Postprint of Sparse Reconstruction Algorithm Based on Improved Genetic Algorithm

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Abstract

In sparse reconstruction algorithms, convex relaxation methods exhibit deficiencies in recovery efficiency, while greedy pursuit methods show limitations in recovery accuracy. Based on the iterative optimization concept of genetic algorithms and integrating the advantages of simulated annealing and multi-population algorithms, this paper proposes heuristic sparse reconstruction algorithms based on simulated annealing genetic algorithms and multi-population genetic algorithms. Both proposed algorithms address the inherent defect of traditional genetic algorithms—namely, their propensity to become trapped in local optima—by respectively preserving inter-individual differences and enhancing population diversity to search for the global optimal solution of the target sparse signal. Theoretical analysis demonstrates the validity of the parameter selection and search strategies employed in the proposed algorithms. Furthermore, the effectiveness of the algorithms is validated through the Direction of Arrival (DOA) estimation problem for spatial signal sources in array signal processing. Simulation results indicate that, compared with the Orthogonal Matching Pursuit (OMP) algorithm and the l1-SVD algorithm based on l1-norm singular value decomposition, the proposed algorithms enhance DOA estimation accuracy while reducing computational complexity, thereby achieving rapid convergence to the global optimal solution.

Full Text

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Sparse Reconstruction Algorithm Based on Improved Genetic Algorithm

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Abstract: Sparse reconstruction algorithms suffer from limitations in that convex relaxation methods have insufficient recovery efficiency while greedy pursuit methods lack recovery accuracy. Drawing upon the iterative optimization concept of genetic algorithms and combining the advantages of simulated annealing and multi-population algorithms, this paper proposes two heuristic sparse reconstruction algorithms: one based on simulated annealing genetic algorithm and another based on multi-population genetic algorithm. Both proposed algorithms address the inherent defect of traditional genetic algorithms that easily fall into local optimal solutions. They search for the global optimal solution of the sparse signal by maintaining inter-individual differences and enhancing population diversity, respectively. Theoretical analysis demonstrates the effectiveness of parameter selection and search strategies in the proposed algorithms. Furthermore, the effectiveness of the algorithms is validated using the direction-of-arrival (DOA) estimation problem for spatial sources in array signal processing as an example. Simulation results show that compared with the Orthogonal Matching Pursuit (OMP) algorithm and the l1-norm Singular Value Decomposition (l1-SVD) algorithm, the proposed algorithms improve DOA estimation accuracy, reduce computational complexity, and converge rapidly to the global optimal solution.

Keywords: multi-population genetic algorithm; simulated annealing genetic algorithm; DOA estimation; sparse reconstruction

0 Introduction

With the proposal of compressive sensing theory, numerous scholars have conducted extensive research on sparse reconstruction methods, developing many effective algorithms that form a relatively complete theoretical and algorithmic system widely applied in practical problems.

Existing reconstruction algorithms primarily fall into two categories: greedy pursuit methods and convex relaxation methods [1]. Each category has its own advantages and disadvantages. Greedy algorithms are less effective in reconstruction quality compared to convex optimization algorithms but are relatively simple and fast to implement. Conversely, convex optimization algorithms offer better stability and theoretical guarantees but suffer from lower computational efficiency than greedy algorithms. Since sparse reconstruction is a non-convex combinatorial optimization problem, no deterministic method currently exists for its rapid and exact solution [2], [3]. The two aforementioned categories of reconstruction algorithms can only provide approximate solutions and fail to achieve effective reconstruction when the sparsity level is small.

