

TRIBHUVAN UNIVERSITY INSTITUTE OF ENGINEERING PULCHOWK CAMPUS

A
REPORT
ON
GENETIC ALGORITHM
FOR
IMAGE EVOLUTION

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Acknowledgments

We would like to express our sincere gratitude to our Artificial Intelligence teacher, **Asst. Prof. Basanta Joshi, Ph.D.**, for his invaluable guidance and support throughout this study. His insightful lectures and expertise have greatly enhanced our understanding of artificial intelligence.

We also extend our heartfelt appreciation to our AI lab instructor, for his continuous assistance and practical demonstrations, which have been instrumental in bridging the gap between theoretical concepts and hands-on implementation

Abstract

Genetic Algorithms (GAs) are population-based optimization techniques inspired by the principles of natural selection and evolution. This report explores the theoretical foundations and practical implementation of GAs, focusing on their ability to efficiently search large solution spaces. The study examines key GA components, including selection, crossover, and mutation, and their role in guiding the evolutionary process. A particular emphasis is placed on hyperplane sampling and implicit parallelism, which enable GAs to explore multiple regions of the search space simultaneously. Furthermore, selection mechanisms such as tournament selection and fitness-proportionate selection are evaluated.

In addition to theoretical exploration, the report presents a practical application through the **Chaotic Canvas** project, which applies GAs for image evolution. The project demonstrates how random initial populations of images evolve over successive generations to closely resemble a target image, using genetic operators and adaptive mutation strategies. The report concludes by discussing the effectiveness of GAs in creative problem-solving tasks, supported by empirical results from the project.

Keywords: Genetic Algorithm, Evolutionary Computation, Selection Mechanisms, Crossover, Mutation, Hyperplane Sampling, Implicit Parallelism, Schema Theorem, Optimization, Search Space

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1. Introduction

1.1 Background

Genetic Algorithms (GAs) are inspired by the principles of natural selection and evolution, a concept formalized by Charles Darwin's theory of evolution. According to Darwin, individuals with traits best suited to their environment have a higher chance of survival and reproduction, passing their genetic information to the next generation. Over multiple generations, beneficial traits become more prevalent in a population.

In biological evolution, the fundamental unit of inheritance is the gene, which exists in different forms called alleles. Each individual has a unique combination of alleles that determine their traits. Similarly, in GAs, a candidate solution, reffered to as 'genotype'[1] or, alternatively as 'chromosome'[2] consists of a sequence of genes (variables), where each gene can take on multiple values (alleles). The genetic diversity of a population influences its ability to adapt and explore the solution space effectively.

GAs, first proposed by John Holland in the 1970s[1], simulate this evolutionary process in computational search and optimization problems. A population of candidate solutions evolves through selection, crossover, and mutation, mimicking the processes observed in natural selection. High-fitness individuals contribute more offspring, ensuring that beneficial traits propagate while maintaining genetic diversity through mutation.

The genetic search space of a GA can be visualized as an L-dimensional hypercube, where each chromosome represents a point. Genetic operations partition this space into hyperplanes, influencing how efficiently the algorithm explores different regions. This brings us to the concept of hyperplane sampling and implicit parallelism, which explains why GAs can process multiple solutions effectively in parallel.

1.2 Problem Statement

Optimization problems often involve navigating vast and complex search spaces to find an optimal or near-optimal solution. Traditional deterministic search methods can be inefficient or impractical, particularly when dealing with nonlinear, multimodal, or high-dimensional problems.

The challenge addressed in this study is to design an efficient and flexible optimization technique capable of evolving solutions over time. Specifically, this report investigates the application of Genetic Algorithms (GAs) to evolve random images into recognizable target images, demonstrating their effectiveness in solving complex optimization tasks.

2. Literature Review

2.1 Hyperplane Sampling in Genetic Algorithms

Genetic Algorithms (GAs) explore the solution space by implicitly processing multiple hyperplanes simultaneously. A hyperplane represents a subset of the search space where certain bit positions in a chromosome remain fixed while others are free to vary. The ability of GAs to sample multiple hyperplanes efficiently is fundamental to their effectiveness in optimization problems.

2.1.1 Hypercube Representation and Search Space

The search space in a Genetic Algorithm is structured as an L-dimensional hypercube, where each chromosome of length L represents a vertex in this space. Each bit position in a chromosome corresponds to a coordinate axis in the hypercube, and adjacent vertices differ by a single bit. This structure allows the genetic operations of selection, crossover, and mutation to navigate the search space systematically[3].

