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# **Quality Diversity Optimization Method for Bilinear Matrix Inequality Problems** in Control System Design

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**ABSTRACT** In this paper, a quality diversity optimization method (QDOM) based on an adaptive bound-searching algorithm and diversity-selecting immune algorithm is proposed for solving bilinear matrix inequality (BMI) problems in control system design. By using the proposed adaptive bound-searching algorithm, appropriate bound values can be obtained for the entries of controller gain matrices or the eigenvalues of closed-loop systems represented by a state space model. Given the bound values, the proposed diversity-selecting immune algorithm can produce the best-so-far controller gain for a given BMI problem. To find the global optimum efficiently and avoid being trapped in a local optimum, the concept of quality diversity is employed in the proposed method. The proposed method was validated through solving some spectral abscissa,  $H_2$ , and  $H_\infty$  optimization problems. The simulation results show that the proposed QDOM achieved better or similar performance in many benchmark problems as compared with existing BMI solution methods.

**INDEX TERMS** Bilinear matrix inequality (BMI), BMI solution methods, novelty search (NS), quality diversity (QD), quality diversity optimization method (QDOM), spectral abscissa optimization.

## I. INTRODUCTION

Linear matrix inequalities (LMIs) can be used for solving control problems. However, certain control problems cannot be written using LMIs. Such problems can instead be written in a general form known as the bilinear matrix inequality (BMI). In recent years, designing BMI controllers has become a popular research area [1], [2], [3], [4]. The use of BMI formulations has many advantages. For instance, these control problems can be solved using BMI formulations with modest complexity [5]. Furthermore, BMI-based controllers exhibit higher performance and robustness than traditional nonlinear controllers [6]. Examples include static output feedback controller design for spectral abscissa optimization,  $H_2$  optimization, and  $H_{\infty}$  optimization [7], [8], [9].

Unfortunately, BMI problems are NP-hard [10], and algorithms for solving these problems can only be applied to problems of modest size. Moreover, computations associated with BMI constraints are more time-consuming and resourceconsuming than those associated with LMI constraints [5]. The limitations of existing BMI solution methods are as follows. First, the decision variables in BMI solution methods such as branch-and-bound-type methods [11] must be written in vector form. However, in controller design, expressing decision variables in matrix form is more convenient than expressing them in vector form [12]. Second, derivations must be performed in some BMI solution methods before some algorithms are applied. For instance, decompositions must be performed in the convex-concave decomposition method (CCDM) [7] before the algorithm is applied; approximations must be performed in the inner convex approximation method (ICAM) [8] before the algorithm is applied. Unfortunately, these derivations can be heuristic or difficult.

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Third, BMI solution methods such as some alternating minimization methods [13] and path-following methods [14], [15] may be suitable only for particular problem structures. When applying these methods to other problem structures, effort must be made to reformulate the problem. Fourth, BMI solution methods such as HIFOO [16], [17], [18], LMIRank [19], and PENBMI [20] only perform local optimization to solve BMI problems with several inherent local optima.

To address the aforementioned drawbacks of existing BMI solution methods, the method of reduction of variables (MRVs) [21] has been proposed. The MRVs adopts stochastic mechanisms based on a hybrid multiobjective immune algorithm (HMOIA) to search for global solutions to BMI problems; however, when stochastic mechanisms are employed, bounds must be set for the entries of controller gain matrices or the eigenvalues of closed-loop systems represented by a state space model. The bounds strongly affect the solutions to BMI problems, and different BMI problems need different bounds that enable efficient search for global optima.

For setting different bounds to solve BMI problems, the concept of quality diversity (QD) is adopted in this work. This concept is used to explore the search space of decision variables while avoiding entrapment in local optima when solving BMI problems. QD algorithms can be used to find the optimal solution with high-novelty behaviors. The QD algorithm is based on the concept of novelty search (NS) used to promote behavioral novelty. NS rewards behaviors that are different from pursuit of the final goal (i.e., the highest-fitness solution). By using NS, different behaviors, that is, different values of bounds and different values of decision variables in our case, can be explored efficiently [22].