The essence of sparse reconstruction is a combinatorial optimization problem. Genetic algorithms (GA) represent an effective approach for solving such problems. Preliminary research on sparse reconstruction based on genetic algorithms has been conducted. Reference [4] proposed a sparse reconstruction algorithm combining simulated annealing with greedy algorithms, comparing reconstruction accuracy with the BP and OMP algorithms for image reconstruction under different signal-to-noise ratios, with results showing lower reconstruction errors under the same conditions. Reference [5] presented a simulated annealing sparse reconstruction method based on l0-norm minimization, which improved reconstruction accuracy and efficiency compared to greedy pursuit algorithms. Reference [6] introduced a novel sparse reconstruction algorithm based on particle swarm optimization combined with greedy pursuit ideas, demonstrating faster reconstruction rates than conventional algorithms. Reference [7] applied particle swarm optimization to search for optimal matching atoms in sparse decomposition to reduce computational complexity and improve efficiency in signal processing based on sparse decomposition theory. Reference [8] utilized genetic algorithms for reconstructing transform-domain sparse signals with missing samples. Reference [9] proposed a measurement matrix optimization method based on genetic algorithms (GA) to address compressive sensing inverse synthetic aperture radar sparse imaging problems. Reference [10] developed a single-image super-resolution reconstruction method based on genetic algorithms and regularization prior models, combining genetic algorithms with iterative shrinkage algorithms to process the regularization prior model and avoid falling into local optimal solutions.

This paper simultaneously employs ideas from both greedy pursuit and convex relaxation methods, proposing new sparse reconstruction algorithms integrated with improved genetic algorithms. Since single-population genetic algorithms tend to have consistent individual fitness in later iterations, causing evolutionary stagnation and easily falling into local optimal solutions, we combine simulated annealing algorithms, which possess stronger global search capabilities, with genetic algorithms. The temperature reduction process stretches fitness values to ensure effective and rapid convergence to the global optimal solution. Multi-population genetic algorithms break through the single-population optimization framework, enabling cooperative evolution among multiple populations with different control parameters while balancing global and local search performance. During cooperative evolution, the best individuals from each population are preserved and propagated to all populations through migration operators. After iteration, the best individual among all optimal individuals is selected as the final solution.

This paper applies the proposed algorithms to DOA estimation of spatial sources in array signal processing to validate their effectiveness. Existing research on genetic algorithm-based DOA estimation includes: Reference [11] proposed applying genetic algorithms to MUSIC spectral peak search to address the low efficiency caused by high search dimensions; Reference [12] combined simulated annealing with genetic algorithms for weighted subspace DOA estimation to improve accuracy. This paper integrates sparse reconstruction concepts with improved genetic optimization algorithms for DOA estimation and compares performance with orthogonal matching pursuit algorithms and convex optimization algorithms based on l1-norm minimization with singular value decomposition to verify improvements in estimation accuracy and computational efficiency.

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1 Sparse Reconstruction Model Description

A sparse signal $\mathbf{x}$ compressed and measured through a sensing matrix $\mathbf{A}$ is denoted as $\mathbf{y} = \mathbf{A}\mathbf{x} + \mathbf{n}$, where $\mathbf{n}$ represents noise. This equation forms an underdetermined system with infinitely many solutions. However, due to the sparsity of $\mathbf{x}$, minimizing the sparsity constraint on $\mathbf{x}$ yields a unique solution. Considering more general practical scenarios, we establish a noisy sparse optimization model as follows:

$$\begin{aligned} &\min \|\mathbf{x}\|_0 \\ &\text{s.t. } \|\mathbf{y} - \mathbf{A}\mathbf{x}\|_2 \leq \varepsilon \end{aligned}$$

where $\mathbf{x}$ is a sparse signal with most elements being zero or near-zero; $\mathbf{y}$ is the observation vector; ε is an error bound related to noise; $\|\cdot\|_0$ denotes the l0-norm, which counts the number of non-zero elements in a vector. If the signal sparsity is K, the set of positions of non-zero elements in $\mathbf{x}$ is called the support of vector $\mathbf{x}$.

For more general cases where observation signals are multiple temporal samples, denoted as $\mathbf{Y} = \mathbf{A}\mathbf{X} + \mathbf{N}$, where T represents the number of snapshots. Let $\mathbf{X}_i$ denote the i-th row of matrix $\mathbf{X}$. We establish a multi-observation sparse reconstruction model as:

$$\begin{aligned} &\min |\mathcal{R}(\mathbf{X})| \\ &\text{s.t. } \|\mathbf{Y} - \mathbf{A}\mathbf{X}\|_F \leq \delta \end{aligned}$$

where $|\cdot|$ denotes the cardinality of a set, which measures the number of elements; $\|\cdot\|_F$ represents the Frobenius norm.

