic uniqueness in the population. The method of duplicate elimination breaks ties in the selection process by making sure an offspring replaces a duplicated string out of the least-fit individuals. The advantage is that the crossover operator does not have to wait to get two different individuals. Very similar to duplicate elimination is duplicate minimisation. In this case, ties are broken such that the least-fit individual that has the highest number of duplicates is removed. This lowers the time to get many pairs of different individuals.

Deterministic crowding always chooses a parent of the current offspring for removal in the selection. This allows to get different individuals more efficiently.
Algorithm 1: ($\mu+1$) GA

1. $P \leftarrow \mu$ individuals, uniformly at random from $\{0, 1\}^n$;
2. while $1^n \notin P$ do
   3. Choose $p \in [0, 1]$ uniformly at random;
   4. if $p \leq p_c$ then
      5. Choose $x, y \in P$ uniformly at random;
      6. $z \leftarrow$ mutate(crossover($x, y$));
   else
      7. Choose $x \in P$ uniformly at random;
      8. $z \leftarrow$ mutate($x, p_m$);
   9. $P \leftarrow P \cup \{z\}$;
10. Remove one element from $P$ with lowest fitness, breaking ties according to the tie-breaking rule, and remove it from $P$;

Note that our result for deterministic crowding is the only analysis which does not extend up to $p_c = \Theta(1)$. Recall that deterministic crowding is here only applied in the tie-breaking rule and not in every generation as in other implementations of deterministic crowding [21, 25].

The second variety of diversity-preserving mechanisms we investigate are based on increasing genotypic distance between individuals in the population. A geometric crossover tends to reduce the size of the convex hull of the population [22]. It is therefore natural to break ties via a convex hull maximisation. Maximising the convex hull can be simulated by maximising the total Hamming distance among the population.

The third and final variety of mechanisms we study is based on relying on parallelism to obtain and preserve diversity. In an island model, diversity is attained by keeping parts of the population on separate processors. We give an upper bound on the expected run time for the the single-receiver island model [23, 32].

The most interesting behaviour of the population presented in this paper occurs after the entire population is stuck at local optima, the so-called plateau. That is because under the right condition the population diversity will emerge during this stage. Then after sufficient progress is made in diversity, crossover and mutation can work together on the plateau to create an optimal solution in $o(n^k)$ time. This is captured by Lemma 15 which will be presented later in the paper.

For the sake of completeness, in the next section, we provide the time bounds for the population to reach the plateau for the different algorithmic settings.

3 Time to plateau

We make the distinction between two cases $p_c = \Omega(1)$, which will be covered by Lemma 2, and $p_c = 1 - \Omega(1)$, which will be covered by Lemma 3. Note that when both $k$ and $\mu$ are constants independent of $n$, the two cases provide the same asymptotic expected time to reach the plateau.

For $p_c = \Omega(1)$, we rely on the steps that crossover occurs and make use of
The following general result, which provides an upper bound on the expected time for the \((\mu + 1)\) GA to reach some region \(A_m\) of the search space. Here we consider a fitness-based partition (see [17] for a formal definition) into levels \((A_i)_{i \in [m]}\) (thus, \(A_m\) is the last level) and define \(A_{\geq j} := \bigcup_{i=j}^{m} A_i\).

**Theorem 1.** Let \((A_i)_{i \in [m]}\) be a fitness-based partition of the search space into \(m \in \mathbb{N}\) levels. If there exist parameters \(\varepsilon, s_1, \ldots, s_{m-1} \in \{0,1\}\) such that for all \(j \in [m-1]\)

1. \(\min_{x,y \in A_{\geq j}, y \in A_{\geq j+1}} \Pr (\text{mutate(crossover}(x,y))) \in A_{\geq j+1}) \geq \varepsilon\) and

2. \(\min_{x,y \in A_j} \Pr (\text{mutate(crossover}(x,y))) \in A_{\geq j+1}) \geq s_j\)

then the expected number of iterations until the entire population of the \((\mu + 1)\) GA with \(p_c = \Omega(1)\) is in \(A_m\) is

\[
O\left(\left(\frac{\mu m}{\varepsilon} \log(\mu) + \sum_{j=1}^{m-1} 1/s_j\right)\right).
\]

**Proof.** The proof follows [4], but we avoid a detailed drift analysis because the algorithm is elitist. Let the current level be the smallest \(j \in [m]\) such that the population contains less than \(\mu/2\) individuals in \(A_{\geq j+1}\). By definition, there are at least \(\mu/2\) individuals in \(A_{\geq j}\), where \(j\) is the current level.

Since the algorithm is elitist, the number of individuals in \(A_{\geq j}\) is non-decreasing for any \(j \in [m]\). For an upper bound, we ignore any improvements where mutation only is used (i.e., lines 8 and 9 in Alg. [1]).

Assume that there are \(i\) individuals in \(A_{\geq j+1}\), hence \(0 \leq i < \mu/2\). If \(i = 0\), then an individual in \(A_{\geq j+1}\) can be created by selecting two individuals from \(A_j\), crossing them over, and mutating them such that the offspring is in \(A_{\geq j+1}\) and an individual not in \(A_{\geq j+1}\) is removed. The probability of this event is \(p_c s_j/4\).

If \(0 < i < \mu/2\), then the number of individuals in \(A_{\geq j+1}\) can be increased by selecting an individual in \(A_{\geq j}\) and an individual in \(A_{\geq j+1}\), crossing them over, and mutating them such that the offspring is in \(A_{\geq j+1}\) and one of the \(\mu - x \geq \mu/2\) individuals not in \(A_{\geq j+1}\) is removed. This event occurs with probability at least \((p_c/2)(i/\mu)\varepsilon\).

The expected time to increase the number of individuals in \(A_{\geq j+1}\) from 0 to \(\mu/2\), i.e., to increase the current level by at least one, is

\[
\frac{4}{(p_c s_j)} + 2\mu/(p_c \varepsilon) \sum_{i=1}^{\mu/2} 1/i.
\]

Hence, the expected time until at least half of the population is in \(A_m\) is

\[
O\left(\left(\frac{\mu m}{\varepsilon} \log(\mu) + \sum_{j=1}^{m-1} 1/s_j\right)\right).
\]

We now consider the time to remove individuals from the lowest fitness level in the population. Assume that there are \(0 < i' < \mu/2\) individuals in the lowest level \(j < m\). The number of individuals in level \(j\) can be reduced by crossing over an individual in level \(j\) and one of the at least \(\mu/2\) individuals in level \(m\), and mutating the offspring so that it belongs to \(A_{\geq j+1}\). By condition 1, this event occurs with probability at least \(p_c (\varepsilon/2) (i'/\mu)\). Hence, the expected time to remove all individuals from the lowest level \(j\) is no more than

\[
(2/p_c \varepsilon) \mu \sum_{i'=1}^{\mu/2} 1/i' = O(\mu/\varepsilon) \log(\mu).
\]

The expected time until all individuals in fitness levels lower than \(m\) have been removed is therefore \(O(\mu (m/\varepsilon) \log(\mu))\).

We apply Theorem 1 to bound the time until the entire population reaches the plateau.
Lemma 2. Consider the (\(\mu+1\)) GA optimizing Jump\(_k\) with \(p_c = \Omega(1)\) and \(p_m = \Theta(1/n)\). Then the expected time until either the optimum has been found or the entire population is on the plateau is \(O\left(n\sqrt{\mu} \log \mu + \log n\right)\).

Proof. We apply Theorem 1 and divide the search space into \(m := n\) levels with the partition

\[
A_j := \begin{cases} 
\{x \in \{0,1\}^n \mid |x|_1 = n - j\} & \text{if } 1 \leq j < k, \\
\{x \in \{0,1\}^n \mid |x|_1 = j - k\} & \text{if } k \leq j < n, \\
\{x \in \{0,1\}^n \mid |x|_1 \in \{n-k,k\}\} & \text{if } j = n,
\end{cases}
\]

where \(|x|_1 := \sum_{i=1}^n x_i\) is the number of 1-bits in bit string \(x\).

We call any search point \(x \in \{0,1\}^n\) with \(n - k < |x|_1 < n\) a gap-individual. We first claim that the probability of producing a gap-individual by crossing over two individuals \(x \in A_{\geq j}\) and \(y \in A_{\geq j+1}\) with \(k \leq j < n + 1\) is bounded from above by

\[
\Pr(n - k < |\text{crossover}(x,y)|_1 < n) < \frac{1}{2} - \frac{1}{4\sqrt{k}}. \tag{1}
\]

To see why this claim holds, we first argue that the probability of producing a gap-individual is highest when the parents \(x\) and \(y\) have \(n - k\) and \(n - k - 1\) 1-bits, respectively. More formally, obtain \(x'\) by flipping an arbitrary 0-bit in \(x\), and \(y'\) by flipping an arbitrary 0-bit in \(y\). Then, we have the stochastic dominance relationships \(|\text{crossover}(x,y)|_1 \leq |\text{crossover}(x',y)|_1\) and \(|\text{crossover}(x,y)|_1 \leq |\text{crossover}(x',y')|_1\). By repeating this argument, we obtain \(|\text{crossover}(x,y)|_1 \leq |\text{crossover}(x'',y'')|_1\) for two bit strings \(x''\) and \(y''\) with \(|x''|_1 = n - k\) and \(|y''|_1 = n - k - 1\). The probability of obtaining a search point with exactly \(k\) 0-bits when crossing over two bit strings with \(k + 1\) 0-bits is minimised when the positions of the 0-bits in the two bit strings differ. Hence, for bit strings \(x''\) and \(y''\), we have the lower bound

\[
\Pr(|\text{crossover}(x'',y'')|_1 = n - k) \geq \frac{2^k - (2k+1)}{2^k} \cdot 2^{-2k+1} = \frac{4^k}{2\sqrt{k}} \cdot 2^{-2k+1} = \frac{1}{4\sqrt{k}}.
\]

The crossover operation between \(x''\) and \(y''\) produces two offspring \(u''\) and \(v''\) where \(|x''|_1 + |y''|_1 = |u''|_1 + |v''|_1\), and returns \(u''\) or \(v''\) with equal probability. Without loss of generality, assume that \(|u''|_1 \geq |v''|_1\). We must have \(|v''| < n - k \leq |u''|_1\) because

\[
2(n - k) - 1 = |x''|_1 + |y''|_1 = |u''|_1 + |v''|_1 \leq 2|u''|_1, \tag{2}
\]

and similarly

\[
2(n - k) - 1 = |u''|_1 + |v''|_1 \geq 2|v''|_1,
\]

hence

\[
\Pr(|\text{crossover}(x'',y'')|_1 \geq n - k) = \frac{1}{2}. \tag{3}
\]
Our claim now follows, because
\[
\Pr(n - k < |\text{crossover}(x, y)|_1 < n) < \Pr(n - k < |\text{crossover}(x, y)|_1) \leq \Pr(n - k < |\text{crossover}(x'', y'')|_1) = \Pr(n - k \leq |\text{crossover}(x'', y'')|_1) - \Pr(|\text{crossover}(x'', y'')|_1 = n - k) \leq \frac{1}{2} - \frac{1}{4\sqrt{k}}.
\]

We now show that condition 1 of Theorem 1 holds for the parameter \(\varepsilon := (1 - p_m)n/(4\sqrt{k}) = \Theta(1/\sqrt{k})\). As before, assume that \(x \in A_{\geq j}\) and \(y \in A_{\geq j+1}\) for \(j \geq k\). As argued in (2), a crossover between \(x\) and \(y\) produces two offspring \(u\) and \(v\) where \(|u|_1 \geq j + 1\). The offspring therefore satisfies
\[
\Pr(\text{crossover}(x, y) \in A_{\geq j+1}) = \Pr(j + 1 \leq |\text{crossover}(x, y)|_1) - \Pr(n - k < |\text{crossover}(x, y)|_1 < n) \geq \frac{1}{4\sqrt{k}}.
\]
Finally, with probability \((1 - p_m)n\), none of the bits are flipped during mutation, which implies
\[
\Pr(\text{mutate}(\text{crossover}(x, y)) \in A_{\geq j+1}) \geq \varepsilon.
\]
The same bound holds for levels \(j < k\), except that we count 0-bits instead of 1-bits, and we do not need to account for the probability of producing gap individuals.