This paper proposes a QD optimization method (QDOM) for efficiently setting different bounds to solve various BMI problems and exploring the search space of the decision variables. The QDOM involves the execution of adaptive bound-searching algorithm and diversity-selecting immune algorithm. The adaptive bound-searching algorithm is used for adaptively searching for bounds of the entries of controller gain matrices and bounds of the eigenvalues of closed-loop systems; it involves three steps: diversity search, quality search, and crossover. Diversity search is used for finding high-novelty bounds. Moreover, quality search and crossover are used to find bounds that correspond to high fitness values. The diversity-selecting immune algorithm is used to efficiently find best-so-far solutions for BMI problems while avoiding becoming trapped in a local optimum.

To validate the proposed methodology, the proposed QDOM was compared with HIFOO, LMIRank, PENBMI, CCDM, ICAM, and the MRVs in solving benchmark BMI problems. Our numerical results show that the QDOM outperformed or had performance similar to most aforementioned BMI solution methods; we conclude that the proposed QDOM method can effectively solve BMI problems in control engineering. The rest of this paper is organized as follows. Section II presents the problem formulation. Section III describes the proposed QDOM. Section IV presents the simulation results. Finally, Section V concludes this study.

# **II. SYSTEM DESCRIPTION AND PROBLEM FORMULATION** In this section, system and controller design is investigated as a BMI optimization problem. The decision variables of BMIs are classified into two types: external variables ( $\alpha$ ) and internal variables (X), where $\alpha$ is a vector or matrix and X is composed of scalar and real-valued symmetric matrix [21].

The inequality

$$\mathcal{BMI}(\boldsymbol{\alpha}, \boldsymbol{X}) < 0 \tag{1}$$

represents a BMI associated with a controller design problem, where the matrix function  $\mathcal{BMI}(\cdot)$  includes two matrix decision variables  $\alpha$  and X. This BMI problem can be reduced to an LMI problem when one decision variable is given (or fixed).

A scalar function  $\mathcal{F}$  can be added to (1) to achieve some optimal controller designs. For the aim, the value of  $\mathcal{F}$  should be as small as possible. Thus, the control problem with BMI constraints can be written as follows:

$$\min_{\boldsymbol{\alpha}, X} \mathcal{F}(\boldsymbol{\alpha})$$
  
subject to  $\mathcal{BMI}(\boldsymbol{\alpha}, X) < 0.$  (2)

The system under investigation is represented in the following form:

$$\begin{cases} \dot{\mathbf{x}} = \mathbf{A}\mathbf{x} + \mathbf{B}_{1}\mathbf{w} + \mathbf{B}\mathbf{u} \\ \mathbf{z} = \mathbf{C}_{1}\mathbf{x} + \mathbf{D}_{11}\mathbf{w} + \mathbf{D}_{12}\mathbf{u} \\ \mathbf{y} = \mathbf{C}\mathbf{x} \end{cases}$$
(3)

where  $\mathbf{x} \in \mathcal{R}^{n_x}$  represents the state vector,  $\mathbf{w} \in \mathcal{R}^{n_w}$  represents the external noise,  $\mathbf{u} \in \mathcal{R}^{n_u}$  represents the control input,  $\mathbf{z} \in \mathcal{R}^{n_z}$  represents the measure output, and  $\mathbf{y} \in \mathcal{R}^{n_y}$  represents the controlled output.

For a static output feedback controller, the following equation is obtained:

$$\mathbf{u} = \mathbf{F}\mathbf{y} = \mathbf{F}\mathbf{C}\mathbf{x} \tag{4}$$

where  $\mathbf{F} \in \mathcal{R}^{n_u \times n_y}$  is the controller gain matrix.