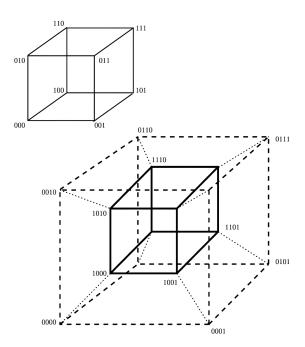


Figure 2.1: A visualization of an L-dimensional hypercube, where each vertex represents a chromosome in the genetic algorithm search space.

2.1.2 Schemata and Their Role in Search

A schema (plural: schemata) is a generalized representation of a set of solutions, using the wildcard symbol '*' to indicate bit positions that can take any value. Each schema corresponds to a hyperplane in the search space.

For example, in a 4-bit chromosome system:

- The schema 1 * 0 * represents the set $\{1000, 1001, 1100, 1101\}$.
- The schema **11 represents the set $\{0011, 0111, 1011, 1111\}$.

According to the **Holland Schema Theorem**, schemata with high fitness values tend to propagate across generations, leading to an increased presence in the population. This process enables the genetic algorithm to focus on promising regions of the search space.

2.1.3 Mathematical Model of Hyperplane Sampling

The expected number of chromosomes belonging to a schema H in the next generation is given by:

$$M(H,t+1) \approx M(H,t) \cdot \frac{f(H)}{\bar{f}} \cdot (1-p_m)^{O(H)}$$
(2.1)

where:

- M(H,t) is the number of chromosomes belonging to schema H at generation t.
- f(H) is the average fitness of schema H.
- \bar{f} is the average fitness of the entire population.
- p_m is the mutation probability.
- O(H) is the order of the schema, defined as the number of fixed positions.

This equation shows that schemata with above-average fitness and lower disruption by mutation will be more likely to propagate across generations.

2.1.4 The Role of Selection, Crossover, and Mutation

Hyperplane sampling is influenced by the three fundamental genetic operators:

- Selection: Increases the representation of high-fitness schemata in the next generation.
- Crossover: Combines segments from parent chromosomes, potentially preserving beneficial schemata while introducing diversity.
- Mutation: Introduces small random changes that can disrupt or create new schemata, balancing exploration and exploitation.

2.1.5 Implicit Parallelism in Genetic Algorithms

One of the most significant advantages of hyperplane sampling is that GAs implicitly process multiple schemata in parallel. Since each chromosome belongs to multiple overlapping schemata, evaluating a single chromosome provides information about multiple hyperplanes. Over generations, this parallel evaluation allows the algorithm to identify and reinforce beneficial patterns without explicitly searching each solution.

2.1.6 How Recombination Moves Through a Hypercube

Recombination in genetic algorithms can be visualized as movement through an L-dimensional hypercube, where each chromosome represents a vertex, and crossover defines paths between them. In a single-point crossover, offspring are generated by swapping genetic material at a single crossover point, which limits movement along predefined edges of the hypercube. This method minimizes schema disruption but restricts exploration. In contrast, uniform crossover allows broader movement across the hypercube by independently inheriting each bit from either parent. While this increases genetic diversity, it also causes higher schema disruption. The trade-off between exploration and exploitation determines the efficiency of genetic algorithms in refining solutions.

Figure 2.2 illustrates how recombination navigates a 4-dimensional hypercube. The dashed lines represent possible offspring paths when performing 1-point crossover between two parent chromosomes, such as 1111 and 0000.

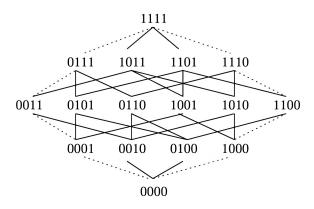


Figure 2.2: Illustration of crossover paths in a 4-dimensional hypercube.

2.2 Mutation and Hill-Climbing in Genetic Algorithms

Mutation plays a crucial role in genetic algorithms (GAs) by introducing random modifications to chromosomes, helping maintain genetic diversity and preventing premature convergence to local optima. Hill-climbing, on the other hand, enhances the refinement of solutions by

iteratively making small improvements to an individual's fitness. The interplay between mutation and hill-climbing determines the balance between exploration and exploitation.