We now show that condition 2 of Theorem 1 holds. Assume that \(x, y \in A_j\) for \(j \geq k\). Then, following the same argument as above
\[
\Pr(\text{crossover}(x, y) \in A_{\geq j}) \geq \frac{1}{4\sqrt{k}}.
\]
The probability that the mutation operator flips at least one of the \(n - j\) 0-bits, and no other bits, is at least \((n - j)p_m(1 - p_m)n^{-1}\). Hence, we can use the parameter \(s_j := (n - j)p_m(1 - p_m)n^{-1}/(4\sqrt{k}) = \Theta((n - j)/(n\sqrt{k}))\). The same bound holds for levels \(j < k\), except that we count 0-bits instead of 1-bits, and we do not need to account for the probability of producing gap-individuals.

The result now follows from Theorem 1.

For \(p_c = 1 - \Omega(1)\), we rely on mutation-only steps, hence, we make use of the result presented in [34].

**Lemma 3.** Consider the \((\mu + 1)\) GA optimising \(\text{Jump}_k\) with \(p_c = 1 - \Omega(1)\). Then the expected time until either the optimum has been found or the entire population is on the plateau is \(O(\mu n + n \log n + \mu \log \mu)\).

**Proof.** Before the population reaches the plateau, \(\text{Jump}_k\) is identical to OneMax. In addition, our \((\mu + 1)\) GA performs the same steps as the \((\mu + 1)\) EA during generations that it does not perform crossover. Therefore, compared to the
any slow-down caused by crossover in (\(\mu + 1\)) GA can only contribute a constant factor to the run time, as long as \(p_c = 1 - \Omega(1)\). It then follows from \cite{34} that the (\(\mu + 1\)) GA also needs \(O(\mu n + n \log n)\) to reach the plateau. After that, similar to the last part of the proof of Theorem \cite{1} we only need an extra \(O(\mu \log \mu)\) term that captures the waiting time until all individuals are on the plateau.

\section{Natural diversity}

We are first interested in the natural setting of Algorithm \cite{1}, i.e., with \(p_c = 1.0\) and without any tailored tie-breaking rule, that is, breaking ties uniformly at random.

\subsection{Population dynamics}

Previous observations of simulations have revealed the following behaviour. Assume the algorithm has reached a population where all individuals are identical. We refer to identical individuals as a species, hence, in this case, there is only one species. Eventually, a mutation will create a different search point on the plateau, leading to the creation of a new species. Both species may shrink or grow in size, and there is a chance that the new species disappears and we go back to one species only.

However, the existence of two species also serves as a catalyst for creating further species in the following sense. Say two parents 0001111111 and 0010111111 are recombined, then crossover has a good chance of creating an individual with \(n - k + 1\) 1s, e.g., 0011111111. Then mutation has a constant probability of flipping any of the \(n - k - 1\) unrelated 1-bits to 0, leading to a new species, e.g., 0011111011. This may lead to a sudden burst of diversity in the population.

Simulations for the standard mutation rate \(1/n\) indicated that the size of the largest species is an important factor for describing this diversity. Due to the ability to create new species, the size of the largest cluster performs an almost fair random walk. Once its size has decreased significantly from its maximum \(\mu\), there is a good chance for recombining two parents from different species. This helps in finding the global optimum, as crossover can increase the number of 1s in the offspring, compared to its parents, such that fewer bits need to be flipped by mutation to reach the optimum. This is formalised in the following lemma.

\textbf{Lemma 4.} The probability that the global optimum is constructed by a uniform crossover of two parents with Hamming distance \(2d\), followed by mutation, is

\begin{equation}
\sum_{i=0}^{2d} \binom{2d}{i} \frac{1}{2^{2d}n^{k+d-i}} \left(1 - \frac{1}{n}\right)^{n-k-d+i} \geq \frac{1}{2^{2d}n^{k-d}} \left(1 - \frac{1}{n}\right)^{n-k+d}.
\end{equation}

\textbf{Proof.} For a pair of search points on the plateau with Hamming distance \(2d\), both parents have \(d\) 1s among the \(2d\) bits that differ between parents, and \(n - k - d\) 1s outside this area. Assume that crossover sets \(i\) out of these \(2d\) bits
to 1, which happens with probability $\binom{2d}{i} \cdot 2^{-2d}$. Then mutation needs to flip the remaining $k + d - i$ 0s to 1. The probability that such a pair creates the optimum is hence

$$\sum_{i=0}^{2d} \binom{2d}{i} \frac{1}{2^{2d}n^{k+d-i}} \left(1 - \frac{1}{n}\right)^{n-k-d+i}.$$  

The second bound is obtained by ignoring summands $i < 2d$ for the inner sum.

Note that even a Hamming distance of 2, i.e., $d = 1$, leads to a probability of $\Omega(n^{-k+1})$, provided that such parents are selected for reproduction. The probability is by a factor of $n$ larger than the probability $\Theta(n^{-k})$ of mutation without crossover reaching the optimum from the plateau.

We will show that this effect leads to a speedup of nearly $n$ for the $(\mu+1)$ GA, compared to the expected time of $\Theta(n^k)$ for the (1+1) EA [11] and other EAs only using mutation.

The idea behind the analysis is to investigate the random walk underlying the size of the largest species. We bound the expected time for this size to decrease to $\mu/2$ and then argue that the $(\mu+1)$ GA is likely to spend a good amount of time with a population of good diversity, where the probability of creating the optimum in every generation is $\Omega(n^{-k+1})$ due to the chance of recombining parents of Hamming distance at least 2.

In the following, we refer to $Y(t)$ as the size of the largest species in the population at time $t$. Define

$$p_+(y) := \Pr(Y(t+1) - Y(t) = 1 \mid Y(t) = y),$$

$$p_-(y) := \Pr(Y(t+1) - Y(t) = -1 \mid Y(t) = y),$$

i.e., $p_+(y)$ is the probability that the size of the largest species increases from $y$ to $y + 1$, and $p_-(y)$ is the probability that it decreases from $y$ to $y - 1$.

The following lemma gives bounds on these transition probabilities, unless two parents of Hamming distance larger than 2 are selected for recombination (this case will be treated later in Lemma 6). We formulate the lemma for arbitrary mutation rates $\chi/n = \Theta(1/n)$ and restrict our attention to sizes $Y(t) \geq \mu/2$ as we are only interested in the expected time for the size to decrease to $\mu/2$.

**Lemma 5.** For every population on the plateau of Jump for $k = o(n)$ the following holds. Either the $(\mu+1)$ GA with mutation rate $\chi/n = \Theta(1/n)$ performs a crossover of two parents whose Hamming distance is larger than 2, or the size $Y(t)$ of the largest species changes according to transition probabilities $p_-(\mu) = \Omega(k/n)$ and, for $\mu/2 \leq y < \mu$,

$$p_+(y) \leq \frac{y(\mu - y)(\mu + y)}{2\mu^2(\mu + 1)} \left(1 - \frac{\chi}{n}\right)^n + O\left(\frac{(\mu - y)^2}{\mu^2 n}\right),$$

$$p_-(y) \geq \frac{y(\mu - y)(\mu + \chi y)}{2\mu^2(\mu + 1)} \left(1 - \frac{\chi}{n}\right)^n.$$

**Proof.** We call an individual belonging to the current largest species a $y$ individual and all the others non-$y$ individuals. In each generation, there is either no change, or one individual is added to the population and one individual chosen
uniformly at random is removed from the population. In order to increase the number of $y$ individuals, it is necessary that a $y$ individual is added to the population and a non-$y$ individual is removed from the population. Analogously, in order to decrease the number of $y$ individuals, it is necessary that a non-$y$ individual is added to the population and a $y$ individual is removed from the population.

Given that $Y(t) = y$, let $p(y)$ be the probability that a $y$ individual is created at time $t+1$, and $q(y)$ the probability that a non-$y$ individual is created. Multiplying by the survival probabilities we have

$$p_-(y) = q(y) \left( \frac{y}{\mu + 1} \right) \quad \text{and} \quad (6)$$

$$p_+(y) := p(y) \left( 1 - \frac{y + 1}{\mu + 1} \right) = p(y) \left( \frac{\mu - y}{\mu + 1} \right). \quad (7)$$

We now estimate an upper bound on $p(y)$. We may assume that the Hamming distance between parents is at most 2 as otherwise there is nothing to prove. A $y$ individual can be created in the following three ways:

- Two $y$ individuals are selected. Crossing over two $y$ individuals produces another $y$ individual, which survives mutation if no bits are flipped, i.e., with probability $(1 - \chi/n)^n$.

- One $y$ individual and one non-$y$ individual are selected. The crossover operator produces a $y$ individual with probability $1/4$, and mutation does not flip any bits with probability $(1 - \chi/n)^n$. If the crossover operator does not produce a $y$ individual, then, to produce a $y$ individual, at least one specific bit-position must be mutated, which occurs with probability $O(1/n)$. The overall probability is hence $(1/4)(1 - \chi/n)^n + O(1/n)$.

- Two non-$y$ individuals are selected. These two individuals are either identical or have Hamming distance 2 (i.e., by assumption). In the first case, they both have one of the $k$ 0-bit positions of a $y$ individual set to 1. In the second case, they either both have one of the $k$ 0-bit positions of a $y$ individual set to 1, or they both have one of the $n - k$ 1-bit positions set to 0. In both cases, crossover cannot change the value of such a bit. Thus, at least one specific bit-position must be flipped, which occurs with probability $O(1/n)$.

