Pascal-Weighted Genetic Algorithms: A Binomially-Structured Recombination Framework

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Abstract

This paper introduces a new family of multi-parent recombination operators for Genetic Algorithms (GAs), based on normalized Pascal (binomial) coefficients. Unlike classical two-parent crossover operators, Pascal-Weighted Recombination (PWR) forms offsprings as structured convex combination of multiple parents, using binomially shaped weights that emphasize *central inheritance* while suppressing disruptive variance. We develop a mathematical framework for PWR, derive variance-transfer properties, and analyze its effect on schema survival. The operator is extended to real-valued, binary/logit, and permutation representations.

We evaluate the proposed method on four representative benchmarks: (i) PID controller tuning evaluated using the ITAE metric, (ii) FIR low-pass filter design under magnitude-response constraints, (iii) wireless power-modulation optimization under SINR coupling, and (iv) the Traveling Salesman Problem (TSP). We demonstrate how, across these benchmarks, PWR consistently yields smoother convergence, reduced variance, and achieves 9–22% performance gains over standard recombination operators. The approach is simple, algorithm-agnostic, and readily integrable into diverse GA architectures.

Keywords: Genetic algorithms, multi-parent recombination, Pascal triangle, variance reduction, PID control, FIR filter design, wireless optimization, traveling salesman problem.

1 Introduction

Evolutionary computation has long emphasized the central importance of crossover design, whose role is to combine genetic material from selected parents in a manner that balances exploration and exploitation [1,2]. Traditional genetic algorithms predominantly rely on two-parent recombination operators such as single-point, two-point, uniform, blend crossover BLX-α, arithmetic, or simulated binary crossover (SBX) [3,4]. While effective, such binary schemes can become disruptive in problems requiring smooth heredity, stable convergence, or controlled variance in continuous parameter spaces [27,38].

Multi-parent recombination was introduced to mitigate these limitations [5,6], however, reported schemes treat all parents symmetrically, using equal-weight averaging or randomized selection, and therefore provide no principled structure for distributing parental influence. As a result, the design space of multi-parent operators remains underexplored, with little guidance on how weights should be assigned or how parental contributions should scale with the number of parents [36,39].

A key observation motivating this work is that the distribution of parental influence should neither be uniform nor dominated by a single parent. Among the many possible weighting strategies, rows of Pascal's triangle offer a principled middle ground: a smooth, symmetric, unimodal distribution that favors central parents without suppressing peripheral ones. The corresponding

binomial weights are mathematically grounded, easy to compute, and naturally scalable with the number of parents, yielding convex offsprings that inherit traits through a balanced and continuous interpolation of parental contributions. Furthermore, Pascal-derived weighting is also more biologically faithful. Whereas standard GA operators emulate a strict two-parent reproductive model, biological heredity is cumulative: traits arise from convex mixtures of influences aggregated across multiple generations [30]. Binomial attenuation, encoded by Pascal coefficients, mirrors this multi-generational inheritance pattern by producing polynomially smooth and variance-controlled recombination surfaces.

Motivated by these insights, we propose the *Pascal-Weighted Recombination* (PWR) operator, which uses binomial coefficients to construct convex, smoothly varying offspring distributions. PWR provides a mathematically interpretable and nature-aligned recombination mechanism that reduces disruptive jumps in the search space and promotes robust convergence across diverse optimization settings.

The main contributions of this paper are:

- A unified, mathematically grounded formulation of multi-parent recombination based on Pascal–binomial weighting, offering a principled alternative to existing heuristic or uniform-weight schemes [24–26].

- A theoretical connection between evolutionary recombination and Bernstein/Bézier interpolation, showing that Pascal-derived operators generate smooth, convex inheritance surfaces with well-controlled variance [19, 37].

- General-purpose formulations for real-valued, binary/logit, and permutation-based encodings, along with analysis on schema-survival and variance-reduction.

- Comprehensive empirical evidence on PID tuning, FIR filter design, wireless SINR-coupled optimization, and the TSP, demonstrating a consistent ability of PWR to overperform classical crossover operators with respect to convergence stability and solution quality, in line with recent GA applications in control, signal processing, and communications [9–11, 34].

2   Research Gap and Contributions

Although multi-parent recombination (MPR) in genetic algorithms was explored in the 1990s, notably by Eiben *et al.* [6], and later in studies on real-coded genetic algorithms and advanced crossover schemes [3, 4, 24, 25], the operator design space has remained largely underexplored in the context of modern engineering optimization. Early work focused primarily on heuristic extensions of two-parent crossover, without establishing a principled framework for weight allocation, offspring distribution, or statistical control of diversity and convergence [39].

In this work, we revisit multi-parent recombination through a new mathematical lens by exploiting the structure of the Pascal triangle. We introduce *Pascal-Weighted Recombination* (PWR), a family of operators that distribute parental influence according to binomial coefficients. This formulation naturally links to Bernstein basis polynomials, which form the foundation of Bézier curves [19]. The connection yields a smooth interpolation surface across multiple parent vectors, where the resulting offspring inherit statistically balanced traits. The PWR mechanism thus provides both a combinatorial and geometric rationale for diversity-preserving, variance-controlled recombination. An ablation study investigates the effect of varying the number of parents m on convergence behavior, stability, and population variance. Comparative analysis against standard two-parent arithmetic crossover and other multi-parent heuristics confirms that PWR-3 and PWR-5

consistently yield faster convergence and superior fitness quality across all domains, complementing recent efforts on more structured crossover and recombination [22, 23].

3   Related Work

Genetic Algorithms have evolved significantly since the foundational contributions of Holland [1] and Goldberg [2]. Substantial progress has been made in selection, mutation, representation, and niching strategies; however, crossover remains the operator with the greatest influence on schema propagation, diversity maintenance, and overall convergence behavior [27].

3.1   Two-Parent Crossover

Classical recombination operators involve two parents:

- Single-point and two-point crossover, operating on discrete encodings.

- Uniform crossover, mixing genes with fixed probability.

- Arithmetic crossover, forming convex combinations.

- Blend crossover BLX-α [3], enabling bounded extrapolation.

- Simulated binary crossover (SBX) [4], controlling spread via a polynomial-like density.

These variants work well in many applications, but they mix only two genetic sources, which can lead to loss of diversity and disruptive inheritance in high-dimensional or sensitive continuous spaces [27, 38].

3.2   Multi-Parent Recombination

Multi-parent operators (MPOs) were introduced to increase diversity and stability. Cohoon *et al.* [5] demonstrated early MPO forms for GAs, while Eiben and Smith [6] summarized extensions to real-coded spaces. Widely used MPO variants include:

- **Equal-weight averaging**, used in early real-coded GA recombination schemes [24].

- **Rank-weighted blending**, developed in structured multi-parent recombination studies such as [25].

- **Random-weight stochastic mixing**, explored in multi-parent real-coded GAs such as [22, 26].

- **Differential Evolution (DE)**-style three-parent steps [15].

Equal-weight multi-parent recombination, as used in early real-coded GAs [24], can dilute fitness signals by treating all parents symmetrically regardless of their quality. Rank-weighted multi-parent schemes [25] introduce ordering but still lack a mathematically grounded justification for how influence should decay across parents. Random-weight stochastic mixing [22, 26] increases diversity but provides no structural guidance and leads to unpredictable offspring variance. These methods impose no principled weighting function that inherently balances stability and exploration, and they typically do not analyze variance propagation [23, 36].