2.2.1 Role of Mutation in Genetic Search

Mutation is often modeled as a stochastic process where each gene in a chromosome undergoes a bit-flip with a probability p_m . The expected number of mutations per chromosome of length L is given by:

$$E_m = Lp_m. (2.2)$$

For effective search, the mutation rate p_m should be neither too high nor too low. Heinz Mühlenbein proposed an optimal mutation rate proportional to chromosome length:

$$p_m = \frac{c}{L},\tag{2.3}$$

where c is a constant that varies depending on problem complexity.

Mutation prevents GAs from getting trapped in local optima by introducing variability. However, excessive mutation disrupts beneficial schemata, reducing the effectiveness of selection and crossover.

2.2.2 Hill-Climbing Strategies in Genetic Algorithms

Hill-climbing in GAs refers to local refinement mechanisms that enhance the fitness of solutions by making small, deterministic changes. A common approach is the *one-bit hill-climbing* method, where each bit flip is accepted if it improves fitness:

$$F(x') \ge F(x),\tag{2.4}$$

where x is the original solution, x' is the mutated solution, and F(x) represents the fitness function.

Hill-climbing can be integrated into a GA using:

- 1. **Hybrid Approaches:** Applying local search techniques after crossover and mutation.
- 2. Adaptive Mutation: Increasing mutation rates near local optima to facilitate escape.
- 3. Elitism and Selection Pressure: Retaining high-fitness individuals while refining suboptimal ones.

2.2.3 Balancing Exploration and Exploitation

The efficiency of a GA depends on its ability to balance global exploration (mutation-driven search) and local exploitation (hill-climbing strategies). This balance is often quantified using

an adaptive mutation scheme:

$$p_m(t) = \alpha e^{-\beta t},\tag{2.5}$$

where α and β are problem-dependent parameters and t represents the generation number.

3. Related Theory

3.1 Basic Components of Genetic Algorithm

A Genetic Algorithm consists of the following components:

• **Population:** A set of candidate solutions (chromosomes). Each chromosome consists of genes, and each gene can take on different values (alleles).

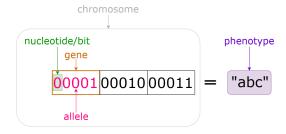


Figure 3.1: Representation of Genes, Alleles, and Phenotype Mapping

- **Selection:** Individuals with higher fitness are chosen for reproduction, ensuring the survival of beneficial traits.
- Crossover (Recombination): Two parent chromosomes exchange segments, creating offspring with mixed genetic information.

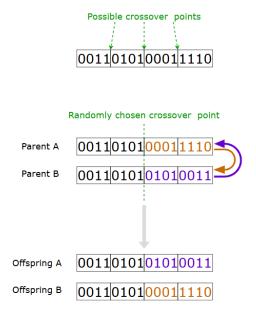


Figure 3.2: Crossover of two parents

- Mutation: A gene in a chromosome is randomly altered, allowing new alleles to appear in the population. This prevents premature convergence.
- **Fitness Function:** A function that evaluates how well a chromosome performs in the given problem domain.

In classical GAs, binary encoding is common, where each gene is either 0 or 1. However, real-valued and multi-allelic representations are also used in more complex problems. The allelic diversity of a population affects its ability to escape local optima and efficiently explore the search space.

3.2 Mathematical Representation

Each chromosome is a bit string of length L:

$$C = (c_1, c_2, ..., c_L), \quad c_i \in \{0, 1\}$$
 (3.1)

The total search space consists of 2^L possible solutions, forming an L-dimensional hypercube. The probability of selecting a chromosome C_i is given by:

$$P(C_i) = \frac{f(C_i)}{\sum_j f(C_j)} \tag{3.2}$$

where $f(C_i)$ is the fitness function.

Crossover occurs at a randomly chosen point p:

$$C_{child1} = (c_1, ..., c_p, c'_{p+1}, ..., c'_L)$$
(3.3)

Mutation flips a bit with probability p_m :

$$c_i' = \begin{cases} 1 - c_i, & \text{with probability } p_m \\ c_i, & \text{otherwise} \end{cases}$$
 (3.4)

3.3 Implicit Parallelism and Hyperplane Sampling

A population of N chromosomes does not just evaluate N solutions but implicitly processes a large number of schemata. A chromosome of length L belongs to L different hyperplanes, contributing to an efficient parallel search. This phenomenon allows GAs to explore multiple regions of the search space simultaneously.