A closed-loop system can be expressed as follows by using the output feedback:

$$\begin{cases} \dot{\mathbf{x}} = (\mathbf{A} + \mathbf{BFC})\mathbf{x} + \mathbf{B}_{1}\mathbf{w} = \mathbf{A}_{F}\mathbf{x} + \mathbf{B}_{1}\mathbf{w} \\ \mathbf{z} = (\mathbf{C}_{1} + \mathbf{D}_{12}\mathbf{FC})\mathbf{x} + \mathbf{D}_{11}\mathbf{w} = \mathbf{C}_{F}\mathbf{x} + \mathbf{D}_{11}\mathbf{w} \end{cases}$$
(5)

where the controller gain matrix **F** can be transformed into an  $n_u n_y \times 1$  vector for solving pole placement problems that occur in closed-loop system design.

In the following text, several BMI problems expressed in the form of (2)–spectral abscissa optimization,  $H_2$  optimization, and  $H_{\infty}$  optimization–are described. The external and internal variables associated with these problems are then identified.

The spectral abscissa of a square matrix is the largest real parts of the matrix's eigenvalues. The spectral abscissa of  $A_F$  in (5) is defined as follows [23]:

$$\alpha_0(\mathbf{A}_{\mathbf{F}}) = \max_{\boldsymbol{\lambda} \in \text{eig}\{\mathbf{A}_{\mathbf{F}}\}} \text{Re}(\boldsymbol{\lambda})$$
(6)

where  $eig\{A_F\}$  is the set of eigenvalues of  $A_F$  and  $Re(\lambda)$  is the real part of eigenvalue  $\lambda$ . To achieve asymptotic stability, spectral abscissa optimization can be performed [23]. If the optimal spectral abscissa value is strictly negative, a feedback control law exists in (4) such that the closed-loop system in (5) is asymptotic stable [9]. Spectral abscissa optimization is formulated as follows:

$$\min_{\mathbf{F}} \alpha_0(\mathbf{A}_{\mathbf{F}}). \tag{7}$$

Based on [9] and [23], the optimization of the spectral abscissa of the square matrix  $A_F$  can be considered an optimization problem over a positive-definite symmetric matrix **P**. The spectral abscissa of  $A_F$  can be expressed as follows [23]:

$$\alpha_0(\mathbf{A}_{\mathbf{F}}) = \inf_{\mathbf{P} \in \mathbf{S}^n, \mathbf{P} > 0} \frac{1}{2} \lambda_{\max}(\mathbf{P}^{\frac{1}{2}} \mathbf{A}_{\mathbf{F}} \mathbf{P}^{-\frac{1}{2}} + \mathbf{P}^{-\frac{1}{2}} \mathbf{A}_{\mathbf{F}}^{\top} \mathbf{P}^{\frac{1}{2}}) \quad (8)$$

where **P** is a positive-definite decision matrix, **S**<sup>*n*</sup> denotes the space of real symmetric matrices, and  $\lambda_{max}$  denotes the maximum eigenvalue of a symmetric matrix.

Let  $\mathcal{F}(\boldsymbol{\alpha}) = \alpha_0(\mathbf{A_F})$  where  $\boldsymbol{\alpha} = \mathbf{F}$  and  $X = (\mathbf{P}, \boldsymbol{\beta})$  denote the external and internal variable of  $\mathcal{F}$  in (2), respectively. The spectral abscissa  $\alpha_0(\mathbf{A_F})$  optimization problem is equal to the following BMI-constrained optimization problem:

$$\min_{\mathbf{F}, \mathbf{P}, \beta} \alpha_0(\mathbf{A}_{\mathbf{F}})$$
  
subject to  $\mathbf{P}\mathbf{A}_{\mathbf{F}} + \mathbf{A}_{\mathbf{F}}^{\top}\mathbf{P} + 2\beta\mathbf{P} < 0, \mathbf{P} > 0$  (9)

where  $\beta$  is related to the decay rate of the system.

Consider a system G(s) whose  $H_2$  norm can be defined as follows [24]:

$$||G(s)||_2 = \sqrt{\frac{1}{2\pi} \int_{-\infty}^{\infty} \operatorname{tr}(G(j\omega)^H G(j\omega)) d\omega} \qquad (10)$$

where  $G(j\omega)^H$  represents the Hermitian of  $G(j\omega)$  and  $tr(G(j\omega)^H G(j\omega))$  represents the trace of  $G(j\omega)^H G(j\omega)$ . Because the  $H_2$  norm is related to the root-mean-square impulse response of the system, this norm can be used to measure the robustness of a closed-loop system under noise or external disturbance [25].