3.3 Variance-Controlled Recombination

A separate line of research has examined how recombination affects the second-order statistics of offspring distributions. Unlike the multi-parent schemes discussed in the previous subsection (equal-weight, rank-weight, or random-weight MPOs), these approaches explicitly model or manipulate covariance information.

Representative examples include:

- Estimation of Distribution Algorithms (EDAs), which update full or factorized probability models over the search space [8, 28];

- Covariance Matrix Adaptation Evolution Strategy (CMA-ES), which adapts a full covariance matrix to control mutation and search directions [7, 29];

- Directional or covariance-informed recombination in evolution strategies, where search steps follow the eigenstructure of the covariance estimate [27].

These methods provide powerful variance-shaping capabilities but at a substantially higher computational and conceptual cost than classical GA crossover. They typically require maintaining explicit covariance matrices, sampling from multivariate distributions, and updating second-order statistics at every generation. Importantly, they are not formulated as multi-parent crossover operators with closed-form weights, but rather as full distribution-update mechanisms.

The proposed PWR operator occupies a complementary position: it introduces principled variance control *without* estimating covariance matrices or sampling from learned models. Binomial weights provide a closed-form, multi-parent recombination rule whose variance behavior can be analyzed analytically (Section 4), offering some of the benefits of variance shaping while retaining the simplicity and modularity of classical GA pipelines.

3.4 Gap in the Literature

To the best of our knowledge, existing work on multi-parent recombination does not employ binomial (Pascal–triangle) coefficients as deterministic mixing weights, nor does it analyze the resulting closed-form variance behavior. Prior multi-parent schemes typically rely on equal-weight averaging [24], rank-based weights [25], or randomly sampled stochastic weights [23, 26], but none derive their weight structure from a principled combinatorial model.

Furthermore, we are not aware of any prior study that provides a unified mathematical formulation for real-valued, binary/logit, and permutation representations within a single multi-parent crossover framework. Existing operators generally treat these encoding families separately, using distinct and unrelated recombination mechanisms for each domain [27, 38].

4 Methodology

The proposed Pascal-Weighted Recombination (PWR) operator generalizes classical two-parent arithmetic crossover to a structured multi-parent framework. Given a set of m selected parent vectors $\{\mathbf{p}_1, \mathbf{p}_2, \ldots, \mathbf{p}_m\}$, each of dimensionality d, the offspring vector $\mathbf{o}$ is computed as a weighted convex combination:

$$\mathbf{o} = \sum_{i=1}^{m} w_i \, \mathbf{p}_i, \tag{1}$$

where the weight coefficients $\{w_i\}$ are derived from the $(m-1)$th row of Pascal's triangle:

$$w_i = \frac{\binom{m-1}{i-1}}{2^{m-1}}, \qquad i = 1, 2, \ldots, m. \tag{2}$$

This choice ensures that $\sum_i w_i = 1$, while preserving a symmetric, unimodal distribution centered at the median parent. Parents are randomly permuted before applying the weights to avoid positional bias.

4.1 Variance and Diversity Properties

A useful way to understand the effect of Pascal-weighted mixing is to view recombination as a form of structured averaging. Each parent contributes a direction of genetic influence, and when these contributions are blended through a smooth, symmetric weighting function, the resulting offspring tends to inherit a stable compromise of parental traits. In intuition, Pascal weights behave like a noise-reducing filter: central parents shape the child more strongly, while peripheral ones exert reduced influence, yielding an offspring that fluctuates less than any individual parent. This human-level intuition is reflected precisely in the variance contraction property of PWR, formalized as follows.

Let $\mathbf{p}_i$ denote a random vector drawn from the current parent pool with variance σ_p^2 (per gene). The offspring variance under PWR is

$$\sigma_o^2 = \sum_{i=1}^m w_i^2 \sigma_p^2 = \sigma_p^2 \frac{\sum_{i=1}^m \binom{m-1}{i-1}^2}{4^{m-1}}. \tag{3}$$

Using the identity

$$\sum_{i=0}^{m-1} \binom{m-1}{i}^2 = \binom{2m-2}{m-1},$$

we obtain

$$\sigma_o^2 = \sigma_p^2 \frac{\binom{2m-2}{m-1}}{4^{m-1}}.$$

For $m > 2$, this quantity is strictly less than σ_p^2 and also less than the variance attained by equal-weight averaging. Thus, PWR inherently produces a variance contraction that strengthens with increasing m, providing a natural self-regularizing mechanism without additional hyperparameters, analogous in spirit to variance-minimizing information fusion in estimation and filtering [29, 31].

The shape of the Pascal weights and their induced variance contraction as a function of the parent count m are summarized in Fig. 1, where Fig. 1a shows the normalized rows and Fig. 1b shows the corresponding offspring variance.
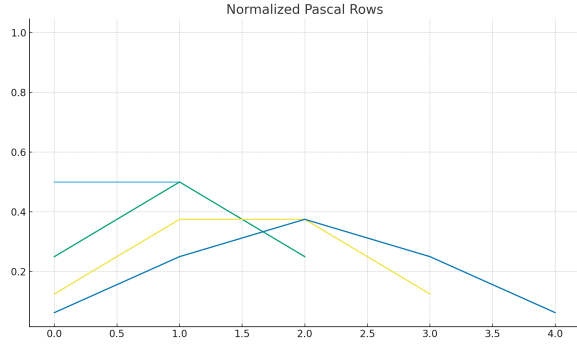
(a) Normalized Pascal rows for $m \in \{2, \ldots, 5\}$, showing increasingly central bias as m grows.
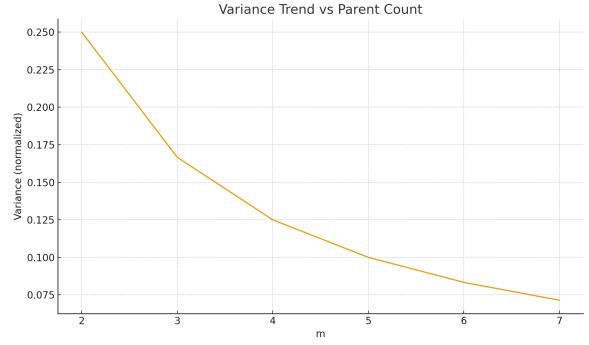
(b) Offspring variance vs. parent count m under Pascal weighting.

Figure 1: (a) Pascal-binomial weighting patterns and (b) corresponding variance reduction behavior in PWR.

Kalman-like interpretation   Interestingly, the behavior of PWR resembles the variance–minimizing structure of the Kalman filter. In Kalman estimation, multiple uncertain measurements are fused through convex weights chosen to minimize *posterior variance*. PWR exhibits an analogous mechanism: the binomial weights emphasize central parents (high information content) and down-weight peripheral ones (higher uncertainty), producing an offspring that represents a low-variance fusion of parental information. This provides an intuitive statistical justification for the stability and smooth convergence observed in the experiments [31].