3.4 Selection Methods

Selection is a fundamental component of evolutionary algorithms that mimics natural selection by preferentially choosing fitter individuals for reproduction. This process creates selection pressure that guides the population toward regions of higher fitness in the search space [4]. Selection methods must balance exploitation of promising solutions with sufficient exploration to maintain genetic diversity [5]. The following subsections detail two prominent selection mechanisms utilized in genetic algorithms.

3.4.1 Roulette Wheel Selection

Roulette wheel selection, also known as fitness proportionate selection, allocates selection probability proportional to an individual's fitness relative to the population. This method conceptually resembles a roulette wheel where each individual occupies a segment proportional to its fitness.

Given a population of n individuals, the probability p_i of selecting individual i with fitness f_i is defined as:

$$p_i = \frac{f_i}{\sum_{j=1}^n f_j} \tag{3.5}$$

This establishes a direct relationship between fitness and selection probability. Implementation generally involves normalizing fitness values, calculating cumulative probabilities, generating a random number $r \in [0,1]$, and selecting the individual whose cumulative probability first exceeds r.

While intuitive and straightforward, roulette wheel selection exhibits limitations including selection pressure reduction in later generations as fitness values converge, and challenges with minimization problems requiring fitness transformation.

3.4.2 Tournament Selection

Tournament Selection[6] is a widely used method in genetic algorithms that selects individuals based on direct competition. Instead of assigning selection probability based on fitness proportion, this method randomly samples a subset (tournament) from the population and selects the best individual from that subset. This process balances exploitation and exploration by adjusting tournament size and selection probability.

Given a population of size n, the process follows these steps:

- 1. Random Sampling: Select t individuals randomly from the population.
- 2. Competition: Compare the fitness values of the selected individuals.
- 3. Selection: The fittest individual from the tournament is chosen for reproduction.

The probability that an individual i with fitness f_i is selected depends on its rank within the tournament rather than absolute fitness. If individuals are ranked in ascending order of fitness, the probability of selecting the best one is determined by:

$$P(i) = s \cdot (1 - s)^{r-1}$$

where:

- s is the selection probability of the best individual in the tournament.
- r is the rank of individual i in the tournament.

The expected number of times an individual i appears in the next generation can be approximated as:

$$E(\text{copies}_i) = n \cdot P(i)$$

where P(i) is the probability of selection in a tournament, and n is the population size.

3.4.3 Remainder Stochastic Sampling

Remainder stochastic sampling, an enhanced version of stochastic universal sampling, combines deterministic and probabilistic selection to improve sampling accuracy while maintaining appropriate selection pressure.

The method proceeds through two phases:

1. **Deterministic Selection**: Each individual i is first allocated a selection count based on the integer portion of its expected count e_i , calculated as:

$$e_i = \frac{f_i}{\bar{f}} = \frac{n \cdot f_i}{\sum_{j=1}^n f_j} \tag{3.6}$$

where \bar{f} is the average population fitness. This integer component guarantees a minimum selection count for high-fitness individuals.

2. Stochastic Selection: The fractional remainder of e_i is then used in a secondary selection process, typically employing stochastic sampling with replacement or placing remainders on a modified roulette wheel for additional selections until the required population size is achieved.

Mathematically, if $\lfloor e_i \rfloor$ represents the integer part of e_i and $e_i - \lfloor e_i \rfloor$ the fractional part, the total expected number of copies of individual i is:

$$copies_{i} = \lfloor e_{i} \rfloor + \begin{cases} 1, & \text{with probability } e_{i} - \lfloor e_{i} \rfloor \\ 0, & \text{with probability } 1 - (e_{i} - \lfloor e_{i} \rfloor) \end{cases}$$
(3.7)

This method provides several advantages: reduced selection variance, improved sampling accuracy, and preservation of expected selection counts. Consequently, remainder stochastic sampling typically demonstrates superior performance in maintaining appropriate selection pressure compared to standard roulette wheel selection [4].

4. Methodology

Methodology for implementing a Genetic Algorithm (GA), inspired by natural selection principles. The process involves encoding potential solutions, evolving them through selection, crossover, and mutation, and iterating towards optimal solutions.

4.1 Planning and Representation

Define how potential solutions are encoded:

- Chromosome Structure: Decide on the representation of solutions (e.g., binary strings, real numbers).
- Gene Definition: Determine the smallest unit of the chromosome affecting traits.
- Fitness Function: Establish a function to evaluate solution quality.

4.2 Parameter Initialization

Set key parameters influencing the GA's performance:

- Population Size: Number of individuals per generation.
- Mutation Rate: Probability of gene alteration.
- Crossover Rate: Likelihood of parent genes combining.
- **Termination Criteria:** Conditions to end the algorithm (e.g., number of generations, satisfactory fitness level).