The  $H_{\infty}$  norm of G(s) can be defined as follows [24]:

$$||G(s)||_{\infty} = \max_{\omega} \bar{\sigma}(G(j\omega)) \tag{11}$$

where  $\bar{\sigma}(G(j\omega))$  represents the maximum singular value of  $G(j\omega)$ . Because the  $H_{\infty}$  norm is related to the peak gain of the frequency response of the system, this norm can be used to guarantee the robust stability or performance of a closed-loop system when model uncertainty exists [25].

To solve  $H_2$  and  $H_{\infty}$  optimization problems, the state-space realization  $G_{cl}(\mathbf{F})$  is used to represent the closed-loop system in (5) as follows:

$$G_{\rm cl}(\mathbf{F}) = \begin{bmatrix} \mathbf{A}_{\rm F} | & \mathbf{B}_{\rm 1} \\ \overline{\mathbf{C}_{\rm F}} | & \mathbf{D}_{\rm 11} \end{bmatrix}.$$
 (12)

Let  $G_{cl}$  denote the transfer matrix of  $G_{cl}(\mathbf{F})$ . The matrix  $\mathbf{F}$  should be determined to minimize  $||G_{cl}||_2$  or  $||G_{cl}||_{\infty}$  under certain BMI constraints.

For the  $H_2$  optimization problem described in [9] and [26], we consider the following optimization problem:

$$\begin{aligned} \min_{\mathbf{F},\mathbf{Q},\mathbf{Y}} & ||G_{c1}||_{2} \\ \text{subject to } \mathbf{A}_{\mathbf{F}}\mathbf{Q} + \mathbf{Q}\mathbf{A}_{\mathbf{F}}^{\top} + \mathbf{B}_{1}\mathbf{B}_{1}^{\top} < 0 \\ & \begin{bmatrix} \mathbf{Y} & \mathbf{C}_{1}\mathbf{Q} \\ \mathbf{Q}\mathbf{C}_{1}^{\top} & \mathbf{Q} \end{bmatrix} > 0, \mathbf{Q} > 0 \end{aligned}$$
(13)

where external variable  $\alpha = \mathbf{F}$ , the internal variable  $X = (\mathbf{Q}, \mathbf{Y})$ , and  $\mathcal{F}(\alpha) = ||G_{cl}||_2$ .

For the  $H_{\infty}$  optimization problem described in [9] and [27], we consider the following optimization problem:

$$\min_{\mathbf{F}, \gamma, \mathbf{Y}} ||G_{cl}||_{\infty}$$
subject to
$$\begin{bmatrix} \mathbf{Y} \mathbf{A}_{\mathbf{F}} + \mathbf{A}_{\mathbf{F}}^{\top} \mathbf{Y} & \mathbf{Y} \mathbf{B}_{\mathbf{I}} & \mathbf{C}_{\mathbf{F}}^{\top} \\ \mathbf{B}_{\mathbf{I}}^{\top} \mathbf{Y} & -\gamma \mathbf{I} & \mathbf{D}_{\mathbf{I}\mathbf{I}}^{\top} \\ \mathbf{C}_{\mathbf{F}} & \mathbf{D}_{\mathbf{I}\mathbf{I}} & -\gamma \mathbf{I} \end{bmatrix} < 0$$

$$\gamma > 0, \mathbf{Y} > 0$$

$$(14)$$

where external variable  $\boldsymbol{\alpha} = \mathbf{F}$ , internal variable  $X = (\gamma, \mathbf{Y})$ , and  $\mathcal{F}(\boldsymbol{\alpha}) = ||G_{cl}||_{\infty}$ .