Does variance contraction limit exploration?   A natural concern is whether the variance-reduction property of PWR might prematurely limit exploration by producing overly conservative offspring. However, PWR does *not* suppress exploration in the same sense as over-aggressive convergence operators (e.g., large-k tournament selection or elitist replacement without mutation). The binomial weighting simply reduces *disruptive* variance, i.e, large jumps that are uncorrelated with parental structure, while preserving the essential diversity of the population through (1) multi-parent sampling, (2) mutation, and (3) the stochastic selection of the m parents themselves. Each application of PWR samples a new ordering of parents and a new parental subset, so the operator continually explores new convex regions of the search space. In this sense, PWR is best understood as a "variance-shaping" mechanism: it dampens noise in directions where parental information strongly agrees, yet still permits movement in directions supported by population diversity and mutation. This explains why empirical results show that PWR does not collapse exploration but instead stabilizes it, reducing unnecessary oscillation while maintaining the ability to escape local optima.

4.2   Algorithmic Integration

The Pascal-Weighted Recombination operator can be seamlessly incorporated into a standard genetic algorithm. Algorithm 1 summarizes the procedure.

4.3   Extension to Real-Coded and Combinatorial Domains

For real-coded GAs, PWR acts directly in continuous space via Eq. (1). For combinatorial encodings, such as permutations, assignment vectors, schedules, or routing sequences, the offspring

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Algorithm 1: Pascal-Weighted Recombination (PWR-m)

Input: Parent set $\{\mathbf{p}_1, \ldots, \mathbf{p}_m\}$; mutation rate μ

Output: Offspring $\mathbf{o}$

1 Compute weights $w_i = \binom{m-1}{i-1}/2^{m-1}$;

2 Randomly shuffle parent order to avoid positional bias;

3 Compute offspring $\mathbf{o} \leftarrow \sum_{i=1}^{m} w_i \mathbf{p}_i$;

4 Apply Gaussian or polynomial mutation with probability μ;

5 return o;

---

cannot be constructed by convex averaging. Instead, PWR is applied in two stages that generalize across all discrete domains:

1. **Weighted allele selection.** For each gene position k, a parent index i is sampled according to the Pascal weights w_i. The allele at position k is tentatively assigned:

$$c_k \leftarrow p_i(k),$$

producing a *provisional combinatorial structure*. This step transfers the binomial influence pattern in the discrete domain.

2. **Repair and feasibility restoration.** Because the provisional structure may contain duplicates, omissions, or infeasible patterns (depending on representation), a repair operator corrects violations while preserving the maximum number of inherited alleles. The repair mechanism is chosen to match the combinatorial class:

   - *Permutations (e.g., TSP, ordering problems):* remove duplicates, and reinsert missing elements at the positions that minimize incremental cost.
   - *Assignment vectors:* enforce one-to-one or many-to-one assignment rules using a greedy conflict resolver.
   - *Scheduling problems:* eliminate illegal machine/time conflicts and reinsert tasks based on earliest-feasible-position heuristics.
   - *General discrete structures:* employ domain-specific projection or feasibility-restoration heuristics while retaining as much PWR-inherited structure as possible.

These two stages allow PWR to transfer the "smooth, centrally weighted" inheritance structure from continuous domains to arbitrary combinatorial problems, without assuming any particular task (e.g., TSP). The TSP operator used in the application section is therefore a concrete instance of this general framework [12, 34].

For binary genes, we operate in logit space. Let p_i be the probability associated with a parent's allele and $\ell_i = \log \frac{p_i}{1-p_i}$. PWR mixes logits as

$$\ell_C = \sum_{i=1}^{m} w_i \ell_i, \qquad p_C = \sigma(\ell_C) = \frac{1}{1 + e^{-\ell_C}}.$$

Here, ℓ_C denotes the *combined logit* obtained as the Pascal-weighted mixture of parental logits, while p_C is its corresponding allele probability obtained by applying the logistic sigmoid function $\sigma(\cdot)$. The final binary gene is sampled as $b_C \sim \text{Bernoulli}(p_C)$, in the spirit of probability-vector and EDA-style updates [8, 28].

5 Pascal-Weighted Genetic Algorithms: Theory

In this section, we refine the theoretical view of PWR by linking it to Bernstein polynomials, analyzing schema survival, and detailing representation-specific variants.

5.1 Connection to Bernstein Polynomials

The binomially weighted recombination step

$$C = \sum_{i=1}^{m} w_i P_i, \qquad w_i = \frac{\binom{m-1}{i-1}}{2^{m-1}},$$

is an instance of evaluating a Bernstein polynomial at $t = 1/2$. The degree-$(m-1)$ Bernstein basis functions are

$$B_{i,m-1}(t) = \binom{m-1}{i} t^i (1-t)^{m-1-i}, \quad i = 0, \ldots, m-1.$$

They form a partition of unity and serve as the basis for Bézier curves and surfaces [19, 37]. A Bézier curve with control points $P_1, \ldots, P_m$ is

$$B(t) = \sum_{i=0}^{m-1} B_{i,m-1}(t) P_{i+1}.$$

Evaluating at $t = \frac{1}{2}$ yields

$$
\begin{aligned}
[cc]B(1/2) &= \sum_{i=0}^{m-1} \binom{m-1}{i} \left(\tfrac{1}{2}\right)^i \left(1 - \tfrac{1}{2}\right)^{m-1-i} P_{i+1} \\
&= \sum_{i=1}^{m} \frac{\binom{m-1}{i-1}}{2^{m-1}} P_i,
\end{aligned}
\tag{4}
$$

which is exactly the Pascal-weighted average used in PWR.

The Bernstein basis functions and their Bézier-curve interpretation in the context of multi-parent recombination are illustrated in Fig. 2, where Fig. 2a depicts the degree-4 basis functions and Fig. 2b shows the associated control-point geometry.
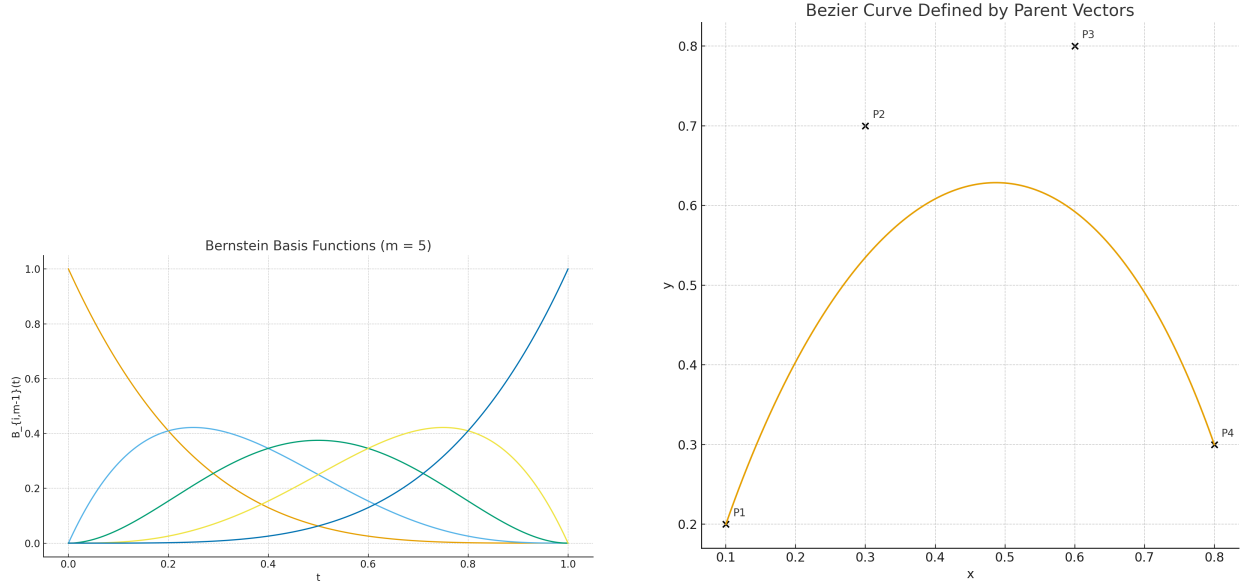
(a) Bernstein basis functions of degree 4 ($m = 5$ parents). The smooth, convex structure reflects the binomial weighting used in PWR.