4.3 Initial Population Generation

Create the initial set of potential solutions, ensuring diversity to explore various regions of the solution space.

4.4 Fitness Evaluation

Assess each individual's fitness using the predefined function, guiding the selection process.

4.5 Selection Process

Choose individuals for reproduction based on fitness, employing strategies like:

- Roulette Wheel Selection: Probability proportional to fitness.
- Tournament Selection: Randomly selected subsets compete for selection.

4.6 Crossover (Recombination)

Combine genetic material from selected parents to produce offspring:

- Single-Point Crossover: Exchange segments at a chosen point.
- Multi-Point Crossover: Exchange segments at multiple points.
- Uniform Crossover: Randomly decide gene inheritance from either parent.

4.7 Mutation

Introduce random gene alterations to maintain genetic diversity and prevent premature convergence.

4.8 Population Replacement

Form a new generation by replacing the old population with offspring, possibly retaining some high-fitness individuals.

4.9 Termination

Repeat the process until termination criteria are met, then select the best-performing individual as the solution.

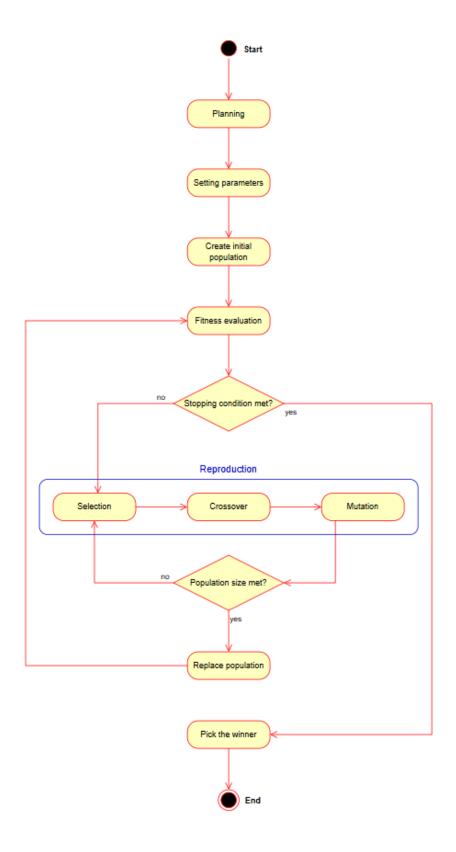


Figure 4.1: Flowchart of Genetic algorithm

5. Genetic Algorithm Image Evolution

5.1 Overview of Chaotic Canvas Project

The Chaotic Canvas project serves as a practical implementation of genetic algorithms specifically tailored to the domain of image evolution. The primary goal of this system is to gradually transform a population of initially random images so that, over multiple iterations, they progressively resemble a predefined target image. This transformation is achieved by applying fundamental genetic operations—namely, selection, crossover, and mutation—across successive generations. By iteratively improving the fitness of individuals within the population, the project demonstrates how biologically-inspired computation can be harnessed for creative problem-solving.

5.2 Evolutionary Strategy and Workflow

The methodology begins with the generation of a population consisting of entirely random images. Each image, referred to as an individual, is encoded as a set of geometric shapes—specifically polygons—with associated attributes such as position, size, and color. As the genetic algorithm proceeds through generations, individuals undergo evaluation and reproduction. The algorithm continuously applies selection, recombination, and mutation operations, ensuring that over time the population as a whole converges toward an optimal solution: an image that closely mirrors the target.

5.3 Core Components Applied in Chaotic Canvas

5.3.1 Population Initialization

In the initial stage, a population of images is generated randomly. Each image is represented internally as a collection of polygons, where each polygon is defined by a set of vertices (points) and a specific RGBA color value. The randomness of this initial population ensures diversity, providing the algorithm with a wide variety of potential genetic material to explore during the search process.

```
// Individual represents a candidate solution in the genetic
    algorithm

type Individual struct {
    Fitness float64
    Image *image.RGBA
    Polygons [] Polygon
}

// Polygon represents a colored polygon

type Polygon struct {
    Points [] image.Point
    Color color.RGBA
}
```