Taking into account the probabilities of the three selection events above, the probability of producing a $y$ individual is

$$p(y) = \left( \frac{y}{\mu} \right)^2 \left( 1 - \frac{\chi}{n} \right)^n + 2 \left( \frac{y}{\mu} \right) \left( 1 - \frac{y}{\mu} \right) \cdot \left( \frac{1}{4} \right) \left( 1 - \frac{\chi}{n} \right)^n + O \left( \frac{1}{n} \right) + \frac{(\mu - y)^2}{\mu^2} O \left( \frac{1}{n} \right)$$

$$= \left( 1 - \frac{\chi}{n} \right)^n \left( \frac{y}{\mu} \right) \left( \frac{y}{\mu} + \frac{\mu - y}{2\mu} \right) +$$

$$+ O \left( \frac{y(\mu - y)}{\mu^2} \cdot \frac{1}{n} \right) + O \left( \frac{(\mu - y)^2}{\mu^2} \cdot \frac{1}{n} \right)$$

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\[
= \frac{y(\mu + y)}{2\mu^2} \left(1 - \frac{\chi}{n}\right)^n + O\left(\frac{\mu - y}{\mu} \cdot \frac{1}{n}\right).
\]

We then estimate a lower bound on \(q(y)\). In the case where \(y = \mu\), a non-\(y\) individual can be added to the population if

- two \(y\) individuals are selected and the mutation operator flips one of the \(k\) 0-bits and one of the \(n - k\) 1-bits. This event occurs with probability

\[
q(\mu) = k(n - k) \left(\frac{\chi}{n}\right)^2 \left(1 - \frac{\chi}{n}\right)^{n-2} = \Omega \left(\frac{k}{n}\right),
\]

where we used that \(k = o(n)\) in the last equality.

In the other case, where \(y < \mu\), a non-\(y\) individual can be added to the population in the following two ways:

- A \(y\) individual and a non-\(y\) individual are selected. Crossover produces a copy of the non-\(y\) individual with probability 1/4, which is unchanged by mutation with probability \((1 - \chi/n)^n\). Secondly, with probability 1/4, crossover produces an individual with \(k - 1\) 0-bits. Mutation then creates a non-\(y\) individual by flipping a single of the \(n - k\) 1-bit positions that do not lead to re-creating \(y\). Thirdly, again with probability 1/4, crossover produces an individual with \(k+1\) 0-bits and mutation then creates a non-\(y\) individual by flipping a single of \(k\) 1-bits that do not lead back to \(y\). The above three events, conditional on selecting a \(y\) individual and a non-\(y\) individual, lead to a total probability of

\[
\frac{1}{4} \cdot \left(1 - \frac{\chi}{n}\right)^n + \frac{1}{4} \cdot (n - k) \cdot \frac{\chi}{n} \left(1 - \frac{\chi}{n}\right)^{n-1} + \frac{1}{4} \cdot k \cdot \frac{\chi}{n} \left(1 - \frac{\chi}{n}\right)^{n-1} \geq \frac{\chi + 1}{4} \cdot \left(1 - \frac{\chi}{n}\right)^n.
\]

- Two non-\(y\) individuals are selected. In the worst case, the selected individuals are different, hence, crossover produces an individual on the plateau with probability at least 1/2, which mutation does not destroy with probability \((1 - \chi/n)^n\).

Assuming that \(\mu/2 \leq y < \mu\) and \(n\) is sufficiently large, the probability of adding a non-\(y\) individual is

\[
q(y) \geq 2 \left(\frac{y}{\mu}\right) \left(1 - \frac{y}{\mu}\right) \cdot \frac{\chi + 1}{4} \left(1 - \frac{\chi}{n}\right)^n
\]

\[
+ \frac{1}{2} \left(1 - \frac{y}{\mu}\right)^2 \left(1 - \frac{\chi}{n}\right)^n
\]

\[
= \frac{(\mu - y)(\mu + \chi y)}{2\mu^2} \left(1 - \frac{\chi}{n}\right)^n.
\]

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Plugging $p(y)$ and $q(y)$ into equations (6) and (7), we get

$$p^-(y) \geq \left[\frac{(\mu - y)(\mu + \chi y)}{2\mu^2} (1 - \frac{\lambda}{n}) \right] \left(\frac{y}{\mu + 1}\right) = \frac{(\mu - y)(\mu + \chi y)y}{2\mu^2(\mu + 1)} (1 - \frac{\lambda}{n})^n.$$

And we also have

$$p^+(y) = \left[\frac{y(\mu + y)}{2\mu^2} (1 - \frac{\lambda}{n}) + O\left(\frac{\mu - y}{\mu} \cdot \frac{1}{n}\right)\right] \left(\frac{\mu - y}{\mu + 1}\right) = \frac{(\mu^2 - y^2)y}{2\mu^2(\mu + 1)} (1 - \frac{\lambda}{n})^n + O\left(\frac{\mu - y}{\mu^2n}\right).$$

Steps where crossover recombines two parents with larger Hamming distance were excluded from Lemma 5 as they require different arguments. The following lemma shows that conditional transition probabilities in this case are favourable in that the size of the largest species is more likely to decrease than to increase.

**Lemma 6.** Assume that $y \geq \mu/2$ and that the $(\mu+1)$ GA on Jump$_k$ with $k = o(n)$ and mutation rate $\chi/n = \Theta(1/n)$ selects two individuals on the plateau with Hamming distance larger than 2, then for conditional transition probabilities $p^*_-(y)$ and $p^*_+(y)$ for decreasing or increasing the size of the largest species, $p^*_-(y) \geq 2p^*_+(y)$.

**Proof.** Assume that the population contains two individuals $x$ and $z$ with Hamming distance $2\ell \leq 2k$, where $\ell \geq 2$. Without loss of generality, let us assume that they differ in the first $2\ell$ bit positions.

In the case that the majority individual $y$ has $\ell$ 0-bits in the first $2\ell$ positions, a $y$ individual may be produced by creating the $\ell$ 0-bits and $\ell$ 1-bits in the exact positions by crossover and no followed mutation. Alternatively, at least 1 exact bit has to be flipped by mutation. Then the probability of producing a $y$ individual from $x$ and $z$ and replacing a non-$y$ individual with $y$ is less than

$$p^*_+(y) \leq \left[\left(\frac{1}{2}\right)^{2\ell} (1 - \frac{\lambda}{n})^n + O\left(\frac{1}{n}\right)\right] \left(\frac{\mu - y}{\mu}\right) \leq \left(\frac{1}{2}\right)^{2\ell + 1} (1 - \frac{\lambda}{n})^n + O\left(\frac{1}{n}\right).$$

On the other hand, the probability of producing an individual on the plateau different from $y$ and replacing a $y$ individual is at least

$$p^*_-(y) \geq \left(\left(\frac{2\ell}{\ell} - 1\right)\left(\frac{1}{2}\right)^{2\ell} (1 - \frac{\lambda}{n})^n \frac{y}{\mu}\right) \geq 3 \left(\frac{1}{2}\right)^{2\ell + 1} (1 - \frac{\lambda}{n})^n \geq 2p^*_+(y)$$

for sufficiently large $n$.

In the other case, assume that the majority individual $y$ does not have $\ell$ 0-bits in the first $2\ell$ bit positions. Then the mutation operator must flip at least one specific bit among the last $n - 2\ell$ positions to produce $y$, which occurs with probability $O(1/n)$, while the probability to produce a non-$y$ individual on the plateau is still $\Omega(1)$.  

\[\square\]
4.2 Standard mutation rate

We first analyse the $(\mu+1)$ GA with the standard mutation rate of $1/n$, i.e., $\chi = 1$. We show that the diversity emerging in the $(\mu+1)$ GA leads to a speedup of nearly $n$ for the $(\mu+1)$ GA, compared to the expected time of $\Theta(n^k)$ for the $(1+1)$ EA [11] and other EAs only using mutation.

**Theorem 7.** The expected optimisation time of the $(\mu+1)$ GA with $p_c = 1$ and $\mu \leq \kappa n$, for some constant $\kappa > 0$, on $\text{Jump}_k$, $k = o(n)$, is

$$O\left(\mu n \sqrt{k} \log(\mu) + n^k / \mu + n^{k-1} \log(\mu)\right).$$

For $k \geq 3$, the best speedup is of order $\Omega(n / \log n)$ for $\mu = \kappa n$. For $k = 2$, the best speedup is of order $\Omega(\sqrt{n / \log n})$ for $\mu = \Theta(\sqrt{n / \log n})$.

Note that for mutation rate $1$, the dominant terms in Lemma 5 are equal, hence the size of the largest species performs a fair random walk up to a bias resulting from small-order terms. This confirms our intuition from observing simulations. The following lemma formalises this fact: in steps where the size $Y(t)$ of the largest species changes, it performs an almost fair random walk.

**Lemma 8.** For the random walk induced by the size of the largest species, conditional on the current size $y$ changing, for $\mu / 2 < y < \mu$, the probability of increasing $y$ is at most $1/2 + O(1/n)$, and the probability of decreasing it is at least $1/2 - O(1/n)$.

**Proof.** We only have to estimate the conditional probability of increasing $y$ as the two probabilities sum up to 1. The sought probability is given by $p_+(y) / (p_+(y) + p_-(y))$, which is strictly increasing in $p_+(y)$. Lemma 6 states that whenever the $(\mu+1)$ GA recombines two parents of Hamming distance larger than 2, the claim on conditional probabilities follows. Hence we assume in the following that this does not happen.

Using the lower bound for $p_+(y)$ and the upper bound from $p_-(y)$ from Lemma 5 with implicit constant $c_+$ in the asymptotic term for $p_+$, we get

$$\frac{p_+(y)}{p_+(y) + p_-(y)} \leq \frac{y(\mu+y)(\mu-y)}{2\mu^2(\mu+1)} \cdot \left(1 - \frac{1}{\mu}\right)^n + \frac{c_+ (\mu-y)^2}{\mu n}$$

$$= 1 + \frac{c_+ (\mu-y)^2}{2\mu n} \cdot \left(1 - \frac{1}{\mu}\right)^n + \frac{c_+ (\mu-y)^2}{\mu^2 n}$$

$$= 1 + \frac{c_+ (\mu-y)^2}{2\mu n} \cdot \left(1 - \frac{1}{\mu}\right)^n + \frac{c_+ (\mu-y)^2}{\mu n}$$

where in the last step we multiplied the last fraction by $\mu/(\mu - y)$. Now the numerator is $O(1/n)$. Since $\mu / 2 < y < \mu$, we have $\frac{y(\mu+y)}{\mu(\mu+1)} = \Theta(1)$. Along with $(1 - \frac{1}{\mu})^n = \Theta(1)$ and $\frac{c_+ (\mu-y)^2}{\mu n} = O(1/n)$, the denominator simplifies to $\Theta(1) + O(1/n) = \Theta(1)$. Hence the last fraction is $O(1/n)$, proving the claim. \(\square\)

We use these transition probabilities to bound the expected time for the random walk to hit $\mu/2$. 

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Lemma 9. Consider the random walk of $Y(t)$, starting in state $X_0 \geq \mu/2$. Let $T$ be the first hitting time of state $\mu/2$. If $\mu = O(n)$, then $\mathbb{E}(T \mid X_0) = O(\mu n + \mu^2 \log \mu)$ regardless of $X_0$.