In the aforementioned examples, when  $\alpha$  is determined, the feasible set of X can be explored internally because of the convexity of LMIs. The variable X does not affect the fitness values but affects the feasibility. If feasibility information can be extracted accurately from  $\alpha$ , X can be considered hidden from the external search. Thus, the problem with two variables (i.e.,  $\alpha$  and X) can be transformed into a new problem with only one variable (i.e.,  $\alpha$ ) [21].

To transform the problem with two variables into a new problem with only one variable, the following eigenvalue problem is considered [21]:

$$(\lambda^*(\alpha), X^*(\alpha)) = \arg\min_{\lambda, X} \lambda$$
  
subject to  $\mathcal{BMI}(\alpha, X) < \lambda \mathbf{I}$  (15)

where  $\lambda^*(\alpha)$  and  $X^*(\alpha)$  are considered functions of  $\alpha$ . Moreover,  $(\lambda^*(\alpha), X^*(\alpha))$  is the pair for which the minimum value of  $\lambda$  in (15) is achieved.

By introducing the reduction theorem in [21], the problem expressed in (2) can be transformed into the following form:

$$\min_{\boldsymbol{\alpha}} \mathcal{F}(\boldsymbol{\alpha})$$
  
subject to  $\lambda^*(\boldsymbol{\alpha}) < 0.$  (16)

In addition, we define the problem expressed in (2) is feasible if and only if there exists an external variable  $\tilde{\alpha}$  such that  $\lambda^*(\tilde{\alpha}) < 0$ .



**FIGURE 1.** Flowchart of the proposed QDOM. The adaptive bound-searching algorithm uses previous bounds to search for new bounds, and the diversity-selecting immune algorithm searches for  $\alpha$  and computes new fitness values of  $\alpha$  that are associated with the new bounds.

#### **III. PROPOSED QDOM**

In last section, we illustrate that a BMI control design problem can be transformed into an optimization problem as shown in (16). This section illustrates how the QDOM solves (16). The QDOM involves the use of the proposed adaptive bound-searching algorithm and diversity-selecting immune algorithm. The adaptive bound-searching algorithm adaptively changes the bounds of the entries of controller gain matrices or the bounds of the eigenvalues of closed-loop systems represented by a state space model. The bound values determined by the aforementioned algorithm are used by the diversity-selecting immune algorithm to compute the fitness function associated with the BMI problem. To find the optimal solution to the BMI problem, the bounds determined by the adaptive bound-searching algorithm and diversity-selecting immune algorithm are applied iteratively.

## A. PROPOSED QDOM

Fig. 1 shows the flowchart of the proposed QDOM. Given the initial bounds  $[g^{\theta} \lambda^{\theta}]^{\top} = [g^{\text{initial}} \lambda^{\text{initial}}]^{\top}$ . The parameter

 $g^{\text{initial}}$  represents the scalar values of the initial bounds of the entries of controller gain matrices, and  $\lambda^{\text{initial}}$  represents the scalar values of the initial bounds of the eigenvalues of closed-loop systems represented by a state space model. The adaptive bound-searching algorithm searches for new bounds. The diversity-selecting immune algorithm then uses the new bounds to compute the fitness values  $f_t^{\text{BMI}}$  associated with the BMI problem.

The variable  $t^{\text{search}}$  represents the number of trials in which the same bounds are used. If  $t^{\text{search}}$  is equal to  $t^{\text{search-end}}$ , which is the maximum number of trials in which the same bounds are used in the diversity-selecting immune algorithm, the average fitness value  $f^{\text{mean}}$  of  $\alpha$  associated with the current bounds is computed as follows:

$$f^{\text{mean}} = \frac{1}{t^{\text{search}}} \sum_{k=t-t^{\text{search}}+1}^{t} f_k^{\text{BMI}}$$
(17)

where t is the index indicating the current trial and  $f_k^{\text{BMI}}$  is the best fitness value of  $\alpha$  in the kth trial. As long as  $t^{\text{search}} < t^{\text{search-end}}$ , the diversity-selecting immune algorithm is used to search for  $\alpha$  and compute new fitness values of  $\alpha$  associated with the current bounds.