Listing 5.1: Definition of the Individual struct

5.3.2 Fitness Evaluation Mechanism

The fitness function is central to guiding the evolutionary process. In the Chaotic Canvas project, fitness is quantitatively evaluated by comparing each candidate image against the target image. This comparison is conducted using pixel-wise difference calculations, often leveraging a metric such as mean squared error (MSE). The lower the cumulative difference between the candidate and target images, the higher the individual's fitness score. This numerical value effectively determines an individual's likelihood of contributing to future generations.

```
// CalculateFitness calculates the fitness using parallel processing
func (ind *Individual) CalculateFitness(targetImage *image.RGBA) {
   bounds := targetImage.Bounds()
   width, height := bounds.Dx(), bounds.Dy()
   numGoroutines := runtime.GOMAXPROCS(0)

   // Divide work into chunks
   rowsPerGoroutine := height / numGoroutines
   differences := make([]float64, numGoroutines)
   var wg sync.WaitGroup

for i := 0; i < numGoroutines; i++ {</pre>
```

```
wg.Add(1)
        startY := i * rowsPerGoroutine
        endY := startY + rowsPerGoroutine
        if i == numGoroutines-1 {
            endY = height
        }
        go func(startY, endY, idx int) {
            defer wg.Done()
            differences[idx] = calculateRegionFitness(ind.Image,
               targetImage, startY, endY)
        }(startY, endY, i)
    }
    wg.Wait()
    // Sum up all differences
    var totalDifference float64
    for _, diff := range differences {
        totalDifference += diff
    }
    ind.Fitness = totalDifference / float64(width*height)
}
```

Listing 5.2: Fitness function

5.3.3 Selection Strategy

Selection is employed to probabilistically favor individuals exhibiting higher fitness. The Chaotic Canvas project utilizes the tournament selection method, wherein small groups of individuals are sampled randomly from the population, and the individual with the best fitness within each group is selected for reproduction. This approach strikes a balance between preserving high-quality solutions and maintaining genetic diversity, as weaker individuals still retain a small chance of being selected.

5.3.4 Recombination through Crossover

Following selection, pairs of parent individuals undergo crossover operations to generate offspring. The project implements two primary crossover techniques: blend crossover and

crossover point. Blend crossover involves creating new individuals by interpolating pixel values between parents, while crossover point divides parent images either horizontally or vertically, combining sections from both parents. These methods ensure that beneficial traits from parent images are combined in various ways, increasing the likelihood of producing improved offspring.

```
// blendCrossover performs a blend crossover operation between two
  parent individuals.
// It creates two children by interpolating pixel values between
  parents using a random alpha value.
func blendCrossover(parent1, parent2 *Individual) (*Individual, *
   Individual) {
    child1 := &Individual{
        Fitness: math.Inf(1),
                 image.NewRGBA(parent1.Image.Bounds()),
        Image:
    }
    child2 := &Individual{
        Fitness: math.Inf(1),
               image.NewRGBA(parent1.Image.Bounds()),
    }
    bounds := child1.Image.Bounds()
    height := bounds.Dy()
    numGoroutines := runtime.GOMAXPROCS(0)
    var wg sync.WaitGroup
    // Process image in parallel strips
    rowsPerGoroutine := height / numGoroutines
    for i := 0; i < numGoroutines; i++ {</pre>
        wg. Add (1)
        go func(startY, endY int) {
            defer wg.Done()
            blendAlpha := rand.Float64()
            bounds := child1.Image.Bounds()
            for y := startY; y < endY; y++ {</pre>
                i := y * child1. Image. Stride
                for x := 0; x < bounds.Dx(); x++ {
                     idx := i + x*4
```

```
Process both children in the same loop
                    for j := 0; j < 4; j++ {
                        p1 := float64(parent1.Image.Pix[idx+j])
                        p2 := float64(parent2.Image.Pix[idx+j])
                         child1.Image.Pix[idx+j] = uint8(p1*(1-
                            blendAlpha) + p2*blendAlpha)
                         child2.Image.Pix[idx+j] = uint8(p1*
                            blendAlpha + p2*(1-blendAlpha))
                    }
                }
            }
        }(i*rowsPerGoroutine, (i+1)*rowsPerGoroutine)
    }
    wg.Wait()
    return child1, child2
}
```

Listing 5.3: Blend Crossover

5.3.5 Diversity through Mutation

To prevent premature convergence and to continuously explore new areas of the solution space, mutation operations are introduced. Mutations in this context involve random alterations to the properties of polygons, such as repositioning vertices or adjusting color attributes. This stochastic process maintains diversity within the population, preventing the algorithm from becoming trapped in local optima.