Proof. Let $E_i$ abbreviate $\mathbb{E}(T \mid X_0 = i)$, then $E_{\mu/2} = 0$ and $E_\mu = O(n) + E_{\mu-1}$ as $p_-(\mu) = \Omega(1/n)$ by Lemma 5.

For $\mu/2 < y < \mu$, the probability of leaving state $y$ is always (regardless of Hamming distances between species) bounded from below by the probability of selecting two $y$ individuals as parents, not flipping any bits during mutation, and choosing a non-$y$ individual for replacement (cf. Lemma 5):

\[ p_+(y) + p_-(y) \geq \frac{y^2}{\mu^2} \cdot \left(1 - \frac{1}{n}\right)^n \cdot \frac{\mu - y}{\mu + 1} \geq \frac{\mu - y}{24\mu} , \]

as $y \geq \mu/2$, $\mu + 1 \leq 3\mu/2$ (since $\mu \geq 2$), and $(1 - 1/n)^n \geq 1/4$ for $n \geq 2$.

Using conditional transition probabilities $1/2 \pm \delta$ for $\delta = O(1/n)$ according to Lemma 8, $E_i$ is bounded as

\[ E_i \leq \frac{24\mu}{\mu - i} + \left(\frac{1}{2} - \delta \right) E_{i-1} + \left(\frac{1}{2} + \delta \right) E_{i+1} . \]

This is equivalent to

\[ \left(\frac{1}{2} - \delta \right) \cdot (E_i - E_{i-1}) \leq \frac{24\mu}{\mu - i} + \left(\frac{1}{2} + \delta \right) \cdot (E_{i+1} - E_i) . \]

Introducing $D_i := E_i - E_{i-1}$, this is

\[ \left(\frac{1}{2} - \delta \right) \cdot D_i \leq \frac{24\mu}{\mu - i} + \left(\frac{1}{2} + \delta \right) \cdot D_{i+1} \]

and equivalently

\[ D_i \leq \frac{24\mu}{\mu - i} + \left(\frac{1}{2} + \delta \right) \cdot D_{i+1} \leq \frac{50\mu}{\mu - i} + \alpha \cdot D_{i+1} \]

for $\alpha := \frac{1+2\delta}{2} = 1 + O(1/n)$, assuming $n$ is large enough. From $E_\mu = O(n) + E_{\mu-1}$, we get $D_\mu = O(n)$, hence an induction yields

\[ D_i \leq \sum_{j=i}^{\mu-1} \frac{50\mu}{\mu - j} \cdot \alpha^{j-i} + \alpha^{\mu-i} \cdot O(n) . \]

Combining $\alpha = 1 + O(1/n)$ and $1 + x \leq e^x$ for all $x \in \mathbb{R}$, we have $\alpha^n \leq e^{O(\mu/n)} \leq e^{O(1)} = O(1)$. Bounding both $\alpha^{j-i}$ and $\alpha^{\mu-i}$ in this way, we get

\[ D_i \leq O(n) + O(\mu) \cdot \sum_{j=i}^{\mu-1} \frac{1}{\mu - j} = O(n + \mu \log \mu) , \]

as the sum is equal to $\sum_{j=1}^{\mu-1} 1/j = O(\log \mu)$.
Now,
\[
D_{\mu/2+1} + D_{\mu/2+2} + \cdots + D_i = (E_{\mu/2+1} - E_{\mu/2}) + (E_{\mu/2+2} - E_{\mu/2+1}) + \cdots + (E_i - E_{i-1}) = E_i - E_{\mu/2} = E_i.
\]

Hence, we get \( E_i = \sum_{k=\mu/2+1}^i D_k \leq O(\mu n + \mu^2 \log \mu). \) \( \square \)

Now we show that when the largest species has decreased its size to \( \mu/2 \) there is a good chance that the optimum will be found within the following \( \Theta(\mu^2) \) generations.

**Lemma 10.** Consider the \((\mu+1)\) GA with \( p_c = 1 \) on Jump_{\mu}. If the largest species has size at most \( \mu/2 \) and \( \mu \leq \kappa n \) for a small enough constant \( \kappa > 0 \), the optimal optimum is found is \( \Omega\left(\frac{1}{\kappa n^{1-1/\mu^2}}\right) \).

**Proof.** We show that during the \( c \mu^2 \) generations the size of the largest species never rises above \( (3/4) \mu \) with at least constant probability. Then we calculate the probability of jumping to the optimum during the phase given that this happens.

Let \( X_i, 1 \leq i \leq c \mu^2 \) be random variables indicating the increase in number of individuals of the largest species at generation \( i \). We pessimistically ignore self-loops and assume that the size of the species either increases or decreases in each generation. Using the conditional probabilities from Lemma 8 we get that the expected increase in each step is
\[
E(X) = \sum_{i=1}^{c \mu^2} X_i = \sum_{i=1}^{c \mu^2} O(1/n) = (c' \mu^2)/n \leq c' \kappa \mu \leq (1/8) \mu,
\]
where we use that \( \mu \leq \kappa n \) and \( \kappa \) is chosen small enough.

By an application of Hoeffding bounds, \( \Pr(X \geq E(X) + \lambda) \leq \exp(-2 \lambda^2/\sum_i c_i^2) \) with \( \lambda = \mu/8 \) and \( c_i = 2 \), we get that \( \Pr(X \geq (2/8)\mu) \leq \exp(-c') = 1 - \Omega(1) \). We remark that the bounds also hold for any partial sum of the sequence \( X_1, \ldots, X_{c \mu^2} \) (Chapter 1, Theorem 1.13), i.e., with probability \( \Omega(1) \) the size never exceeds \((3/4) \mu \) in the considered phase of length \( c \mu^2 \) generations.

While the size does not exceed \((3/4) \mu \), in every step there is a probability of at least \( 1/4 \cdot 3/4 = \Omega(1) \) of selecting parents from two different species, and by Lemma 4 the probability of creating the optimum is \( \Omega(n^{-k+1}) \).

Finally, the probability that at least one successful generation occurs in a phase of \( c \mu^2 \) is, using \( 1 - (1-p)^\lambda \geq (\lambda p/(1+\lambda p)) \) for \( \lambda \in \mathbb{N}, p \in [0,1] \) Lemma 10], the probability that the optimum is found in one of these steps is
\[
1 - \left(1 - \frac{1}{\Omega(n^{-k+1})}\right)^{c \mu^2} \geq \Omega\left(\frac{\mu^2 \cdot n^{-k+1}}{1 + \mu^2 \cdot n^{-k+1}}\right). \quad \square
\]
Finally, we assemble all lemmas to prove our main theorem of this section.

Proof of Theorem 7. The expected time for the whole population to reach the plateau is $O(\mu n \sqrt{k \log(\mu)} + n \sqrt{k \log n})$ by Lemma 2.

Once the population is on the plateau, we wait till the largest species has decreased its size to at most $\mu/2$. According to Lemma 9, the time for the largest species to reach size $\mu/2$ is $O(\mu n + \mu^2 \log \mu)$. By Lemma 10, the probability that in the next $c\mu^2$ steps the optimum is found is $\Omega(1/(1+nk-1/\mu^2))$. If not, we repeat the argument. The expected number of such trials is $O(1 + n^k/\mu + n^k - 1 \log(\mu))$, and the expected length of one trial is $O(\mu n + \mu^2 \log(\mu) + n^k/\mu + n^{k-1} \log(\mu))$.

Adding up all times and subsuming terms $\mu^2 \log(\mu) = O(\mu n \sqrt{k \log(\mu)})$ and $n \sqrt{k \log n} = O(n^k/\mu + n^{k-1} \log(\mu))$, noting that $k = o(n)$ completes the proof.

4.3 High mutation rates

We now consider the run time of $(\mu+1)$ GA with mutation rate $\chi/n = (1+\delta)/n$ for an arbitrary constant $\delta > 0$. The following theorem states that in this setting the algorithm has at least a linear speedup compared to the $(\mu+1)$ EA without crossover [34]. By assuming a slightly higher mutation rate, we not only obtain a bound which is by a log-factor better than Theorem 7, but the analysis is also significantly simpler.

Theorem 11. The $(\mu+1)$ GA with mutation rate $(1+\delta)/n$, for a constant $\delta > 0$, and population size $\mu \geq ck \ln(n)$ for a sufficiently large constant $c > 0$, has for $k = o(n)$ expected optimisation time $O(n^k \mu \log(\mu) + \mu^2 + n^k - 1)$ on Jump$_k$.

We again study the random walk corresponding to the size of the largest species on the plateau. For mutation rate $1/n$, this is almost an unbiased random walk. For slightly higher mutation rates, we will see that the random walk changes to an unfair random walk where the size of the largest species decreases by $\Omega(1/\mu)$ in expectation. Formally, our analysis assumes the following condition.

Condition 12. For a constant $\delta > 0$ and all $y, \mu/2 \leq y \leq \mu$,

$$p_-(y) \geq \begin{cases} 
\Omega(1/n) & \text{if } y = \mu, \\
\Omega(1/\mu) & \text{if } \mu/2 \leq y < \mu, \text{ and} \\
(1+\delta)p_+(y) & \text{if } \mu/2 \leq y < \mu.
\end{cases}$$

(10)

The following lemma states that it is sufficient to increase the mutation rate slightly above $1/n$ to satisfy the diversity condition.

Lemma 13. If $\chi/n \geq (1+\delta)/n$ for any constant $\delta > 0$, then Condition 12 holds.
Proof. The first two inequalities follow directly from Lemma 5 and Lemma 6. For any constant \( \varepsilon > 0 \), Lemma 5 implies that

\[
p_+(y) \leq \frac{y(\mu - y)(\mu + y)(1 + \varepsilon)}{2\mu^2(\mu + 1)} \left(1 - \frac{\chi}{n}\right)^n \quad \text{and} \quad p_-(y) \geq \frac{y(\mu - y)(\mu + \chi y)(1 - \varepsilon^2)}{2\mu^2(\mu + 1)} \left(1 - \frac{\chi}{n}\right)^n.
\]

Thus, given that \( \mu/2 < y < \mu \) and \( \chi \geq 1 + \delta \),

\[
\frac{p_-(y)}{p_+(y)} \geq \left(\frac{\mu + \chi y}{\mu + y}\right) (1 - \varepsilon) \geq 1 + \delta'
\]

for some constant \( \delta' > 0 \) when \( \varepsilon \) is sufficiently small.

Given Condition 12, a drift argument implies that the largest species quickly decreases to half the population size.

Lemma 14. If Condition 12 holds, then the expected time until the largest species has size at most \( \mu/2 \) is \( O(\mu^2 + n) \).

Proof. Let \( Y(t) \) denote the size of the largest species at time \( t \). We consider the drift with respect to the distance function \( h(y) := y + (n/\mu)e^{-\kappa(y - \mu)} \), where \( \kappa := \ln(1+\delta) \) over the interval \( y \in [\mu/2, \mu] \). The total distance is \( h(\mu) - h(\mu/2) = O(\mu + n/\mu) \), hence, we need to prove that the drift of the process \( h(Y(t)) \) is \( \Omega(1/\mu) \).