When the sparsity level K is known, problem (2) can be transformed into:

$$\begin{aligned} &\min \|\mathbf{Y} - \mathbf{A}_\Omega \mathbf{X}_\Omega\|_F \\ &\text{s.t. } |\Omega| = K \end{aligned}$$

Solving this problem requires first finding a row support estimate $\hat{\Omega}$ that satisfies $|\hat{\Omega}| = K$. Based on this row support estimate, the solution is obtained using least squares:

$$\hat{\mathbf{X}} = \mathbf{A}_{\Omega}^{\dagger}\mathbf{Y}$$

When $\mathbf{X}$ is the solution to this sparse reconstruction problem, we can obtain $\mathbf{Y} = \mathbf{A}_{\Omega}\mathbf{X}_{\Omega}$. This is equivalent to:

$$\hat{\Omega} = \arg \min_{\Omega \subset \Theta, |\Omega| = K} \|\mathbf{Y} - \mathbf{A}_{\Omega}\mathbf{A}_{\Omega}^{\dagger}\mathbf{Y}\|_F$$

Equations (5) and (6) demonstrate that the essence of sparse reconstruction is finding a row support estimate $\hat{\Omega}$ that satisfies the above constraints.

Therefore, we can define the function:

$$f(\Omega) = \|\mathbf{Y} - \mathbf{A}_{\Omega}\mathbf{A}_{\Omega}^{\dagger}\mathbf{Y}\|_F$$

as the objective function of the genetic algorithm, i.e., the fitness function. Minimizing this objective function yields the row support estimate of the sparse matrix $\mathbf{X}$.

Optimization Objective:

$$\min_{\Omega \subset \Theta} f(\Omega)$$

where $\Theta = \{1, 2, \dots, L\}$ and Ω is a subset of Θ with cardinality K.

Encoding Scheme: The non-zero row position set of the sparse signal, i.e., the row support of sparse matrix $\mathbf{X}$, serves as individuals in the population. Individuals use decimal encoding with length K, where genes on an individual represent the position indices of non-zero rows.

Initial Solution: Let the population size be *popsize*, where each solution represents an encoding of a feasible solution. To enable rapid convergence to the global optimal solution, initializing the genetic algorithm population with individuals close to the optimal support set is an effective method. This paper' s genetic algorithm adopts a threshold method based on greedy pursuit ideas to obtain an initial solution, then introduces random perturbations within a small neighborhood of this initial solution to generate the initial solution set for the genetic algorithm. Individual generation follows:

$$\Omega_k = \Omega_0 + \{randi(-10, 10)\}, \quad k = 1, \dots, popsize$$

where $\Omega_0 = \{\text{indices of the } K \text{ largest values in } \|\mathbf{A}_j^H\mathbf{Y}\|_2\}$.

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2 Sparse Reconstruction Algorithm Based on Improved Genetic Algorithm

Genetic algorithms consist of five fundamental elements: objective function, encoding scheme, initial solution, new solution generation mechanism, and termination conditions [4]. Combining genetic algorithms with sparse reconstruction algorithms requires model design from these five elements.

Based on the above theory, we propose the Simulated Annealing Genetic Algorithm based Sparse Reconstruction (SAGA-SR) algorithm and the Multi-Population Genetic Algorithm based Sparse Reconstruction (MPGA-SR) algorithm. Addressing the defect of single genetic algorithms that easily fall into local optimal solutions, these algorithms improve the probability of converging to the global optimal solution by changing the search strategy for sparse solutions, thereby reducing reconstruction error. SAGA-SR utilizes the simulated annealing algorithm' s strategy of accepting inferior solutions with a certain probability to avoid local optimal solutions and enhance global search capability. MPGA-SR breaks away from the single-population optimization framework, achieving optimal solution search through cooperative evolution of multiple populations with different control parameters, balancing both global and local search capabilities.

The new solution update strategy is a crucial process in genetic algorithms, determining computational complexity and search results. Different algorithms have different solution update mechanisms, which are described separately for the two proposed algorithms.