5.4 Computational Considerations and Parallel Processing

Given the computational intensity of evaluating and evolving large populations over many generations, the project incorporates parallel processing strategies. Specifically, the population is divided into manageable batches, allowing genetic operations on different subsets of the population to be executed concurrently. This parallelization significantly reduces execution time and allows for larger population sizes to be feasibly processed, without compromising the quality of the evolutionary process.

5.5 Implementation Details and Technical Aspects

The Chaotic Canvas project is implemented in the Go programming language. Go's inherent support for concurrency, via goroutines and channels, is leveraged to facilitate efficient parallel execution of genetic operations. The image processing tasks, including pixel manipulation and polygon drawing, are managed using appropriate libraries to ensure accurate fitness evaluation and image generation. The overall architecture is modular, with separate components handling fitness evaluation, selection, crossover, mutation, and adaptive mutation strategies.

5.6 Challenges Encountered and Design Considerations

5.6.1 Maintaining Balance between Exploration and Exploitation

A critical consideration during the project's development was tuning parameters to achieve a balance between exploration and exploitation. Excessive mutation rates can lead to a random search behavior, eroding beneficial genetic structures. Conversely, insufficient mutation or overly strong selection pressure risks rapid convergence to suboptimal solutions. Adaptive mutation strategies were employed to dynamically adjust mutation rates based on population diversity and improvement stagnation.

5.6.2 Handling Computational Overhead

Managing computational resources efficiently posed another challenge. Processing large images with complex fitness calculations is resource-intensive. To mitigate this, image sizes were optimized, and parallel processing was strategically used. Nevertheless, limitations in memory usage and CPU core availability had to be considered carefully to avoid bottlenecks or excessive execution times.

6. Results

This work explores the results of applying the Chaotic Canvas genetic algorithm to the iconic portrait of the Afghan Girl. The algorithm was run for 50,000 generations, with a population size of 500 individuals. The objective was to evolve random polygon-based images to gradually resemble the target portrait.

6.1 Comparison of Target and Evolved Image

Figure 6.1 illustrates the comparison between the original target image and the evolved result after 50,000 generations. The left side shows the target portrait, while the right side displays the most fit individual produced by the algorithm at the 50,000th generation.





Figure 6.1: Comparison between target image and evolved output at 50,000th generation.

The evolutionary process effectively reduces the visual difference between the generated image and the target. Although not perfect, the structure and dominant colors are preserved, demonstrating the ability of genetic algorithms to approximate complex visual patterns.

6.2 Intermediate Evolution Stages

Intermediate results across generations are presented in the Appendix (see Appendix A), showcasing the gradual improvement and structural refinement at different milestones.

7. Discussion & Conclusion

This report explored the principles and applications of Genetic Algorithms (GAs), emphasizing their potential in optimization problems and creative tasks. Beginning with a thorough review of foundational theories such as hyperplane sampling, schemata, and implicit parallelism, we examined how GAs efficiently navigate large search spaces by favoring high-fitness schemata while maintaining genetic diversity through crossover and mutation.

The Chaotic Canvas project provided a practical implementation of these concepts, applying GAs to the domain of image evolution. Through the process of fitness evaluation, tournament selection, adaptive mutation, and recombination, random populations were iteratively refined to resemble a target image. The results demonstrate that, even without explicit guidance, GAs can effectively approximate complex visual patterns.

Several challenges were encountered, including balancing exploration and exploitation, and optimizing computational resources. These were addressed by adaptive mutation strategies and parallel processing techniques. Nevertheless, the project highlighted the inherent trade-offs and design considerations involved in evolutionary algorithms.

In summary, Genetic Algorithms offer a robust framework for solving complex, multidimensional problems across various fields. This study reaffirms their flexibility and power, illustrating their applicability not only in technical optimization but also in creative domains such as art and design.

8. Future Works

While the current implementation of the Chaotic Canvas project successfully demonstrates the application of Genetic Algorithms (GAs) for image evolution, several areas offer opportunities for further enhancement and exploration:

8.1 Scalability Improvements

Processing larger image resolutions and more complex target images remains computationally intensive. Future work can explore optimized parallel processing techniques or GPU acceleration to improve scalability and efficiency.

8.2 Enhanced Genetic Operators

The current system employs basic crossover and mutation techniques. Investigating more advanced genetic operators, such as multi-point crossover, adaptive mutation based on fitness gradients, or hybrid methods combining evolutionary strategies with other optimization algorithms, could further improve convergence rates.