We first bound the drift of \( Y(t) \).

Case 1: \( Y(t) = \mu \). Since \( Y(t + 1) \leq \mu \), the drift in this case is

\[
E(Y(t) - Y(t + 1) | Y(t) = \mu) \geq 0.
\]

Case 2: \( \mu/2 < Y(t) < \mu \). By [10], the drift in this case is

\[
E(Y(t) - Y(t + 1) | Y(t) = y, \mu/2 < y < \mu)
= p_-(y) - p_+(y) > \delta p_-(y) = \Omega(1/\mu).
\]

Consider the drift according to \( g(y) := (n/\mu)e^{-\kappa(y - \mu)} \).

Case 1: \( Y(t) = \mu \). By [10],

\[
E(g(Y(t)) - g(Y(t + 1)) | Y(t) = \mu) = \Omega(1/n)(n/\mu)(1 - e^{-\kappa}) = \Omega(1/\mu).
\]

Case 2: \( \mu/2 < Y(t) < \mu \). By [10], \( p_+(y)e^{\kappa} \leq p_-(y) \). The drift with respect to \( g \) is therefore

\[
E(g(Y(t)) - g(Y(t + 1)) | \mu/2 < Y(t) < \mu)
= p_+(y)(g(y) - g(y + 1)) + p_-(y)(g(y) - g(y - 1))
= (n/\mu)e^{-\kappa(y - \mu + 1)} (e^{\kappa} - 1) (p_-(y) - p_+(y)e^{\kappa}) > 0.
\]

The drift is always \( \Omega(1/\mu) \), and the theorem follows.
After the population diversity has increased sufficiently on the plateau, an optimal solution can be produced with the right combination of crossover and mutation. This is captured by the following lemma.

**Lemma 15.** Consider a population $P$ on the Jump$_k$ plateau ($f(x) = n - k$ for all $x \in P$). We partition $P$ into species. For any constant $0 < c < 1$, if the largest species has size at most $c\mu$, then the optimal solution is created by uniform crossover followed by mutation with probability $\Omega((\chi/n)^{k-1})$ assuming the mutation rate is $\chi/n = \Theta(1/n)$.

**Proof.** Since the size of the largest species is no larger than $c\mu$, the probability that two distinct parents are selected for crossover is $\Omega(1)$. For the remainder of the proof, we assume that two parents $x$ and $y$ are selected with $x \neq y$.

Let $2d > 0$ denote the Hamming distance between $x$ and $y$. Then $x$ and $y$ have $d$ 1s among the $2d$ bits that differ between parents and $n - k - d$ 1s outside this area. Assume that crossover sets exactly $i$ out of these $2d$ bits to 1, which happens with probability $\binom{2d}{i}2^{-2d} \left(\frac{X}{n}\right)^{k+d-i} \left(1 - \frac{X}{n}\right)^{n-k-d+i} = \Omega((\chi/n)^{k-1})$

where we bound the sum by dropping all but the last term ($i = 2d$) and use $4^{-d} \geq \frac{1}{4} \left(\frac{X}{n}\right)^{d-1}$, since $d > 0$ and we take $n$ to be large enough.

We are now in a position to complete the run time analysis of the algorithm. By Lemma 2 and Lemma 14, we quickly reach a diverse population on the plateau. From this configuration, there is a sufficiently high probability that before the diversity is lost the algorithm has crossed over an appropriate pair of individuals and jumped to the optimum. If the diversity is lost, we can repeat the argument.

**Proof of Theorem 11.** By Lemma 2 the expected time for the entire population to reach the plateau is $O\left(n\sqrt{k\mu \log \mu}\right)$, and by Lemma 13 Condition 12 is satisfied.

Assume $c'$ sufficiently large so that $\mu \geq (c'k/x) \log(n)$ implies $(1 + \delta)^{\mu/4} \geq 4cn^{k-1} + 1$ for a constant $c$ that will be determined. We consider a phase of length $c(\mu^2 + 2n^{k-1})$ iterations and define the following three failure events.

The **first failure** occurs if within the first $c(\mu^2 + n)$ iterations the largest species has not become smaller than $\mu/2$ individuals. By Lemma 14, the expected time until less than $\mu/2$ individuals belong to the largest species is $O(\mu^2 + n)$. Hence, by Markov’s inequality, the probability of this failure is less than $1/4$ when $c$ is sufficiently large.

The **second failure** occurs if within the next $cn^{k-1}$ iterations there exists a sub-phase which starts with $\mu/2 + 1$ individuals in the largest species and ends with the largest species larger than $(3/4)\mu$ without first reducing to $\mu/2$. We call such a sub-phase a **failure**. We model the number of individuals in the largest species by a Gambler’s ruin argument [12], where, by [10], the probability of losing an individual in the largest species is at least a $(1 + \delta)$-factor larger than the probability of winning such an individual. From standard results about
the Gambler’s ruin process \cite{12}, the probability that a sub-phase is a failure is
\( \delta /((1 + \delta)^{\mu/4} - 1) \). By a union bound, the probability that any of the at most \( cn^{k-1} \) sub-phases is a failure is no more than \( cn^{k-1}/((1 + \delta)^{\mu/4} - 1) < 1/4 \).

The third failure occurs if the optimum is not found during a sub-phase of length \( cn^{k-1} \) iterations where the largest species is always smaller than \((3/4)\mu\) individuals. In this configuration, two individuals with Hamming distance at least \( 2 \) are selected with probability at least \( (3/4)^{-1} \).

Hence, the probability of obtaining the optimum from two such individuals is \( \Omega(1/n^{k-1}) \). By Lemma 15, the probability of not obtaining the optimum during the sub-phase of length \( cn^{k-1} \) is \( (1 - \Omega(1/n^{k-1}))^{cn^{k-1}} \leq 1/4 \) for sufficiently large \( c \).

By a union bound, given a sufficiently large constant \( c > 0 \), the probability that none of the failures occur and the optimum is found within a phase of length \( cl(\mu^2 + 2n^{k-1}) \) iterations is at least \( 1/4 \). Therefore, the expected number of phases until the optimum is found is no more than \( 4 \).

\[ \square \]

5 Reinforced diversity

The aim of this section is to analyse how different tie-breaking rules in line 11 of Algorithm 1 affect further the population diversity and the expected time to optimise the function.

We first consider diversity mechanisms that correspond to tie-breaking rules that try to promote having unique individuals in the population either by explicitly eliminating duplicates or by enforcing selection to occur between parent and offspring, who are more likely to be non-unique.

5.1 Duplicate elimination

In this setting, we consider the \((\mu+1)\) GA using duplicate elimination as a tie-breaking mechanism that operates as follows. When breaking ties on the lowest-fitness individual in line 11 of Algorithm 1, if there are no duplicates among the least-fit individuals, one is chosen at random to remove. Otherwise, we always choose one so that the number of duplicated strings decreases.

**Theorem 16.** Consider the \((\mu+1)\) GA using duplicate elimination to break ties and a population size of \( \mu < k(n-k)/2 \). The expected optimisation time on Jump\(_k\) with \( k = o(n) \) is \( O(\mu^2 n + n \log n + n^{k-1}) \) if \( p_c = 1 - \Omega(1) \) and \( O(\mu n (\sqrt{k} \log \mu + \mu) + n \sqrt{k} \log n + n^{k-1}) \) if \( p_c = \Omega(1) \).

**Proof.** We assume all individuals in the population are at the plateau. Let \( 0 < c < 1 \) be an arbitrary constant. We argue that after \( O(\mu^2 n) \) generations in expectation, there are at most \( c\mu \) duplicates in the population. A **duplicate pair** is a pair \((x, y)\) such that \( x = y \). For all \( z \in \{0, 1\}^n \), we define the (possibly empty) set \( S_2(z) = \{ y \in \{0, 1\}^n : f(y) = n - k \land d_H(z, y) = 2 \} \), where \( d_H \) denotes the Hamming distance. Let \( x \in P \) be conditioned on the event that every point in \( P \) is contained on the plateau. Then \( |S_2(x)| = k(n-k) \), so due to our bounds on \( \mu \), \( |S_2(x) \cap P| \geq k(n-k)/2 \).

If there are duplicates in the population, a new plateau point can be generated as follows. First, select a duplicate pair \( x, x' \) as parents and perform crossover to obtain \( x'' \). Obviously \( x = x' = x'' \). Now, mutation flips exactly two
specific bits of $x''$ to create one of the points in $S_2(x'') \setminus P$. We call such a mutation a novel mutation. The probability for any novel mutation on $x''$ is at least

$$\frac{1}{n^2} \left(1 - \frac{1}{n}\right)^{n-2} \mid S_2(x'') \setminus P \mid \geq \frac{1}{n^2} \frac{k(n - k)}{2e} = \Omega(1/n).$$

As long as there are at least $c\mu$ duplicates, the probability of choosing a duplicate pair for parents can be bounded as follows. Consider a partition of the population at time $t$ such that each partition contains all copies of a particular string. Let $s_1 \geq s_2 \geq \cdots \geq s_a \geq 1$ denote the sequence of partition sizes. Let $l^* = \max\{i : s_i > 1\}$. If $\sum_{i=1}^{l^*} s_i \geq c\mu$, then the number of duplicate pairs is at least

$$\sum_{i=1}^{l^*} \frac{s_i}{2} \geq \frac{1}{2} \sum_{i=1}^{l^*} s_i \geq c\mu/2.$$

Therefore, under the condition that there are at least $c\mu$ duplicates, the probability that a duplicate pair is selected for recombination is at least $(c\mu/2)/(\mu^2) = \Omega(1/\mu)$.

If a novel mutation occurs in the offspring, then it will be accepted and, consequently, a duplicate will be removed from the population. The number of duplicates cannot increase. Moreover, it decreases in each generation with probability $\Omega(1/(\mu n))$. Hence, the expected waiting time until all but $c\mu$ duplicates have been removed from the plateau is $O(\mu^2 n)$.

After this time, we maintain the invariant that the size of the largest equivalence class cannot be higher than $c\mu$. Thus, in each subsequent generation, the probability of generating the optimal string is bounded from below by Lemma 15. The expected number of generations until the optimal string appears in the population after this point is thus $O(n^{k-1})$.

The expected number of generations to reach the optimum from the plateau is then $O(\mu^2 n + n^{k-1})$, and the results follow by taking into account the time for the population to reach the plateau in first place, i.e., by Lemma 2 for $p_c = \Omega(1)$ and Lemma 3 for $p_c = 1 - \Omega(1)$ (and here by noting that $\mu \log \mu$ is first subsumed into $O(\mu n)$ and later $O(\mu^2 n)$ since $\mu = \text{poly}(n)$).

\section{5.2 Duplicate minimisation}

Duplicate minimisation is similar to duplicate elimination, except that, when breaking ties, we do not choose an arbitrary duplicate but an individual that has the highest number of duplicates.