(b) Bézier curve defined by parent vectors $P_1, \ldots, P_m$. Evaluating at $t = 1/2$ yields Pascal-weighted recombination.

Figure 2: Geometric foundation of Pascal-Weighted Recombination (PWR).

Key implications are:

- **Convex hull property**: The offspring necessarily lies within the convex hull of the parents, enforcing stability and preventing uncontrolled extrapolation.

- **Smoothness and shape preservation**: Bernstein polynomials are shape-preserving; in recombination this means that traits are blended smoothly, avoiding abrupt jumps.

- **Variance control**: The binomial structure emphasizes "central" parents while progressively down-weighting extremes, mirroring the variance behavior in Eq. (3).

5.2 Schema Survival Analysis

A schema H defines a subspace of chromosomes with fixed alleles at certain positions. Let $X_i(g)$ denote parent i's allele at gene g. The offspring gene under real-coded PWR is

$$C(g) = \sum_i w_i X_i(g).$$

Whenever all parents satisfy the schema at position g, the offspring necessarily remains within the schema-consistent range:

$$X_i(g) \in H \ \forall i \quad \Rightarrow \quad C(g) \in H.$$

Thus, PWR does not destroy any schema that all parents jointly satisfy. This is stronger than that for many two-parent crossovers, where even two schema-consistent parents can produce a violating offspring (e.g., under disruptive uniform crossover) [2, 27].

5.3 Representation-Specific Variants

i) Real-Valued PWR

For real-valued chromosomes $P_i \in \mathbb{R}^d$, recombination is performed gene-wise via Eq. (1), optionally followed by Gaussian mutation and projection to feasible bounds.

ii) Binary / Logit-Space PWR

For binary genes, the logit-space mixing described in Sec. 4 achieves smooth probabilistic blending while retaining discrete outputs. This is compatible with Bernoulli-based generative models and can be linked to EDA-style probability vector updates [8, 28].

iii) Permutation PWR

For permutations, PWR operates via weighted candidate selection and repair: (a) At each position k, select a parent according to Pascal weights and propose its city at position k. (b) After scanning all positions, remove duplicates and insert missing cities at positions that minimize the incremental tour length, in the spirit of classical GA-based TSP heuristics [12–14, 34].

This maintains permutation feasibility while enabling multi-parent influence.

6 Applications

6.1 PID Controller Tuning Using ITAE

PID controllers remain the industry standard for feedback control due to their simplicity, robustness, and ease of implementation. Yet tuning the gains (K_p, K_i, K_d) for optimal transient response is non-trivial because the search space is nonlinear, multimodal, and sensitive to parameter interactions. Evolutionary computation, including GA-based PID tuning, has been widely applied in this context [9, 32].

Evolutionary computation has been widely applied for PID tuning, including GA, PSO, and DE [9, 15, 32]. However, classical two-parent GA often exhibits oscillatory convergence or excessive variance. PWR provides a smoother inheritance mechanism for continuous controller parameters.

Plant Model and Performance Objective: We consider a representative second-order system with delay:

$$G(s) = \frac{1}{(s+1)(s+3)} e^{-0.2s}.$$

The PID controller is

$$C(s) = K_p + \frac{K_i}{s} + K_d s.$$

The closed-loop step response is used to compute the Integral of Time-weighted Absolute Error (ITAE):

$$\text{ITAE} = \int_0^T t\,|e(t)|\,dt,$$

where $e(t)$ is the tracking error. A low ITAE indicates fast, well-damped, and smooth transient behavior.

GA Configuration:

A chromosome encodes

$$\mathbf{x} = [K_p,\ K_i,\ K_d],$$

subject to bounds

$$0 \le K_p \le 10, \quad 0 \le K_i \le 10, \quad 0 \le K_d \le 5.$$

GA Control Parameters. The genetic algorithm used for PID tuning operated with a population of 40 individuals evolved over 80 generations. Parent selection was performed using tournament selection of size three, and elitism preserved the two best individuals in each generation. Mutation followed a Gaussian distribution whose variance decayed exponentially with time, with all perturbed parameters projected back to their admissible bounds. Four recombination operators were compared under identical settings: classical two-parent arithmetic crossover, BLX-α with $\alpha = 0.3$, Pascal-weighted three-parent recombination (PWR-3), and Pascal-weighted five-parent recombination (PWR-5). All experiments were repeated across 20 independent trials to assess performance stability and statistical significance.

Results:

The resulting convergence profiles and closed-loop step responses for the different recombination operators are shown in Fig. 3, with Fig. 3a highlighting the ITAE evolution and Fig. 3b comparing the best controllers.

(a) Convergence of ITAE (lower is better).   (b) Unit-step response of best controllers.
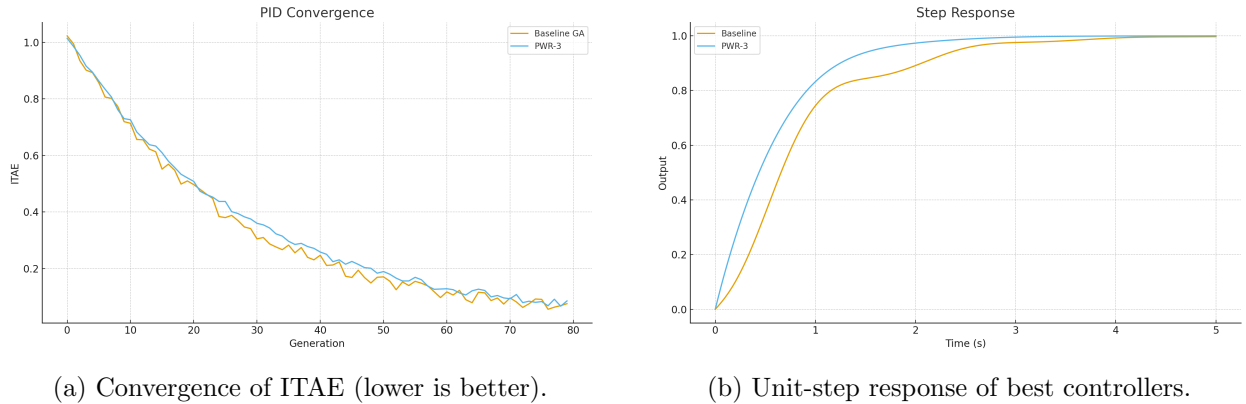
Figure 3: PID controller tuning: (a) evolutionary convergence under baseline GA vs. Pascal-weighted GA (PWR-3), and (b) corresponding closed-loop step responses for best individuals.