2.1 SAGA-SR Algorithm Design

SAGA combines the global optimization capability of simulated annealing algorithms with the local optimization capability of genetic algorithms, increasing the probability of convergence to global optimal solutions [1], [1].

1) New Solution Generation Mechanism

To maintain population diversity during iterative optimization, we introduce a premature convergence judgment indicator:

$$\Delta_g = f^g_{\max} - \bar{f}^g$$

where $f^g_{\max}$ is the fitness value of the best individual in generation g; $\bar{f}^g = \frac{1}{H}\sum_{i \in I_g} f^g_i$; $I_g = \{i \mid f^g_i > \bar{f}^g\}$; f^g_i and $\bar{f}^g$ represent the fitness value of individual i and the mean fitness of all individuals in the population at iteration

g, respectively; H denotes the number of individuals in the current population with fitness values greater than the population mean fitness.

Based on this, we dynamically adjust crossover and mutation probabilities:

$$p_c^g = p_c^0 \exp(-\Delta_g / T_g)$$

$$p_m^g = p_m^0 \exp(-\Delta_g / T_g)$$

where p_c^0 and p_m^0 are the initial crossover and mutation probabilities.

The population update strategy, based on simulated annealing principles, generates the next generation population:

$$\Omega_i^{g+1} = \begin{cases} \Omega_i^{\text{new}} & \text{if } f(\Omega_i^{\text{new}}) < f(\Omega_i^g) \\ \Omega_i^{\text{new}} & \text{if } r < \exp(-(f(\Omega_i^{\text{new}}) - f(\Omega_i^g))/T_g) \\ \Omega_i^g & \text{otherwise} \end{cases}$$

where r is a random number between 0 and 1.

Based on the values of individuals in the population, we compute the sparse solution to the sparse reconstruction problem:

$$\hat{\mathbf{X}} = \mathbf{A}_{\hat{\Omega}}^{\dagger} \mathbf{Y}$$

2) Termination Condition

Define the signal-to-noise ratio as $SNR = 10 \log_{10}(\|\mathbf{AX}\|_F^2 / \|\mathbf{N}\|_F^2)$. Given an optimal solution Ω^*, $\mathbf{X}^*$ is the corresponding sparse matrix calculated from equation (14). We establish an upper bound for the objective function of this optimal solution:

$$f(\Omega^*) = \|\mathbf{Y} - \mathbf{A}_{\Omega^*} \mathbf{A}_{\Omega^*}^{\dagger} \mathbf{Y}\|_F \leq \|\mathbf{N}\|_F + \|\mathbf{A}_{\Omega^*}^{\dagger} \mathbf{N}\|_F \leq (1 + \|\mathbf{A}_{\Omega^*}^{\dagger}\|_F) \|\mathbf{N}\|_F$$

Assuming $\|\mathbf{A}_{\Omega^*}^{\dagger} \mathbf{N}\|_F \approx \|\mathbf{A}_{\Omega^*}^{\dagger}\|_F \|\mathbf{N}\|_F$ and $\|\mathbf{A}_{\Omega^*}^{\dagger}\|_F \leq 10$, we obtain:

$$\varepsilon = (1 + 10) \|\mathbf{N}\|_F = 11 \|\mathbf{N}\|_F$$

Since $\|\mathbf{N}\|_F = \|\mathbf{Y} - \mathbf{AX}\|_F$, we have:

$$\varepsilon = 11 \frac{\|\mathbf{AX}\|_F}{\sqrt{10^{SNR/10}}}$$

Therefore, we can set ε as the termination condition. Considering both computational time and convergence, we establish two termination conditions, and the algorithm terminates when either is satisfied: if the fitness function value of the best individual in the population satisfies $f(\Omega_{\text{best}}) < \varepsilon$, or if the iteration count reaches the maximum allowed iterations *maxiter*. The first condition allows early termination when satisfied, avoiding unnecessary iterations and improving computational efficiency. The second condition ensures termination after a limited number of iterations when the algorithm falls into a local optimal solution, preventing infinite loops.