8.3 Fitness Function Refinement

While mean squared error (MSE) serves as an effective fitness evaluation metric, alternative evaluation strategies such as perceptual similarity metrics or deep learning-based loss functions may better capture structural and semantic similarity between candidate and target images.

8.4 User Interaction and Customization

Introducing user-defined parameters, such as adjustable mutation rates, polygon complexity, or fitness criteria, could make the system more interactive and applicable to a broader range of creative tasks.

8.5 Application to Other Domains

The core framework of the Chaotic Canvas project can be extended beyond image evolution to other creative and optimization challenges, such as procedural content generation, texture synthesis, or automated design optimization.

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Appendix A. Intermediate results

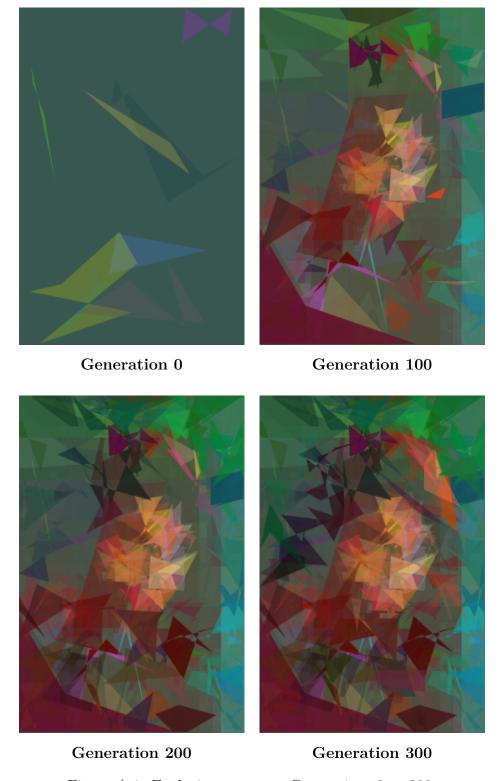


Figure A.1: Evolution progress: Generations 0 to 300.

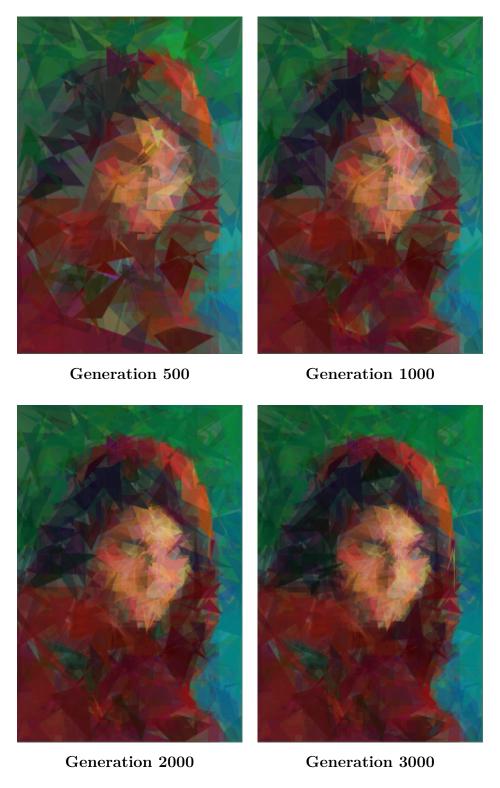


Figure A.2: Evolution progress: Generations 500 to 3000.

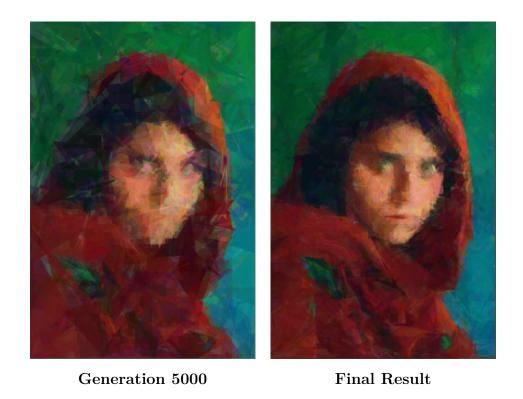


Figure A.3: Final stages: Generation 5000 and Final Evolved Image.

Appendix B. Source Code

The source code for this project is available on GitHub:

 ${\bf Chaotic\text{-}Canvas:}\ {\tt https://github.com/bishal0602/chaotic\text{-}canvas}$