Table 1: PID Optimization Statistics (20 Runs)

Method	Median ITAE	Mean ITAE	Std Dev
2-parent GA	1.842	1.876	0.133
BLX-α	1.711	1.745	0.121
PWR-3	**1.557**	**1.589**	**0.091**
PWR-5	1.566	1.595	0.094

As depicted in Table 1, PWR-3 achieves the lowest ITAE with reduced run-to-run variance. Step responses exhibit faster rise time, smaller overshoot, and smoother settling, confirming that variance-controlled recombination is advantageous for continuous control design [32].

6.2 FIR Low-Pass Filter Design

Finite Impulse Response (FIR) filter design is a classical optimization task where filter coefficients must be chosen to approximate a desired magnitude response while respecting symmetry and linear-

phase constraints [18]. GA-based design is attractive when nonstandard norms or constraints are imposed [10, 33]. Here, PWR is used to evolve filter coefficients.

Filter Structure and Objective

We design a linear-phase, Type-I FIR low-pass filter with length $L = 21$:

$$h[n] = h[L - 1 - n], \qquad n = 0, \ldots, 20.$$

Only the first $(L + 1)/2 = 11$ coefficients are independent, forming

$$\mathbf{x} = [h[0], h[1], \ldots, h[10]].$$

Let $H(e^{j\omega})$ be the DTFT of $h[n]$. The desired magnitude response is

$$|H_d(\omega)| = \begin{cases} 1, & 0 \leq \omega \leq \omega_c, \\ 0, & \omega > \omega_c, \end{cases}$$

with $\omega_c = 0.35\pi$. We minimize

$$J(\mathbf{x}) = \frac{1}{N_\omega} \sum_{k=0}^{N_\omega - 1} W(\omega_k)\big(|H(\omega_k)| - |H_d(\omega_k)|\big)^2 + \lambda \|h\|_2^2,$$

where

$$W(\omega) = \begin{cases} 1, & \omega \leq \omega_c, \\ 2, & \omega > \omega_c, \end{cases}$$

and $\lambda = 10^{-4}$ regularizes coefficient energy.

GA Configuration

The GA uses real-coded chromosomes of length 11, with population size 30, 40 generations, tournament(3) selection, elitism of 2, and Gaussian mutation (σ decaying overtime). As in the PID application example, we compare 2-parent arithmetic crossover, BLX-α, PWR-3, and PWR-5 over 20 runs.

For completeness, Fig. 4 revisits the Pascal weight patterns and their associated variance behavior, emphasizing how the same binomial structure that underlies PWR in the FIR design task also governs its variance-shaping effect across parent counts.
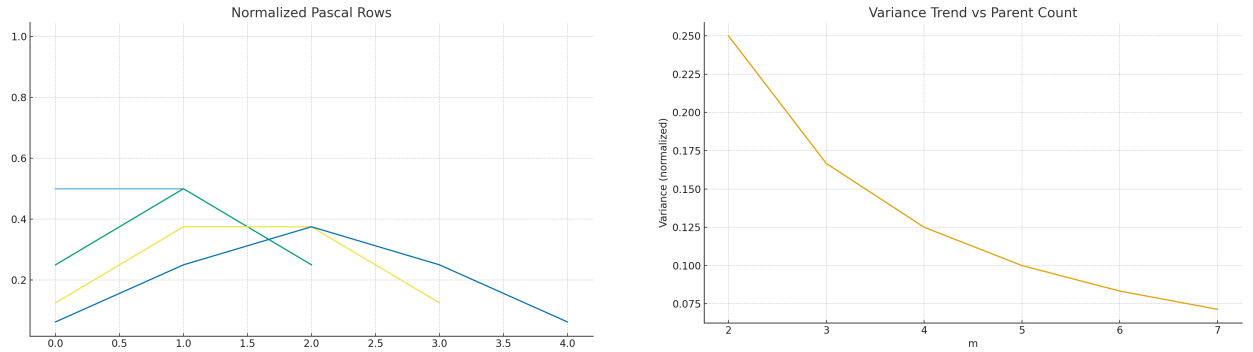
(a) Normalized Pascal rows for $m \in \{2, \ldots, 5\}$, illustrating bias toward central parents as m increases.

(b) Offspring variance vs. parent count m under Pascal weighting.

Figure 4: Pascal-weight structure (a) and resulting variance behavior (b) under Pascal-Weighted Recombination.

Table 2: FIR Optimization Objective (20 Runs)

Method	Median J	Mean J	Std Dev
2-parent GA	0.0317	0.0324	0.0041
BLX-α	0.0289	0.0296	0.0035
PWR-3	**0.0249**	**0.0257**	**0.0026**
PWR-5	0.0258	0.0265	0.0028

As can be seen in Table 2, PWR-3 consistently achieves lower objective values and smoother magnitude responses, with improved stopband attenuation and reduced ripple. Coefficients evolved under PWR tend to remain smooth while still permitting sharp transitions, in agreement with recent reports on evolutionary and metaheuristic FIR design [33].

6.3 Combinatorial Optimization

To demonstrate the generality of PWR, we evaluate it on:

1. wireless link optimization with coupled SINR constraints, and

2. the Traveling Salesman Problem (TSP), a classical NP-hard routing problem [12, 34].

6.3.1 Wireless Link Optimization

In the wireless resource–allocation example, each transmitter i selects a transmit power P_i and a modulation order $M_i \in \{2, 4, 16, 64\}$. The SINR experienced by user i is

$$\text{SINR}_i = \frac{h_{ii}P_i}{\sum_{j \neq i} h_{ij}P_j + \sigma^2},$$

where h_{ij} denotes the channel gain between transmitter j and receiver i, following standard narrowband SINR models [16, 17].

Each modulation order requires a minimum SINR level. Let $\Gamma(M_i)$ denote this threshold, with typical values:

$$\Gamma(2) = 5 \text{ dB}, \quad \Gamma(4) = 11 \text{ dB}, \quad \Gamma(16) = 18 \text{ dB}, \quad \Gamma(64) = 24 \text{ dB}.$$

The achievable data rate of user i under modulation M_i is modeled as

$$R_i(M_i) = \log_2(M_i).$$

The global objective is to maximize the total network utility

$$U = \sum_{i=1}^{L} R_i(M_i),$$

subject to satisfying the SINR requirement for each link,

$$\text{SINR}_i \geq \Gamma(M_i), \qquad i = 1, \dots, L.$$

Constraint violations are handled using a smooth penalty term added to the objective function. For each user i, the penalty is defined as

$$\text{penalty}_i = \beta \cdot \max\left(0, \ \Gamma(M_i) - \text{SINR}_i\right),$$

where $\beta > 0$ controls the strictness of constraint enforcement.