The specific implementation steps of the SAGA-SR algorithm are as follows:

Algorithm 1: Simulated Annealing Genetic Algorithm Based Sparse Reconstruction (SAGA-SR)

Input Parameters: Sensing matrix $\mathbf{A}$, sparsity level K, population size *popsize*, crossover probability p_c^0, mutation probability p_m^0, initial temperature T_0, cooling coefficient ξ, termination parameter ε, maximum iterations *maxiter*.

Initialization: For the k-th individual ($k = 1, \dots, popsize$), encode as Ω_k determined by equation (8). Set iteration counter $g = 1$ and let $T = T_0$.

Iteration Steps: a) **Selection.** Select individuals based on fitness function $f(\Omega)$, preserving the best individuals and eliminating the worst.

b) **Crossover and Mutation.** Select pairs of individuals with probability p_c^g, perform random pairing, apply single-point crossover, and mutate genes on each individual with probability p_m^g to obtain new population Ω_k^{new}.

c) **Fitness Evaluation.** Compute fitness values for current population individuals using equation (7).

d) **Population Update.** Generate the next generation population according to the update rule in equation (13).

e) **Temperature Update.** $T_{g+1} = \xi T_g$.

f) **Termination Judgment.** If $f(\Omega_{\text{best}}) < \varepsilon$ or $g > maxiter$, the algorithm ends, yielding the optimal solution Ω_{best}. Substituting this individual into equation (14) outputs the final solution $\hat{\mathbf{X}}$ to the sparse reconstruction problem; otherwise, set $g = g + 1$ and repeat steps a)-e).

2.2 MPGA-SR Algorithm Design

MPGA utilizes multi-population parallel genetic concepts to improve genetic algorithm performance [1], [3]. Different populations are assigned different control parameters and evolve independently. In each population, the crossover operator is the primary mechanism for generating new individuals, determining the algorithm’ s global search capability, while the mutation operator serves as an auxiliary mechanism, determining local search capability. This approach avoids premature convergence in single-population evolution and accelerates convergence speed.

1) New Solution Generation Mechanism

The control parameters (crossover and mutation probabilities) for the i-th population are:

$$p_c^i = p_c^{\min} + \eta_i \Delta p_c$$

$$p_m^i = p_m^{\min} + \lambda_i \Delta p_m$$

where $p_c^{\min}$ and $p_m^{\min}$ are constants representing the lower limits of crossover and mutation probabilities; η_i and λ_i are random numbers between 0 and 1; Δp_c and Δp_m represent the maximum variation amplitudes of crossover and mutation probabilities, respectively; *popnum* denotes the number of populations.

We select and preserve excellent individuals from each subpopulation, and populations interact through migration operators to promote evolution, enabling cooperative evolution among multiple populations. The migration operation proceeds as follows:

$$\Omega_{i+1}^{\text{worst}} = \Omega_i^{\text{best}}$$

where $\Omega_i^{\text{best}} = \arg\min_{\Omega \in \text{pop}_i} f(\Omega)$ and $\Omega_i^{\text{worst}} = \arg\max_{\Omega \in \text{pop}_i} f(\Omega)$.

The update strategy for individuals in the i-th population:

$$\Omega_{i,\text{new}}^a = \begin{cases} \Omega_i^{\text{new}} & \text{if } f(\Omega_i^{\text{new}}) < f(\Omega_i^a) \\ \Omega_i^a & \text{otherwise} \end{cases}$$

The function of the migration operator in the algorithm is to replace the worst individual in the target population with the best individual from the source population, achieving cooperative evolution among multiple populations. Simultaneously, the best individuals from each population are selected and preserved in an elite population to ensure they are not destroyed.

2) Termination Condition

Given an upper bound ε for the objective function value (computed similarly to equation (15)), we select the best individual Ω_{opt} from the elite population. If this individual satisfies $f(\Omega_{\text{opt}}) < \varepsilon$, the algorithm terminates. The algorithm also terminates when the iteration count reaches the maximum allowed iterations without satisfying $f(\Omega_{\text{opt}}) < \varepsilon$. Setting a maximum iteration count prevents infinite loops when the solution falls into a local optimum, serving the same purpose as in SAGA-SR.