\textbf{Theorem 17.} Consider the $(\mu+1)$ GA using duplicate minimisation to break ties, and a population size of $\mu < k(n - k)/2$. The expected optimisation time on $\text{Jump}_k$ with $k = o(n)$ is $O((\mu n + n \log n + n^{k-1})$ if $p_c = 1 - \Omega(1)$ and $O\left(\mu n \sqrt{k} \log \mu + n \sqrt{k} \log n + n^{k-1}\right)$ if $p_c = \Omega(1)$.

\textbf{Proof.} The proof is identical to the proof of Theorem 16 except how we handle the initial gain of diversity on the plateau. In the case of duplicate minimisation, we have the extra property that the size of the largest species cannot increase over time. Hence, we only have to wait until the size of the largest species is at most $c\mu$ (instead of the entire duplicate count, as with duplicate elimination).
This saves us an extra $\mu$-factor in the waiting time to reach a point where we can apply Lemma 15.

Again, we assume that the entire population has already reached the plateau. Let $X_t$ be the count of duplicates in the population at time $t$. Let $Y_t$ denote the size of the largest species, that is, the cardinality of the largest species in the population at time $t$. Let $x$ be the offspring generated at time $t$. If $x$ belongs to one of the partitions of size $Y_t$, then the size of one of these partitions is temporarily increased before survival selection, but then duplicate minimisation ensures $Y_{t+1} = Y_t$ since one of the members of the partition of size $Y_t + 1$ is removed uniformly at random. In every other case, the size of the largest partition stays the same or decreases.

Thus, we only must wait until $Y_t \leq c\mu$ to apply Lemma 15. In each iteration, $X_t$ is decreased by one if a novel point is created. As stated in the proof of Theorem 16, the probability of a novel mutation given a duplicate pair for parents is $\Omega(1/n)$. Conditional on $Y_t > c\mu$, the probability of selecting a duplicate pair and subsequently creating a novel offspring is at least $\left(\frac{Y_t}{2}\right)/(\binom{n}{2}) > \left(\frac{n}{2}\right)/(\binom{n}{2}) = \Omega(1/n)$.

Let $(\hat{X}_t)_{t \geq 0}$ be the stochastic process defined by

$$\hat{X}_t = \begin{cases} X_t & \text{if } Y_t > c\mu, \\ 0 & \text{otherwise}. \end{cases}$$

Since $\hat{X}_t - \hat{X}_{t+1} \geq 0$ and decreases by at least one with probability $\Omega(1/n)$, the waiting time until $Y_t \leq c\mu$ is $O(\mu n)$. From this point and beyond, the size of the largest species is at most $c\mu$ and the proof is completed by applying Lemma 15 then Lemma 16 for $p_c = \Omega(1)$ and Lemma 18 for $p_c = 1 - \Omega(1)$.

5.3 Deterministic crowding

We consider deterministic crowding as described in [13]. In effect, this tie-breaking rule always chooses a parent individual of the current offspring for removal in the selection phase (in particular, the offspring always survives if it is not worse than its parents). Thus, if offspring and parent have the same fitness, for mutation, the parent is always removed; for crossover, one parent uniformly chosen at random is removed.

**Theorem 18.** Consider the $(\mu+1)$ GA with $p_c = k/n$. Suppose that ties in the selection procedure are handled by deterministic crowding. Then the expected number of iterations until an optimal individual is created when running on Jump$_k$, $k = \omega(\sqrt{n})$, is $O(\mu n + n \log n + \mu \log \mu + n e^{5k} \mu^{k+2})$.

**Proof.** According to Lemma 16 after $O(\mu n + n \log n + \mu \log \mu)$ rounds, all individuals are on the plateau.

The remaining part of this proof follows the ideas presented in the one from Theorem 7 of [20]. We want to make sure that we end up having two individuals that do not have a 0 in common and that these get chosen for crossover that succeeds in creating the optimum.

---

1In this proof, we set $p_c = k/n$ instead of bounding it only from above. This corrects an error that appears in the proof of Theorem 7 of [20], in which the reciprocal of the crossover probability erroneously does not appear in the run time bound.
This process is divided into two phases. Phase 1 considers the probability of mutating two individuals such that they end up sharing no 0. Phase 2 then considers the probability of a crossover to occur that chooses the two individuals of phase 1. The phases are, too, separated into several events that are sufficient for the desired outcome.

Phase 1 lasts \( n \) rounds without any crossover and should generate two different individuals that do not share a single 0. Phase 2 goes on for \( n/k \) rounds and should generate the optimum. Therefore, a harmful mutation, i.e., one that changes at least one of the two designated individuals, must not occur.

We start off with phase 1 and decompose this phase into the events E1–E5.

**E1:** The event that no crossover occurs in \( n \) rounds. Its probability is 
\[
(1 - p_c)^n \geq (1 - k/n)^n \geq e^{-k(1 - o(1))}.
\]

**E2:** The event, conditional on E1, that there are at least \( k \) mutations during phase 1 that flip two bits such that a 1-bit and a 0-bit get flipped. Note that an individual generated this way is on the plateau.

A single such mutation happens with probability 
\[
q := k/n \cdot (n-k)/n \cdot (1 - 1/n)^{n-2} \geq k/n \cdot 3^{-1} \text{ if } n \text{ is large enough.}
\]
Trivially, \( q \leq k/n \) holds.

The probability of E2 happening is therefore at least
\[
\binom{n}{k} q^k (1 - q)^{n-k} \geq \frac{n^k}{k^k} \left( \frac{k}{n} \cdot \frac{1}{3} \right)^k \left( 1 - \frac{k}{n} \right)^{n-k} \geq 3^{-k} \left( 1 - \frac{k}{n} \right)^{\left( \frac{3}{2} - 1 \right)k} \geq (3e)^{-k}.
\]

**E3:** The event, conditional on E1, that any mutation that creates a new individual on the plateau does so by just flipping a single 0 (and of course a single 1), i.e., it is unlikely that at least two 0s get flipped, the probability of which would be at most \( \frac{k^2}{n} \cdot 1/n^2 \leq k^2/n^2 \).

The probability of this never happening during phase 1 and, thus, the probability of E3 is therefore bounded by
\[
\left( 1 - \frac{k^2}{n^2} \right)^n \geq 1 - O \left( \frac{k^2}{n} \right)^k = o\left( \frac{1}{\sqrt{n}} \right) \geq 1 - o(1).
\]

**E4:** The event, conditional on E1, E2, and E3, that two designated individuals get chosen for the \( k \) mutations. In the end, these individuals should be the ones chosen for crossover. The probability of choosing the correct individuals for mutation is at least \( (2/\mu)^k \).

Our tie-breaking rule is deterministic crowding, so the offspring will always survive because the parent will be removed. Hence, the probability for E4 is at least \( (2/\mu)^k \).

**E5:** The event, conditional on E1 through E4, that the two individuals from E4 actually drift apart such that, in the end, they do not share any of their 0s. To do so, the individuals must increase their Hamming distance to one another by 2. Let \( i \) denotes the number of 0-bits that do not have to be
mutated anymore. This probability is at least

\[ \prod_{i=1}^{k-1} \left( \frac{k-i}{k} \cdot \frac{n-k-i}{n-k} \right) \geq \left( \frac{n-2k}{n-k} \right)^{k-1} \prod_{i=1}^{k-1} \frac{k-i}{k} \]

\[ \geq \left( 1 - \frac{k}{n-k} \right)^{k-1} \cdot \frac{(k-1)!}{k^{k-1}} \]

\[ \geq \left( 1 - \frac{k^2}{n-k} \right) \cdot \frac{(k-1)!}{k^k} \geq e^{-k} \cdot (1 - o(1)) \cdot \left( \frac{2}{e} \right)^k \geq e^{-k} \cdot (1 - o(1)) \cdot \left( \frac{2}{e} \right)^k \]

We now focus on phase 2 and condition on the events E1 through E5.

**E6:** The event that during the next \( n/k \) rounds no accepting mutation occurs and that at least one crossover choosing the correct two individuals is performed.

We first consider the mutations that could be harmful. Note that for such a mutation it is necessary to flip at least one 0-bit. Thus, we calculate the probability that during each mutation none of the \( k \) 0s of any individual get flipped. The probability of this happening is at least \( (1 - k/n) \cdot \left( \frac{2}{e} \right)^k \geq e^{-1} \cdot (1 - o(1)) \).

We now look at the crossover. The probability of at least one crossover choosing the two correct individuals is at least \( (1 - (1 - p_c)^{n/k}) \cdot \left( \frac{1}{\mu^2} \right)^k \geq (1 - e^{-1})/\mu^2 \geq e^{-1} \cdot \mu^{-2} \). The probability that the crossover creates the optimum is \( 2^{-2k} \cdot 1/n^k \geq 2^{-2k} \cdot e^{-1} \). All in all, the probability of E6 is at least \( e^{-3} \cdot 2^{-2k} \cdot e^{-1} \cdot \mu^{-2} \).

The probability of all of the events E1 through E6 happening is thus at least \( \Omega(e^{-5k} \cdot \mu^{-k-2}) \), and the length of such an event is \( n + n/k = O(n) \). Hence, the expected time to create the optimum, once the plateau is reached, is in \( O\left(ne^{5k} \cdot \mu^{k+2}\right) \).

If we have \( \mu \leq n/k \), then it is possible for the population to be perfectly spread, i.e., any two individuals do not share a position with a 0. We will see that this state is obtained quickly with the next three diversity mechanisms. Once any two individuals do not share a position with a 0, every crossover operation has a probability of \( 4^{-k} \) to generate the optimum.

### 5.4 Convex-hull maximisation

Given two bit strings \( x, y \in \{0, 1\}^n \), uniform crossover can produce any bit string \( z \) such that, for all \( i \leq n \), \( z_i \in \{x_i, y_i\} \); in this sense, any such \( z \) is in between \( x \) and \( y \). Accordingly one can define the convex hull of a set \( P \subseteq \{0, 1\}^n \) as the set of all those bit strings which are producible with repeated application of uniform crossover. In this sense, evolutionary search with crossover means searching the convex hull of the population \( \{x \} \).

Thus, it makes sense to consider a tie-breaking rule which maximises the size of this convex hull. Since the size of the convex hull of a set \( P \) of bit strings is determined by the number of positions \( i \) for which there is an \( x \in P \) with \( x_i = 0 \) and a \( y \in P \) with \( y_i = 1 \), we can formalize this tie-breaking rule as follows. Given a population \( P \) of bit strings with worst fitness, remove an individual
$z \in P$ such that 
\[ \sum_{i=1}^{n} [\exists x, y \in P \setminus \{z\} : x_i = 0 \land y_i = 1] \]
is maximised, where $[B]$ denotes the Iverson bracket (indicator function) for a proposition $B$.

**Theorem 19.** Consider the $(\mu+1)$ GA with $\mu \leq n/k$ and $p_c = 1 - \Omega(1) > 0$. Suppose that ties in the selection procedure are handled by maximising the convex hull. Then the expected number of iterations until an optimal individual is created when running on $\text{Jump}_k$, $k \leq n/2$, is $O(\mu n^2 \log n + 4k p^{-1}_c)$.