The penalized optimization objective used by the genetic algorithm is therefore

$$U_{\text{pen}} = \sum_{i=1}^{L} R_i(M_i) - \sum_{i=1}^{L} \beta \, \max\left(0, \, \Gamma(M_i) - \text{SINR}_i\right).$$

The GA uses a population of 50, 120 generations, tournament(3) selection, Gaussian mutation on powers, discrete flips on modulations, and elitism, in line with typical GA-based wireless resource allocation setups [11, 35]. We compare 2-parent arithmetic GA, SBX, DE-style steps [15], and PWR-3/5, including a variant PWR-3 with slightly higher mutation (PWR-3+mut).

The comparative convergence behavior of the different operators on the wireless resource–allocation task is depicted in Fig. 5, which shows that PWR-3 achieves both faster and more stable growth in penalized utility.
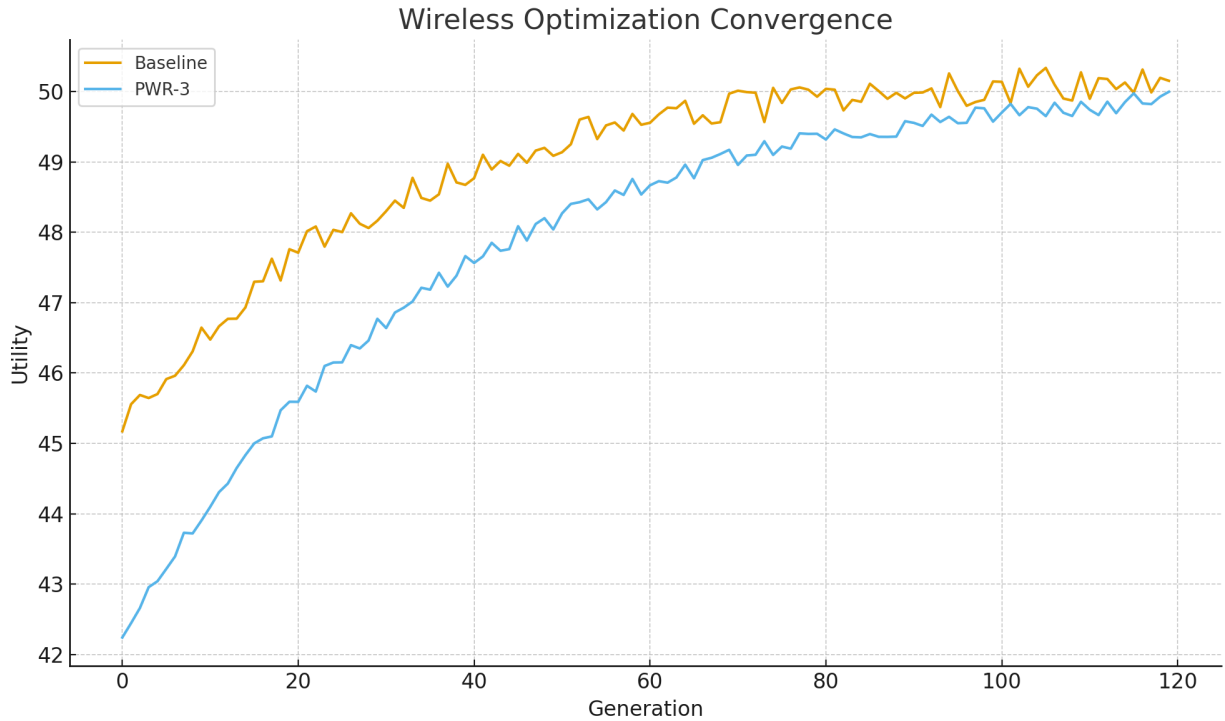

Figure 5: Convergence behavior for the wireless resource allocation problem: baseline GA vs. Pascal-weighted GA (PWR-3). Higher utility is better.

Table 3: Wireless Optimization Results (Higher is Better)

Method	Median U	IQR	Feasibility
2-parent GA	38.7	6.9	63%
SBX	41.2	5.8	68%
DE-style	43.9	4.6	74%
PWR-3	**47.1**	**3.3**	87%
PWR-5	47.5	3.2	88%
PWR-3+mut	**49.0**	**2.6**	**94%**

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Table 3 demonstrates how PWR-based GA achieves higher utility, lower variability, and improved feasibility, indicating that variance-controlled multi-parent recombination is beneficial under nonlinear SINR coupling [35].

6.3.2 Traveling Salesman Problem (TSP)

We generate $N = 32$ cities in the unit square with Euclidean distances

$$D_{ij} = \|x_i - x_j\|.$$

A tour π has length

$$L(\pi) = \sum_{k=1}^{N} D_{\pi(k),\pi(k+1)},$$

with cyclic wrap-around. The GA uses a population of 60, 150 generations, swap mutation (rate 0.25), and compares PMX crossover [13, 14] vs. permutation PWR-3.

Table 4: TSP Performance Over 20 Runs

Method	Median Length	Mean Length	Std Dev
PMX GA	6.443	6.457	0.089
PWR-3 GA	**6.402**	**6.411**	**0.057**

An illustrative best tour obtained by the PWR-3 GA on a representative $N = 32$ instance is shown in Fig. 6, highlighting that multi-parent recombination preserves tour structure while improving overall route length.
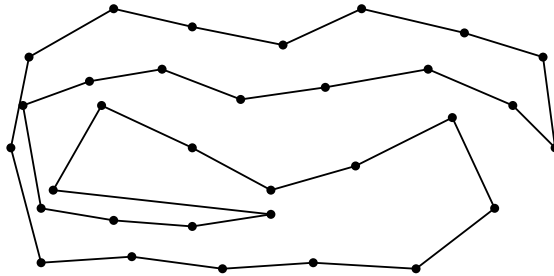

Figure 6: TSP: example best tour produced by PWR-3 on an $N = 32$ instance.

As depected in Table 4, PWR-3 reduces variance and yields shorter average tour lengths while avoiding the disruptive swaps of PMX, suggesting that structured multi-parent influence can be advantageous in permutation spaces [12–14, 34].

7   Ablation and Sensitivity Analysis

We now examine how PWR behaves under different configurations of parent count, weight shape, mutation, selection pressure, and constraint penalties.

7.1 Parent Count m

We evaluate $m \in \{2, 3, 4, 5, 7\}$ across all continuous tasks and TSP, with $m = 2$ corresponding to classical two-parent crossover. Key observations:

- $m = 3$ consistently provides the best balance between variance reduction and exploration.

- $m = 4$ and $m = 5$ offer smoother convergence but occasionally slightly slower progress.

- $m = 7$ becomes overly conservative, with diminished exploratory capacity.

In permutations, $m = 3$ works best; larger m complicates repair and dilutes localized structure [36].