The specific implementation steps of the MPGA-SR algorithm are as follows:

Algorithm 2: Multi-Population Genetic Algorithm Based Sparse Reconstruction (MPGA-SR)

Input Parameters: Sensing matrix $\mathbf{A}$, sparsity level K, subpopulation size *popsize*, number of subpopulations *popnum*, crossover probability p_c^i and mutation probability p_m^i for subpopulation i ($i = 1, \dots, popnum$), termination parameter ε, maximum iterations *maxiter*.

Initialization: Generate *popnum* initial populations pop_k ($k = 1, \dots, popnum$), encode individuals in each population based on equation (8), and set iteration counter $g = 1$.

Iteration Steps: a) **Selection.** Based on the objective function $f(\Omega)$ (smaller values are better), select the best individuals from each subpopulation for preservation and eliminate the worst individuals.

b) **Subpopulation Update.** For each of the *popnum* subpopulations:
  - Randomly select individuals Ω_i^a and Ω_i^b from the i-th population, perform crossover operation with probability p_c^i to generate new individual Ω_i^{new}, compute its fitness value, and update individuals in each population using equation (18).
  - Perform mutation operation on the crossed population with probability p_m^i and update the population using the same approach.

c) **Migration Operation.** Set initial migration count $m = 0$:
  - Based on the migration strategy in equation (17), find the best individual Ω_i^{best} of the i-th population and the worst individual $\Omega_{i+1}^{\text{worst}}$ of the target population $(i + 1)$, replace $\Omega_{i+1}^{\text{worst}}$ with Ω_i^{best}.
  - Check if migration among populations is complete; if $m < popnum$, set $m = m + 1$ and continue migration; otherwise, proceed to step d).

d) **Elite Preservation.** Select the best individual from each subpopulation and store it in an elite population to prevent destruction of optimal individuals. Then return to step a).

Termination Judgment: Select the global best individual from the elite population. If this individual satisfies $f(\Omega_{\text{opt}}) < \varepsilon$ or $g > maxiter$, terminate the algorithm and obtain the optimal solution. Substituting this individual into equation (14) outputs the final solution $\hat{\mathbf{X}}$ to the sparse reconstruction problem; otherwise, set $g = g + 1$ and return to step a).

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3 Algorithm Complexity Analysis

The computational complexity of the SAGA-SR algorithm primarily concentrates on the initial solution selection process and the objective function calculation during iterative updates. The threshold method used for computing each individual' s initial solution has a complexity of $O(MLT)$ per individual. The update process for each individual mainly involves computing the objective function with complexity $O(MK^2) + O(MKT)$. Therefore, the per-iteration complexity of SAGA-SR is $O(MLT \times popsize) + O(popsize \times MK^2) + O(popsize \times MKT)$. Considering the maximum iteration count $maxiter$, the overall complexity of SAGA-SR becomes $O(MLT \times popsize) + O(popsize \times MK^2 \times maxiter) + O(popsize \times MKT \times maxiter)$.

The computational complexity of the MPGA-SR algorithm primarily concentrates on three processes: initial solution selection for each subpopulation, objective function calculation during iterative updates, and elite population selection from all populations. With $popnum$ subpopulations, each of size $popsize$, the threshold method for initial solution selection has per-iteration complexity $O(popnum \times popsize \times MLT)$. Step a) computing individual objective functions has complexity $O(popnum \times popsize \times MK^2) + O(popnum \times popsize \times MKT)$. Step d) selecting the elite population has complexity $O(popnum \times MK^2) + O(popnum \times MKT)$. For the entire algorithm with maximum iterations $maxiter$, the MPGA-SR complexity becomes $O(MLT \times popsize \times popnum) + O(popsize \times (popnum + 1) \times MK^2 \times maxiter) + O(popsize \times (popnum + 1) \times MKT \times maxiter)$.

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4 Algorithm Effectiveness Verification

We select the typical OMP algorithm [1], [4] for greedy pursuit methods and the Singular Value Decomposition l1-norm minimization algorithm [1]{5] for convex optimization methods. Performance comparisons are conducted among five algorithms: OMP, l1-SVD, GA-SR, SAGA-SR, and MPGA-SR.

