Extending Evolutionary Polynomial Point Searching to the Complex Plane

Jonathan Rampersad

January 31, 2026

Abstract

This paper presents an extension to the **PolySolve** genetic algorithm, enabling the simultaneous discovery of real and complex roots for polynomials of degree n. By expanding the search space from the real number line $\mathbb{R}$ to the complex plane $\mathbb{C}$, the algorithm leverages the **Fundamental Theorem of Algebra** to find all n roots. We demonstrate that this increase in dimensionality does not degrade the accuracy of strictly real roots. The implementation utilizes an **independent component evolution** strategy for crossover and mutation, thereby *decoupling* the 2D optimization into parallel 1D subproblems and preserving the convergence characteristics of the original algorithm.

1 Introduction

Polynomial root finding is a fundamental problem in computational mathematics. While analytical solutions exist for degrees $n \leq 4$, higher-degree polynomials require numerical approximation methods. The previous iteration of PolySolve successfully applied a **Genetic Algorithm (GA)** to find roots on the real line. However, this approach is fundamentally limited by the nature of polynomials, which often possess roots with *non-zero imaginary components*.

The **Fundamental Theorem of Algebra** states that every non-zero, single-variable, degree n polynomial with complex coefficients has exactly n roots in $\mathbb{C}$ [1]. Searching strictly in $\mathbb{R}$ ignores a significant portion of the solution space. This update extends the strictly real-valued evolutionary strategy to the complex plane, denoted as $z = x + iy$.

2 Mathematical Formulation

Let $P(z)$ be a polynomial of degree n with complex coefficients c_k:

$$P(z) = \sum_{k=0}^{n} c_k z^k \tag{1}$$

We seek the set of values $\{z_j\}_{j=1}^{n}$ such that $P(z_j) = 0$.

2.1 Search Bounds (Cauchy's Bound)

To efficiently initialize the population, we must define a bounded region in the complex plane that contains all roots. We utilize **Cauchy's Bound**, which provides a disk of radius R centered at the origin [2]:

$$R = 1 + \text{max}\left(\left| \frac{c_{n-1}}{c_n} \right|, \left| \frac{c_{n-2}}{c_n} \right|, \ldots, \left| \frac{c_0}{c_n} \right| \right) \tag{2}$$

where c_n is the leading coefficient. The search space is defined as the *square region* $S = \{z \in \mathbb{C} \mid |\text{Re}(z)| \leq R, |\text{Im}(z)| \leq R\}$, ensuring uniform coverage of potential root locations.

2.2 Fitness Function

The objective is to minimize the modulus of the polynomial evaluation $|P(z)|$. We maximize a **fitness function** $F(z)$, defined as:

$$F(z) = \frac{1}{|P(z)| + \epsilon} \tag{3}$$

where $|P(z)| = \sqrt{\text{Re}(P(z))^2 + \text{Im}(P(z))^2}$ and ϵ is a small constant to prevent division by zero.

3 2D Genetic Algorithm Implementation

The transition from 1D to 2D requires adapting core evolutionary operators.

3.1 Population Initialization

The population consists of N individuals. Each individual I_k is a complex number initialized uniformly within the bounds determined by **Cauchy's Bound**:

$$\text{Re}(I_k) \sim U(-R, R), \quad \text{Im}(I_k) \sim U(-R, R)$$

3.2 Independent Component Crossover

Standard vector crossover techniques can be applied to complex numbers, but they often treat the complex number as a *strongly coupled vector*. To maintain fine-grained search capability, we employ **Independent Component Crossover**. Given parents $P_1 = x_1 + iy_1$ and $P_2 = x_2 + iy_2$, we apply the **BLX-α (Blend Crossover)** operator to the real and imaginary parts *independently*. This operator, originally designed for real-coded GAs, allows for effective exploration of interval-schemata [3, 4].

Let $x_{\text{min}} = \text{min}(x_1, x_2)$ and $x_{\text{diff}} = |x_1 - x_2|$. The range for the child's real component is:

$$[x_{\text{min}} - \alpha \cdot x_{\text{diff}}, \quad x_{\text{max}} + \alpha \cdot x_{\text{diff}}] \tag{4}$$

This creates a **rectangular probabilistic region** for offspring, allowing the algorithm to explore "off-axis" solutions effectively.

3.3 Independent Component Mutation

Mutation is similarly decoupled. For $z = x + iy$, we apply **independent Gaussian noise**:

$$x' = x \cdot (1 + \mathcal{N}(0, \sigma)) \tag{5}$$

$$y' = y \cdot (1 + \mathcal{N}(0, \sigma)) \tag{6}$$

This allows for simultaneous scaling and rotation in the complex plane.

4 Accuracy Analysis

A concern with increasing dimensionality is the potential **"curse of dimensionality,"** where the solution space becomes too sparse to search effectively. Our implementation mitigates this through **independent component processing**.

4.1 Real Root Preservation

For a strictly real root x_r, the target is $z = x_r + 0i$. Since the selection pressure drives $|P(z)| \to 0$, the imaginary component y is driven towards 0. Because mutation $y' = y(1 + \delta)$ scales with the current value, as y becomes negligible (e.g., $< 10^{-15}$), the 2D search **dynamically collapses** into a 1D search, preserving precision.

5 Conclusion

The extension of PolySolve to the complex plane represents a *robust generalization* of the underlying evolutionary strategy. By treating components as **independent genetic traits**, we avoid the pitfalls of higher dimensional sparse searching. The algorithm correctly identifies the full set of n roots for an n-th degree polynomial, fulfilling the **Fundamental Theorem of Algebra** [1] without sacrificing the precision of real-valued solutions.

References

[1] H. Derksen, *The Fundamental Theorem of Algebra and Linear Algebra*, University of California, Berkeley. [Online]. Available: https://math.berkeley.edu/~ribet/110/f03/derksen.pdf

[2] A. Setia, V. Sharma, and Y. Liu, ”Numerical method to solve Cauchy type singular integral equation with error bounds,” *AIP Conference Proceedings*, vol. 1798, no. 1, p. 020141, 2017. https://doi.org/10.1063/1.4972733

[3] L. J. Eshelman and J. D. Schaffer, ”Real-Coded Genetic Algorithms and Interval-Schemata,” *Foundations of Genetic Algorithms*, vol. 2, pp. 187-202, 1893.

[4] H. Kita, I. Ono, and S. Kobayashi, ”Theoretical Analysis of the Unimodal Normal Distribution Crossover for Real-coded Genetic Algorithms,” *Transactions of the Society of Instrument and Control Engineers*, vol. 35, no. 1333, pp. 1333–1339, 1999. https://doi.org/10.9746/sicetr1965.35.1333