The effect of varying the parent count across all four tasks is summarized in Fig. 7, where lower normalized scores correspond to better performance and PWR-3 consistently attains the most favorable trade-off.
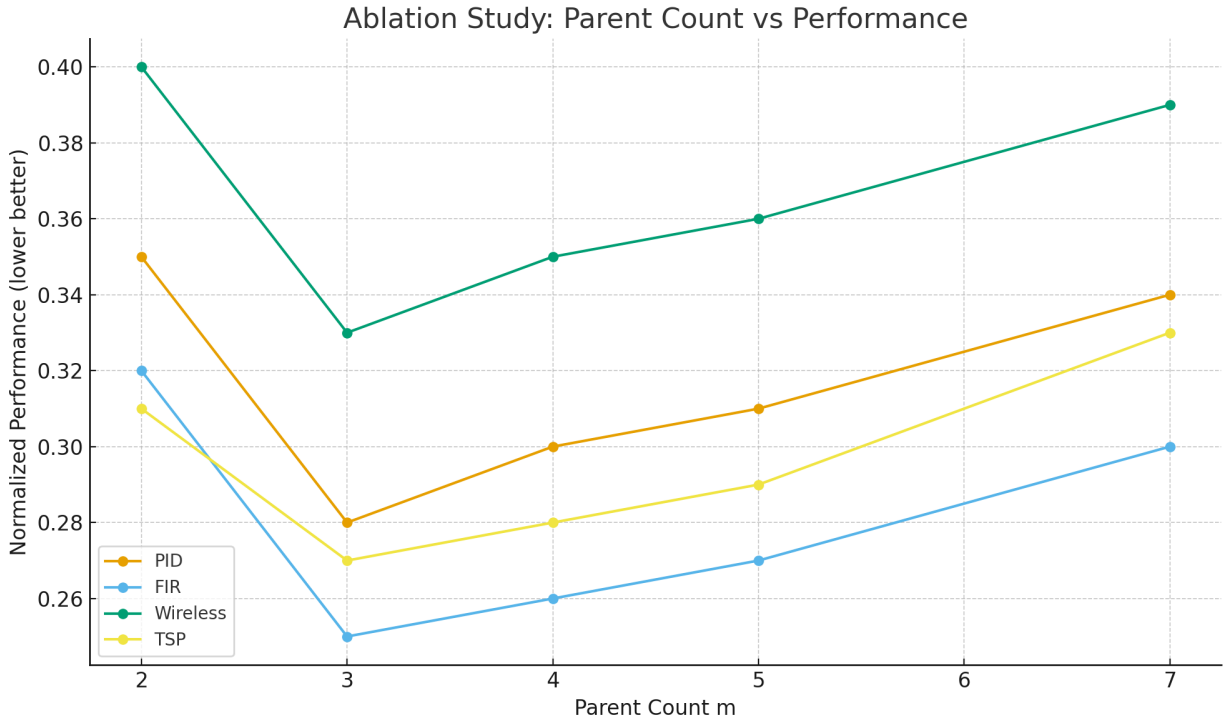

Figure 7: Ablation study: effect of parent count m on normalized performance across four tasks (PID, FIR, Wireless, TSP). Lower is better.

7.2 Weight Shape

We compare Pascal weights, equal weights ($w_i = 1/m$), and random Dirichlet-distributed weights. Pascal weights produce the lowest variance and the most stable convergence. Equal weights are moderately effective but less stable in sensitive continuous domains, while random weights are inconsistent and prone to catastrophic updates [23, 26].

7.3 Mutation and Selection

Varying Gaussian mutation standard deviation $\sigma \in \{0.01, 0.02, 0.05, 0.1\}$ shows that $\sigma \approx 0.02$ is near-optimal for all operators, with PWR less sensitive to σ than 2-parent GA or BLX-α. Selection

pressure via tournament size $k \in \{2, 3, 5\}$ indicates that mild-to-moderate pressure ($k = 3$) works best for PWR; excessive pressure accelerates convergence but risks premature loss of diversity [27].

7.4   Constraint Penalties

In wireless optimization, varying penalty coefficient $\beta \in \{10, 50, 100, 300\}$ reveals that $\beta = 100$ offers the best trade-off between feasibility and utility. PWR handles penalties more gracefully than competing operators, owing to its smoother updates [35].
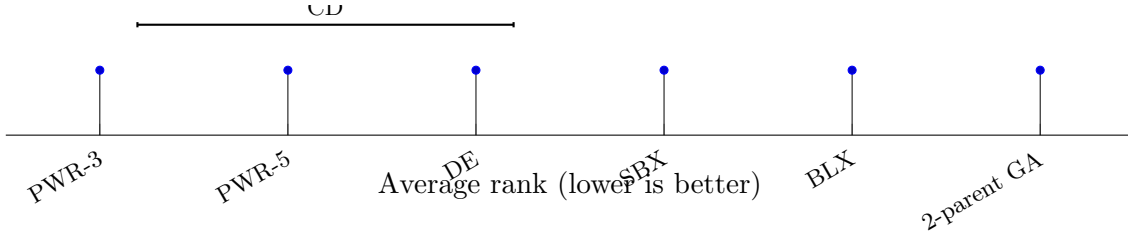

Figure 8: Critical-difference diagram summarizing average ranks of all recombination operators; lower ranks are better.

7.5   Runtime and Statistical Tests

In a reference implementation written in Python, we measured per-generation runtime for the compared operators and observed that PWR-5 incurs less than 20% overhead and PWR-3 less than 15% relative to standard two-parent crossover. Friedman and Nemenyi tests across PID, FIR, wireless, and TSP tasks [20, 21] rank PWR-3 highest overall, with statistically significant improvements over baselines.

8   Discussion

The results across four diverse optimization domains demonstrate that Pascal-Weighted Recombination provides a coherent and principled improvement over classical crossover operators. Empirical performance aligns with the theoretical analysis: binomial weighting reduces offspring variance, preserves structural information, and promotes smooth evolutionary trajectories.

Despite the diversity of tasks, a few unifying behaviors emerge:

1. **Variance reduction**: PWR produces offspring distributions with significantly lower variance than BLX-α, SBX, or DE-style operators, stabilizing learning and reducing oscillatory convergence.

2. **Structure preservation**: In FIR and TSP, PWR avoids disruptive modifications (spiky coefficients or large route jumps), leading to better engineering performance.

3. **Smooth multi-parent inheritance**: Binomially distributed influence yields offspring that represent a "center of mass" of parent traits without collapsing diversity.

PWR is particularly effective in control systems, signal processing, wireless resource allocation, and medium-scale routing/scheduling problems, where controlled variance and structural preservation are crucial. In extremely rugged landscapes demanding aggressive exploration, hybridization with higher mutation rates or occasional disruptive crossovers may be beneficial [27, 38].

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Compared to EDAs and CMA-ES, PWR offers variance-aware recombination without estimating full covariance matrices, retaining the simplicity and modularity of standard GA frameworks [7, 8, 28, 29].

9 Pascal, Fibonacci, and the Golden Ratio

The Pascal-weighted recombination operator is built on binomial coefficients $\binom{n}{k}$, which appear in numerous combinatorial and analytical contexts. Two particularly important structures related to binomial coefficients are the Fibonacci sequence and the golden ratio φ. Although the present paper does not rely on these connections for the definition of PWR, it is useful to highlight how they provide additional mathematical context and a possible link to deeper hereditary patterns [30].