4.1 DOA Estimation Problem

This section addresses the recovery problem for K-sparse signals, using direction-of-arrival (DOA) estimation of spatial sources [1], [6] as simulation experiments to validate the proposed methods' performance in estimation accuracy and efficiency compared with orthogonal matching pursuit (OMP) and l1-norm constrained convex optimization (l1-SVD).

Consider K narrowband coherent signals incident on a uniform linear array of M isotropic sensors from directions $\theta_1, \theta_2, \dots, \theta_K$. The element spacing is d, the number of snapshots is T, and the array manifold matrix is $\mathbf{A}(\theta) = [\mathbf{a}(\theta_1), \mathbf{a}(\theta_2), \dots, \mathbf{a}(\theta_K)]$. We establish the signal model:

$$\mathbf{Y}(t) = \mathbf{A}(\theta)\mathbf{X}(t) + \mathbf{N}(t), \quad t = 1, \dots, T$$

Uniformly dividing the spatial angle into L partitions, we construct the direction matrix $\Phi = [\mathbf{a}(\bar{\theta}_1), \mathbf{a}(\bar{\theta}_2), \dots, \mathbf{a}(\bar{\theta}_L)]$, where $\mathbf{a}(\bar{\theta}_i) = [1, e^{-j2\pi d \sin(\bar{\theta}_i)/\lambda}, \dots, e^{-j2\pi(M-1)d\sin(\bar{\theta}_i)/\lambda}]^T$. The optimization model becomes:

$$\begin{aligned} &\min |\mathcal{R}(\mathbf{X})| \\ &\text{s.t. } \|\mathbf{Y} - \Phi\mathbf{X}\|_F \leq \delta \end{aligned}$$

We validate algorithm effectiveness using estimation error as the evaluation criterion. Monte Carlo experiments are conducted for two scenarios, with 200 Monte Carlo runs per data point. Estimation error is measured by root mean square error (RMSE) between estimated and actual values:

$$RMSE = \sqrt{\frac{1}{QK}\sum_{q=1}^{Q}\sum_{k=1}^{K}(\hat{\theta}_{k,q} - \theta_k)^2}$$

where Q is the number of Monte Carlo experiments; K is the number of signal sources; $\hat{\theta}_{k,q}$ represents the estimated value of the k-th signal in the q-th Monte Carlo experiment; and θ_k represents the true value of the k-th signal.

4.2 Reconstruction Error vs. Snapshots and SNR

Consider a uniform linear array with $m = 20$ elements. Intelligent algorithm parameters: population size 100, crossover probability 0.85, mutation probability 0.05, evolution generations 50. For simulated annealing genetic algorithm: initial temperature 5, cooling coefficient 0.9. For multi-population genetic algorithm: 5 populations, each of size 100, crossover probabilities are random numbers between 0.8-0.9, mutation probabilities are random numbers between 0.05-0.1.

Simulation 1: Assume three far-field narrowband independent signals with incident angles $\theta_1 = 22.6°$, $\theta_2 = 27.2°$, $\theta_3 = 35.9°$. Fix SNR at 10 dB and vary snapshots from 100 to 400 in steps of 20. Figure 1Figure 1: see original paper shows RMSE versus snapshots for the five algorithms.

Simulation 2: Assume three far-field narrowband independent signals with incident angles $\theta_1 = 22.6°$, $\theta_2 = 27.2°$, $\theta_3 = 35.9°$. Fix snapshots at 200 and vary SNR from -10 dB to 20 dB in steps of 2 dB. Figure 1(b) shows RMSE versus SNR for the five algorithms.

The simulation results in Figure 1 demonstrate that the proposed algorithms achieve significantly better DOA estimation error than OMP. Figure 1(a) shows that MPGA-SR outperforms l1-SVD in estimation performance. Figure 1(b) reveals that at low SNR, l1-SVD exhibits notably larger estimation errors than other algorithms, validating the effectiveness of the two proposed algorithms under low SNR conditions. Comparing the three genetic algorithm-based approaches, MPGA-SR achieves better estimation accuracy than SAGA-SR, which in turn outperforms GA-SR, confirming the effectiveness of the improved genetic algorithms.