**Proof.** First, we determine the time needed until all individuals are on the plateau. By Lemma 3, this is $O(\mu n + n \log n + \mu \log \mu)$. Note that $\mu \log \mu$ gets dominated by $\mu n$ because we bound $\mu$ by a polynomial in $n$.

The rest of this proof is similar to the one of Theorem 3 in [14]. We first introduce some terms that come in handy for the rest of the proof.

We define bad 0s as 0s at a bit position such that there exists another individual having a 0 at that same position. We do not want to have such 0s, because they contradict our goal of all individuals ultimately having their 0s at unique positions.

Analogously we define a good 1 as a 1 at a bit position such that there exists no individual that has a 0 at that same position. We call such a position good as well. During mutation, good 1s can be used to turn into 0s that no other individual has.

We proceed via drift analysis and define our potential $h$ to be the number of good positions. Let $h'$ denote the potential after one iteration of the algorithm, and let $A$ denote the event that $h' < h$. Note that $h'$ cannot increase as each good position decreases the value of the convex hull by one, thus decreasing the convex hull if we end up with more good positions than before. Hence, we can easily estimate

\[ E[h - h' | h] \geq E[h - h' | h, A] \Pr(A | h) \geq \Pr(A | h) . \]

We decompose the analysis of $\Pr(A | h)$ into four smaller events.

**E1:** The event to choose an individual with a bad 0 for mutation. If total diversity has not been reached, there is at least one individual having a bad 0. Thus, the probability of E1 is at least $1/\mu \cdot (1 - p_c)$.

**E2:** The event that the mutation flips exactly one 0 and exactly one 1 (hence, the mutated individual is on the plateau). Note that E2 does not focus on the 0 being a bad one and the 1 being a good one. The probability of any two-bit-flip mutation is $k/n \cdot (n-k)/n \cdot (1 - 1/n)^{n-2}$.

**E3:** The event, conditional on E1 and E2, to choose a bad 0 for mutation. The probability to do so is at least $1/k$.

**E4:** The event, conditional on E1 and E2, to choose a good 1. Due to the definition of $h$, the probability of E4 is $h/(n-k)$.

Taking all of this together, we get that the probability of $A$, given $h$, is at least

\[ \frac{1 - p_c}{\mu} \cdot \frac{1}{n} \cdot \frac{h}{n} \cdot \left(1 - \frac{1}{n}\right)^{n-2} = \Omega\left(\frac{h}{\mu n^2}\right) . \]
Using the multiplicative drift theorem [10], we get a run time of $O(\mu n^2 \log n)$ until reaching maximal diversity.

At last, time needed to perform crossover after reaching maximum diversity takes expected $p_c^{-1}$ rounds. Since all two different individuals have no 0s in common, such a crossover is successful with probability $1/2^{2k}$. This results in an overall waiting time of $4^k p_c^{-1}$ in the end. □

5.5 Total Hamming distance

In the section before we looked at the maximisation of the convex hull of a population $P$. The convex hull operator only looks, per position, for two individuals having different bits at said position.

A more thorough operator can take all the bits per individual into account to give a more detailed view on the diversity of $P$. Such an operator is the one maximising the total Hamming distance of all individuals in $P$.

For any set of bit strings $P$, we let

$$g(P) = \sum_{x \in P} \sum_{y \in P} d_H(x, y)$$

be the total Hamming distance of $P$. We consider the tie-breaking rule which, given a population $P$, removes an individual $z \in P$ such that $g(P \setminus \{z\})$ is maximised.

**Theorem 20.** Consider the $(\mu+1)$ GA with $\mu < n/(2k)$ with $p_c = 1 - \Omega(1) > 0$. Suppose that ties in the selection procedure are handled by maximising total Hamming distance. Then the expected number of iterations until an optimal individual is created when running on Jump$_k$, $k \leq n/8$, is $O(n \log n + \mu^2 kn \log(\mu k) + 4^k p_c^{-1})$.

**Proof.** This proof is similar to the one of Theorem 19 and uses the same terms of bad 0s and good 1s.

Using Lemma 3, all individuals are on the plateau within $O(\mu n + n \log n + \mu \log \mu)$ steps. The $\mu \log \mu$ term is dominated by $\mu n$ because of our bound on $\mu$.

The remaining analysis is, again, done via a drift argument. Note that the maximum of $g(P)$ is $2k\mu(\mu - 1)$; thus, we let our potential function $h$ be $2k\mu(\mu - 1) - g(P)$ and show that this potential reaches 0.

The initial potential is at most $2k\mu(\mu - 1)$ and $h$ cannot increase, due to the selection operator always choosing an individual to discard such that the total Hamming distance is not decreased.

As before, let $h'$ denote the potential after a mutation and let $A$ denote the event that the potential decreased. We have $E(h - h' \mid h) \geq \Pr(A \mid h)$. Again, we decompose $\Pr(A \mid h)$.

**E1:** The event that an individual having a bad 0 is chosen for mutation. Each bad 0 adds at most $2(\mu - 1)$ to $h$. Since each individual can have up to $k$ bad 0s, there are at least $h/(2k(\mu - 1))$ individuals having at least one bad 0. The probability of E1 is therefore at least $h/(2k\mu(\mu - 1)) \cdot (1 - p_c)$.

**E2:** The event that mutation creates an individual on the plateau by flipping a 0- and a 1-bit. The probability of E2 is thus at least $k/n \cdot (n - k)/n \cdot (1 - 1/n)^{\mu - 2}$.
E3: The event, conditioned on E1 and E2, to choose a bad 0 during mutation. The respective probability is at least $1/k$.

E4: The event, conditioned on E1 and E2, to choose a good 1 during mutation. We pessimistically assume that the total Hamming distance ($= 2k\mu(\mu - 1) - h$) divided by $(\mu - 1)$ is the number of 1s that are no longer good because each good 1 adds $(\mu - 1)$ to the total Hamming distance. The mutation must choose one of the remaining good 1s. Thus, the probability of E4 is at least

$$\frac{n - k - \frac{2k\mu(\mu - 1) - h}{\mu - 1}}{n - k} = \frac{n + \frac{h}{\mu - 1} - k(2\mu + 1)}{n - k}.$$ 

Note that the numerator is always nonnegative for $\mu < n/(2k)$. Because we need $\mu \geq 3$, it follows that $k \leq n/8$.

Overall, the probability of A is at least

$$\frac{h(1 - p_c)}{2k\mu(\mu - 1)} \cdot \frac{1}{n} \cdot \frac{n + \frac{h}{\mu - 1} - k(2\mu + 1)}{n} \cdot \left(1 - \frac{1}{n}\right)^{-2} \geq \frac{h(1 - p_c)}{2\mu^2kn} \cdot \left(1 + \frac{h}{\mu - 1} - \frac{2\mu + 1}{n}k\right) \cdot \left(1 - \frac{1}{n}\right)^{-2} \geq \frac{h(1 - p_c)}{2\mu^2kn} \cdot e^{-1},$$

which is positive as long as maximal diversity ($h = 0$) has not been reached. Note that this is our desired drift and that $1 - p_c = \Omega(1) > 0$.

We can now bound the expected time until maximal diversity has been reached by using the multiplicative drift theorem [10]. This yields an expected number of rounds in $O(\mu^2kn \log(\mu k))$.

Now all that is left is that a crossover is performed that generates the optimum. Again, the expected number of steps for this event is $4^k p_c^{-1}$. This completes the proof.

5.6 Fitness sharing

We consider a tie-breaking rule that makes use of fitness sharing as described in [13] rather than how it is used in [26]. The actual fitness $f(x)$ of an individual $x$ gets skewed by how similar it is with respect to a certain measure $d$ to other individuals. The new shared fitness $\bar{f}(x)$ is the basis of the tie-breaking mechanism, where we just delete one individual with worst shared fitness.

The general scheme of the fitness sharing mechanism is parameterised with a metric $d$ and two numbers $\alpha$ and $\sigma$. Given a population $P$ of individuals with worst fitness, we want to remove an individual $z \in P$ such that

$$\sum_{x \in P \setminus \{z\}} \frac{f(x)}{\sum_{y \in P \setminus \{z\}} \max \left\{0, 1 - \left(\frac{d(x, y)}{\sigma}\right)^\alpha\right\}}$$

is maximised. That means that there is a penalty for the similarity of $x$ to all other individuals $y$ up to a distance of $\sigma$; $\alpha$ determines the shape of the penalty.

In this paper, we consider the Hamming distance, i.e., $d = d_H$, and we set $\alpha = 1$, that is, we have a linear penalty. Note that we only use this fitness sharing rule for breaking ties (this ensures that the initial climb to the plateau is undisturbed). We call this tie-breaking rule Hamming fitness sharing.
Lemma 21. Given a population $P$ of individuals all having the same fitness; suppose that any two individuals of $P$ differ by at most $\sigma$. Then the Hamming fitness sharing tie-breaking rule maximises the total Hamming distance of $P$.

Proof. Since all individuals $x \in P$ have the same fitness, we can ignore the impact of the fitness on the tie-breaking rule. Furthermore, since individuals can differ by at most $\sigma$, the maximum in the fitness sharing expression is not necessary. So we want to remove an individual $z \in P$ such that

$$\sum_{x \in P \setminus \{z\}} \left( \sum_{y \in P \setminus \{z\}} \left( 1 - \frac{d_H(x,y)}{\sigma} \right) \right)^{-1}$$

is maximised. That is the same as minimising the term $\sum_{x \in P \setminus \{z\}} \sum_{y \in P \setminus \{z\}} d_H(x,y)$ since we just change the monotony and remove the offset of $\sum_{y \in P \setminus \{z\}} 1$ and the common factor $1/\sigma$; this is just the same as maximising the total Hamming distance of $P$.

Thanks to this lemma, we now know that Hamming fitness sharing and maximising the Hamming distance are equivalent. Thus, we can immediately carry over all run time results from the maximisation of the Hamming distance to fitness sharing, as stated in the following theorem.

Theorem 22. Consider the $(\mu+1)$ GA with $\mu < n/(2k)$ with $p_c = 1 - \Omega(1) > 0$. Suppose that ties in the selection procedure are handled by Hamming fitness sharing with $\sigma \geq 2k$. Then the expected number of iterations until an optimal individual is created when running on Jump$_k$, $k \leq n/8$, is $O(n \log n + \mu^2 kn \log(\mu k) + 4^k p_c^{-1})$.

Proof. The time needed to reach the plateau is by Lemma 3 in $O(\mu n + n \log n + \mu \log \mu)$. As we bound $\mu$ by a polynomial in $n$, the $\mu \log \mu$ term is dominated by $\mu n$.

After reaching the plateau, Lemma 21 yields that on the plateau Hamming fitness sharing is just maximisation of total Hamming distance. Thus, the statement follows from the proof of Theorem 20.