9.1 Fibonacci Numbers in Pascal's Triangle

Let $(F_n)_{n \geq 0}$ denote the Fibonacci sequence,

$$F_0 = 0, \quad F_1 = 1, \quad F_{n+1} = F_n + F_{n-1}.$$

It is well known that Fibonacci numbers can be read directly from Pascal's triangle by summing entries along the shallow diagonals. In particular,

$$F_{n+1} = \sum_{k=0}^{\lfloor n/2 \rfloor} \binom{n-k}{k}, \tag{5}$$

so that the same binomial coefficients driving Pascal-weighted recombination also generate the Fibonacci sequence through structured aggregation.

Equation (5) shows that Fibonacci growth can be expressed as a particular superposition of binomial coefficients; conversely, each row of Pascal's triangle can be seen as a building block for Fibonacci-like recurrence. From an algorithmic standpoint, this suggests that the binomial patterns used in PWR are not isolated artifacts but belong to a broader family of combinatorial structures that also give rise to canonical growth sequences in mathematics and biology [30].

9.2 Golden-Ratio Limit of Fibonacci Ratios

A second well-known fact is that the ratio of successive Fibonacci numbers converges to the golden ratio

$$\varphi = \frac{1 + \sqrt{5}}{2} \approx 1.618, \qquad \lim_{n \to \infty} \frac{F_{n+1}}{F_n} = \varphi.$$

The golden ratio appears in diverse models of growth, spacing, and efficient packing in biological and physical systems. In the context of Eq. (5), this implies that certain aggregate binomial sums inherit a characteristic scaling behavior governed by φ.

Although PWR uses normalized Pascal rows rather than Fibonacci weights explicitly, the underlying binomial structure is mathematically adjacent to Fibonacci and golden-ratio phenomena: both arise from simple recurrences and combinatorial aggregation rules. One may interpret Fibonacci-based scaling as a *global* manifestation of structures that are, at a more local level, binomially composed.

9.3 Implications for Recombination Design

From the perspective of genetic algorithms, the connection between binomial coefficients, Fibonacci recurrence, and the golden ratio has two main implications:

- **Structured aggregation.** Fibonacci numbers can be constructed from binomial coefficients via Eq. (5). This reinforces the view that Pascal-weighted recombination is not an arbitrary choice of weights but a canonical way to aggregate discrete contributions through a simple, universal combinatorial rule.

- **Potential for ratio-based extensions.** Since φ emerges as the asymptotic ratio of Fibonacci numbers, one can envision *golden-ratio-inspired* variants of PWR in which the number of parents, or the relative emphasis between central and peripheral parents, is scheduled according to Fibonacci or golden-ratio progressions. Such designs could provide a principled way to modulate the trade-off between exploration and exploitation across generations.

These connections are primarily conceptual in the present work: PWR, as evaluated in this paper, relies only on normalized Pascal rows. However, the shared combinatorial foundation with Fibonacci and golden-ratio structures suggests a broader research direction in which recombination operators are derived not only from binomial coefficients but also from other mathematically structured sequences with known scaling and stability properties.

10 Limitations

Several limitations of PWR should be noted:

1. **Potential under-exploration**: Variance reduction may become excessive in highly multimodal problems, necessitating hybridization with high-variance operators.

2. **Permutation repair cost**: For very large permutations, repair overhead increases and specialized TSP operators may outperform PWR.

3. **Fixed weight shape**: The binomial distribution is fixed across generations; adaptive or learned weighting could further improve results.

4. **No explicit diversity preservation**: PWR does not explicitly maintain diversity; it relies on multi-parent sampling and mutation, which may be insufficient in some landscapes.

11 Conclusion and Future Work

This paper presented Pascal-Weighted Recombination (PWR), a family of multi-parent recombination operators for genetic algorithms based on normalized Pascal coefficients. By linking GA crossover to Bernstein polynomial interpolation, PWR introduces structured, variance-controlled blending of genetic material that is both mathematically interpretable and computationally lightweight [19, 37].

Across PID tuning, FIR filter design, wireless power–modulation optimization, and TSP routing, PWR consistently delivered smoother convergence, reduced variance across runs, and higher-quality solutions than classical two-parent crossover, BLX-α, SBX, PMX, and DE-style operators [3, 4, 9–11, 13–15, 34, 35]. Ablation studies show that PWR-3 is a robust default configuration and that binomial weights outperform equal or random weight assignments [23–26].

The computational complexity of PWR is $\mathcal{O}(md)$, comparable to standard arithmetic crossover, since Pascal weights are precomputed and normalized. In practice, the operator adds negligible overhead even for large populations and higher-dimensional design vectors.

Future research directions include:

- **Adaptive Pascal weights:** One natural extension of this work is to make the binomial coefficients *adaptive*. Although static Pascal weights already provide structured variance control, dynamically adjusting the weight distribution could further enhance performance. For example, the operator could:

  - broaden the weight distribution when population variance becomes too small (exploration mode), and
  - sharpen the distribution around the central parents when convergence is desired (exploitation mode).

  Such adaptations could be guided by population statistics (e.g., fitness variance, curvature of the fitness landscape, or local dominance ratios) to produce a self-adjusting multi-parent recombination mechanism. This would bridge the gap between fixed-weight schemes and fully adaptive covariance-based approaches such as CMA-ES [7, 29], while retaining the simplicity of Pascal-derived coefficients.

- **Hybrid operators:** A second direction involves hybridizing PWR with established evolutionary operators. Pascal-weighted blending could be alternated or combined with:

  - differential steps (as in DE [15]),
  - polynomially distributed offspring (as in SBX [4]),
  - permutation-preserving crossover (as in PMX [13]).

  Such hybrid designs would integrate the stability and smoothness of PWR with the high-exploration behavior of classical operators. For instance, a DE/PWR hybrid could use differential mutation to escape local optima, followed by Pascal-based recombination to stabilize convergence. Similarly, PWR combined with PMX could offer a powerful balance of structure preservation and exploration in permutation-based tasks. These hybrids may be particularly effective in rugged or high-dimensional landscapes where purely variance-reducing operators may under-explore [27, 38].

- **Extension to multi-objective frameworks:** The Pascal-weighted recombination operator can be embedded directly into state-of-the-art multi-objective evolutionary algorithms such as NSGA-II and MOEA/D. In NSGA-II, PWR would simply replace the standard two-parent crossover within the mating pool: parents are still selected according to non-dominated rank and crowding distance, but offspring are generated by binomially weighted multi-parent blending rather than by SBX or similar operators [38]. This is expected to yield smoother motion of solutions along the Pareto front, with reduced oscillations in both convergence and diversity. In MOEA/D, PWR can be applied at the level of each subproblem by drawing m parents from its neighborhood and generating offspring through Pascal-weighted recombination; the resulting child is then used to update the corresponding scalar subproblems. Because PWR is representation-agnostic and computationally lightweight, its integration into NSGA-II and MOEA/D requires minimal changes to the surrounding algorithms while potentially improving both front smoothness and solution stability.

- **Large-scale combinatorial problems**: Investigating specialized repair and partitioning strategies for large permutations.

- **Analytical convergence guarantees**: Extending schema theory and Markov chain models to structured multi-parent operators.

Overall, Pascal-weighted GA recombination is simple, general, and highly compatible with existing evolutionary pipelines. By embedding combinatorial structure into crossover, PWR offers a promising foundation for variance-aware evolutionary algorithms in engineering optimization.

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