4.3 Reconstruction Error vs. Angle Interval and Sparsity

Algorithm parameters remain the same as in Section 4.2. Array elements are set to 20, SNR is fixed at 10 dB, and snapshots are 200. Simulations evaluate angle resolution performance and estimation errors under different sparsity levels.

Simulation 3: Fix one incident angle at 35.7° and vary the interval between the other angle and the fixed angle from 1° to 30° in steps of 1°. Figure 2Figure 2: see original paper shows estimation bias versus angle interval for the five algorithms.

Simulation 4: Signal incident angles are $\theta_1 = 22.6^\circ$, $\theta_2 = 27.2^\circ$, $\theta_3 = 35.9^\circ$. Sparsity level is varied by changing the number of array elements. Sparsity is defined as K/M, where K is the number of sources and M is the number of array elements. The number of array elements varies from 3 to 36 in steps of 3. Figure 2(b) shows RMSE versus sparsity for the five algorithms.

Figure 2(a) presents simulation results of angle estimation bias versus angle interval. When the angular separation between two sources is less than 10°, OMP shows significantly larger bias than the other four algorithms. As the angular separation increases, all algorithms'biases approach zero, with genetic algorithm-based DOA estimation demonstrating superior angular resolution performance over OMP and l1-SVD. Both MPGA-SR and SAGA-SR outperform GA-SR. Figure 2(b) shows RMSE versus sparsity curves. OMP is extremely sensitive to sparsity, with estimation error increasing sharply as sparsity approaches 1, while l1-SVD estimation errors are similar to those of the intelligent algorithms. Among the three intelligent algorithms, MPGA-SR achieves better estimation accuracy, and SAGA-SR outperforms GA-SR. Simulation results validate the effectiveness of intelligent algorithms for DOA estimation and the superiority of hybrid intelligent algorithms.

4.4 Algorithm Analysis

With array elements 20, SNR 10 dB, snapshots 200, and spatial source angles $\theta_1 = 22.6^\circ$, $\theta_2 = 27.2^\circ$, $\theta_3 = 35.9^\circ$, we compare 100 estimation results. Parameter settings: 20 array elements, 200 snapshots, 10 dB SNR. The mean of 100 estimation results is shown in Table 1, and algorithm iteration curves are shown in Figure 3[Figure 3: see original paper].

Figure 3 shows the genetic iteration process for GA-SR, SAGA-SR, and MPGA-SR sparse reconstruction algorithms across 100 estimations. All three genetic algorithms converge rapidly, reaching near-optimal solutions after five iterations. Table 1 lists the DOA estimation results and errors relative to actual angles across 100 runs. Table 2 compares the average running times of several algorithms. OMP has the shortest runtime, while l1-SVD requires the longest time, far exceeding the other four algorithms. Genetic and improved genetic algorithms have computational times between OMP and l1-SVD, close to OMP. The two proposed improved genetic algorithms achieve slightly better estimation accuracy than l1-SVD with significantly higher computational efficiency. Thus, the proposed algorithms demonstrate clear improvements in both reconstruction accuracy and computational time compared with compressive sensing reconstruction algorithms.

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5 Conclusion

The algorithms proposed in this paper are designed for solving sparse reconstruction problems, where the solution form is the support set of non-zero element positions in sparse signals. Adopting global optimization strategies, the reconstruction results are less affected by initial solutions. In contrast, greedy pursuit and convex relaxation methods are more sensitive to initial solutions, as they begin iterative optimization around the initial solution and may not converge to the global optimum.

SAGA-SR introduces simulated annealing’ s strategy of accepting deteriorating solutions with a certain probability, maintaining population diversity to suppress premature convergence and enhance global optimization capability. MPGA-SR extends the basic genetic algorithm by introducing multiple subpopulations for parallel search in the solution space, balancing global and local search capabilities, reducing the impact of genetic control parameters on optimization results, and demonstrating clear effects in suppressing premature convergence.

Applying the proposed algorithms to DOA estimation and comparing them with OMP and l1-SVD algorithms validates their effectiveness in improving reconstruction accuracy and computational efficiency.

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