5.7 Island model

An easy way to ensure diversity in a population is to keep different parts strictly separate. Previous results [23] have shown that island models can provide enough diversity that can be subsequently leveraged by crossover. We consider a single-receiver island model, described in [32], as follows. We have $\mu+1$ islands, $\mu$ of them running a (1+1) EA independently from one another. Furthermore, there is one island which is the receiver island. Each iteration, it chooses two of the $\mu$ islands uniformly at random, copies their respective best-so-far individuals, and then performs uniform crossover on those, hence $p_c = 1$. The resulting offspring replaces the resident individual if it has higher fitness. We say that the island model succeeds if the receiver island produces the optimum. We do not employ any particular tie-breaking rule on the islands (and, in the case of a tie, choose a survivor uniformly at random).

Theorem 23. Consider the island model with $p_c = 1$, $\mu = O(n^c)$ islands for any $c$, and $\mu \geq 2$. For optimizing Jump$_k$, $k = o(\sqrt{n}/\mu)$, the expected run time until the optimum is produced is $O(n \log n + \mu^2 kn + \mu^2 4^k)$.
Proof. In this proof, we follow the same language as in the proof of Theorem 19.

In expectation, after \( O(n \log n^d) \) steps, for a constant \( d > 0 \), a single \((1+1)\) EA is on the plateau with probability \( 1 - 1/n^d \). Hence, the probability of \( \mu \) independently running \((1+1)\) EAs being all on the plateau after \( O(n \log n^d) \) steps is \((1 - 1/n^d)^\mu\), which goes toward 1 as \( n \) goes to infinity, because of our constraint on \( \mu \) and because we can choose \( d > c \).

Once all \((1+1)\) EAs are on the plateau, we proceed via drift analysis: we define a potential for the island model and show that there is a bias toward 0. Fix two islands under consideration. The potential \( X_t \) at point \( t \) (starting from the plateau) is defined as follows: it is 0 if the receiver island produced the optimum. If not, we have a look at the individuals of the two fixed islands. Assume that these individuals have \( i \leq k \) of their 0s in common. \( X_t \) is then \( i \mu^2 n e^2 + \mu^2 4^k e \).

The drift is the expected change in potential, i.e., \( \text{E}(X_t - X_{t+1} | X_t) \). We make a case distinction to whether the potential decreases or increases. In order to compute the drift, we assume \( X_t > 0 \) to be given. Let \( i \) be such that \( X_t = i \mu^2 n e^2 + \mu^2 4^k e \).

First, we consider \( i > 0 \). Whenever the potential decreases, it decreases by at least \( \mu^2 n e^2 \).

We now lower-bound the probability of the potential decreasing, i.e., the two individuals increase their Hamming distance: we assume that only one individual flips a bad 0 and a good 1 and that our two individuals are chosen. No other bits are mutated. Therefore, the probability is at least
\[
\frac{2}{\mu^2} \left(1 - \frac{1}{n}\right)^{n-2} \frac{n - 2(k - i) - i}{n} \frac{1}{n} \left(1 - \frac{1}{n}\right)^{n} \geq \frac{1}{\mu^2 n e^2}.
\]
Thus, the overall positive drift is at least 1.

If we now consider \( i = 0 \), we easily get a positive drift of at least 1 as well, since then all that is left to create the optimum is to have the uniform crossover always choose the correct bits of the \( 2k \) positions where the two individuals differ and not mutating any bit after crossover, resulting in a probability of at least \( 1/(\mu^2 4^k e) \).

We now upper-bound the negative drift. We only consider the case that \( i \) increases by 1. An increase by more than 1 is possible but far more unlikely since more bit flips have to occur, leading to an additional factor of \( 1/n^2 \) in the probability for each additional 1. We make up for the so lost terms by multiplying our negative drift with a constant \( c \).

The change in potential conditioned on a decrease as we defined it is \(-\mu^2 n e^2\), and the probability of such a decrease is at most \( ck^2/n^2\): each of the two individuals can only decrease the distance to the other one by flipping one of its own 0s and flipping a 1 where the other individual has a 0. The absolute value of the negative drift is thus at most \( c(\mu k e)^2/n \). Using our assumption regarding \( k \), this results in a negative drift in \( o(1) \). The additive drift theorem \([16]\) hence yields an expected run time of \( O(\mu^2 k n + \mu^2 4^k) \) when starting from the plateau. Taking the time needed for all islands to be on the plateau into account, we get the desired run time of \( O(n \log n + \mu^2 k n + \mu^2 4^k) \). \( \square \)
6 Experiments

Since the theoretical results presented in the previous section are asymptotic and they only provide upper bounds on the run time of the algorithms, we also implemented the $(\mu + 1)$ GA with the different diversity mechanisms and conducted experiments on Jump$_k$ for various values of $k$, $n$, and $p_m$.

In each tested setting of the algorithm and the function, the run is replicated 100 times with different random seeds. The number of function evaluations, denoted ‘# evaluations’, is reported as the run time. The population size is set to $\mu = c \ln n$, in which $c$ is chosen so that $\mu$ is not too small for some small $n$, i.e., $c = 4e$.

6.1 Impact of crossover and mutation rates

Figure 1 (a) and (b) depict the performance of the GA ($p_c = 1.0$) compared to the algorithm using only mutation ($p_c = 0.0$) under the same setting ($p_m = 1/n$). The range of $n$ in this experiment is set to $n = [50 \ldots 300]$ with a step size of 10, and $k$ is in $\{2, 3\}$. Even with these small values of $k$ and $n$, a strong reduction of the average run time can be observed, up to a multiplicative factor of $10^4$.

The impact of the jump length $k$ on the run time is illustrated in Figure 2 (a). The experiment was set with $n$ in $[100 \ldots 5000]$ (with a step size of 100) and $k$ is in $\{3, 4, 5\}$. We notice that the increase of $k$ does not imply a large change in the average run time. The average run time seems to still scale linearly with $n$ in this setting even for $k = 4$. By fixing $k = 3$, we also experimented with different mutation rates, i.e., $p_m$ in $\{0.9/n, 1/n, 1.1/n, 2/n\}$. The results are displayed in Figure 2 (b). We notice that the mutation rates above $1/n$ reduce the average run time while a slightly lower mutation rate increases it.
considerably. With mutation rate $2/n$, the average run time and the stability of the runs are distinctively improved.

On the other hand, an excessive increase of the mutation rate may deteriorate the average run time because of the likelihood of multiple bit flips which imply harmful mutations. This can be observed in the experiment depicted in Figure 3 (in log-scale) for $n = 500$. In this experiment, $k$ is in {2, 3, 4}, and the range of $\chi = p_m \cdot n$ is set to [0.6...8] (with a step size of 0.1). We note that the more $k$ is increased, the stronger the negative effect of high mutation rates can be noticed. Moreover, too low mutation rates are also bad for the run time. This can be related to our theoretical analysis, in which a low mutation rate could have made the random walk associated with the size of the largest species biased toward the wrong direction. This may lead to the reduction of the population diversity and the loss of benefit from crossover.

6.2 Impact of diversity mechanisms

Full crossover is enabled ($p_c = 1.0$), the problem size $n$ is varied in [100, 1000] (with a step size of 25), and the standard mutation rate ($p_m = 1/n$) is used. In each tested setting, the run is replicated 100 times with different random seeds and the number of function evaluations, denoted as ‘# evaluations’, is reported as the run time. The result for $k = 4$ is shown in Figure 4.

On average, the highest contribution to the reduction of the run time in order is fitness sharing, then convex hull maximisation, deterministic crowding, and, finally, duplicate elimination and minimisation have quite similar average run times. We also notice that the the island model with $\mu = 2$ requires approximately the same average number of evaluations as deterministic crowding. Overall, compared to the standard ($\mu+1$) GA, all the diversity mechanisms con-
Figure 3: Impact of different mutation rates \( p_m = \chi/n \) with crossover for problem size 500.

Contribute to the reduction of the average run time, as well as to the stability of the result. In addition, we also compare the diversity mechanisms to the high mutation rate setting \( p_m = 2.6/n \) (the best choice for \( n = 500 \) and \( k = 4 \), suggested by Figure 3) of the \((\mu+1)\) GA. The high mutation rate setting is able to perform better than four diversity mechanisms and it is only less efficient than convex hull maximisation and fitness sharing.

7 Conclusion

A rigorous analysis of the \((\mu+1)\) GA has been presented showing how the use of, first, only crossover and mutation and, second, the use of diversity mechanisms considerably speeds up the run time for Jump\(_k\) compared to algorithms using mutation only.

With regard to the first setting, traditionally it has been believed that crossover may be useful only if sufficient diversity is readily available and that the emergence of diversity in the population is due to either mutation alone or should be enforced by the introduction of diversity mechanisms [13, 29]. Indeed, previous work highlighting that crossover may be beneficial for Jump\(_k\) used unrealistically low crossover probabilities to allow mutation alone to create sufficient diversity. Conversely, our analysis shows that the interplay between crossover and mutation on the plateau of local optima of the Jump\(_k\) function quickly leads to a burst of diversity that is then exploited by both operators to reach the global optimum. The right balance between the amount of mutation
and crossover impacts the run time considerably.

While mutation rates lower than the standard $1/n$ rate considerably increase the expected run time, rates that are slightly higher than $1/n$ lead to improved performance. These rates also depend on the presence of crossover. For instance, for $k = 4$, the best rate for a mutation-only algorithm is $4/n$ while the best rate for the $(\mu+1)$ GA with $p_c = 1$ is considerably lower than $4/n$ and higher than $1/n$. Our experiments also reveal that the expected run time of the $(\mu+1)$ GA does not increase considerably with the increase of the gap length $k$. Hence, it is an open problem to provide tighter bounds on the expected run time than those presented in this paper.

Second, we have considered the role of selection-based diversity mechanisms used together with crossover for escaping local optima. We prove rigorous upper bounds on the run time of the $(\mu+1)$ GA for seven well-known diversity mechanisms optimising the Jump$_k$ function. Our results reveal a qualitative difference in the ability of the different diversity mechanisms to escape local optima.

In contrast to previous theoretical work on crossover for Jump$_k$, our upper bounds do not rely on unreasonably small (e.g., vanishing with $n$) crossover probabilities but instead cover the more practical case of constant crossover probabilities. Furthermore, our proofs provide insight into the ways that di-

Figure 4: Performance of the diversity mechanisms for jump length 4, the mutation rate $p_m$ is set to $1/n$ unless specified.
versity mechanisms, when applied as a tie-breaking rule in selection, can quickly spread the population out over the Jump plateau in order to get enough diversity for crossover to combine the correct solution components to escape the set of local optima.

Acknowledgements

The research leading to these results has received funding from the European Union Seventh Framework Programme (FP7/2007-2013) under grant agreement no. 618091 (SAGE) and from the EPSRC under grant no. EP/M004252/1. This research benefitted from Dagstuhl seminar 16011 “Evolution and Computing” and is based upon work from COST Action CA15140 ‘Improving Applicability of Nature-Inspired Optimisation by Joining Theory and Practice (ImAppNIO)’ supported by COST (European Cooperation in Science and Technology).

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