If the current average fitness value  $f^{\text{mean}}$  is the best average fitness value, the best average fitness value  $f^{\text{best}}$  is updated (i.e.,  $f^{\text{best}} = f^{\text{mean}}$ ), and the values of bounds  $g^{\text{best}}$  and  $\lambda^{\text{best}}$  are also updated (i.e.,  $g^{\text{best}} = g^{\theta}$  and  $\lambda^{\text{best}} = \lambda^{\theta}$ ). The diversity-selecting immune algorithm is terminated after it has been executed  $t = T^{\text{max}}$  times, where  $T^{\text{max}}$  represents the maximum number of trials. Finally, the  $\alpha$  value with the best fitness  $f^{\text{BMI-best}}$  is output to minimize the objective function  $\mathcal{F}$  in (16). The controller gain matrix  $\alpha = \mathbf{F}$  is then obtained as the approximate solution to the BMI problem.

#### B. OVERVIEW OF NS AND QD

NS, which is inspired by nature's trend toward diversity, is a method that can be implemented by neuroevolution of augmenting topologies [22], [28], [29] or genetic programming [30], [31] to search only for individuals with novel behaviors [22]. In NS, the fitness function of evolutionary algorithms is replaced by a measure of solution novelty [32]. NS focuses on obtaining behaviorally diverse solutions instead of high-fitness ones (high-quality solutions). This method is particularly efficient for solving problems that involve deceptive or sparse rewards.

In NS, a behavior characterization vector  $\mathbf{b}(\cdot)$  is used to store behavioral information. The behavioral information that must be stored in  $\mathbf{b}(\cdot)$  is user-defined. In NS, new characterization vectors are generated through crossover or mutation. If  $\boldsymbol{\alpha}$  denotes a behavior, the novelty of  $\mathbf{b}(\boldsymbol{\alpha})$  can be measured using a novelty function  $\rho$  as follows:

$$\rho(\mathbf{b}(\boldsymbol{\alpha})) = \frac{1}{k} \sum_{l=1}^{k} \operatorname{dist}(\mathbf{b}(\boldsymbol{\alpha}), \mathbf{b}(\boldsymbol{\alpha}_{l}))$$
(18)

where  $\mathbf{b}(\boldsymbol{\alpha}_l)$  is the *l*th-nearest neighbor of  $\mathbf{b}(\boldsymbol{\alpha})$  in the archive with respect to a similarity measure dist( $\cdot$ ,  $\cdot$ ). Moreover, *k* 



**FIGURE 2.** Adaptive bound search. The black "+" signs represent the b<sup>bounds</sup> values that are currently being used to search for new b<sup>bounds</sup> values, the green " $\Delta$ " signs denote the new b<sup>bounds</sup> values, and the orange " $\bullet$ " signs represent the b<sup>bounds</sup> value that has been stored in the archive. The blue "X" marks represent local optima, and the red " $\star$ " signs represent the global optimum. (a) In diversity search, exploration is conducted in the purple dashed rectangle to search for new b<sup>bounds</sup> values. (b) In quality search, new b<sup>bounds</sup> values are found along a certain direction. (c) In the crossover operation, the two best b<sup>bounds</sup> values are used to search for new b<sup>bounds</sup> values.

denotes the number of neighbors. The novelty value  $\rho(\mathbf{b}(\alpha))$  is its average distance to the *k* nearest neighbors in the archive. If the novelty value of a new characterization vector satisfies a certain threshold  $\rho^{\min}$ , the vector is stored in the archive.

NS algorithms avoid exploring search space regions that have already been explored by calculating the similarity between new and previous characterization vectors. Over generations, these algorithms encourage the population to spread out across the space of diverse behaviors.

Because NS algorithms only attempt to find high-novelty behaviors, the concept of QD can be employed to find an optimal solution while searching for high-novelty behaviors.

# C. PROPOSED ADAPTIVE BOUND-SEARCHING ALGORITHM

For dynamically adjusting search bounds of QDOM, Algorithm 1 shows the proposed adaptive bound-searching algorithm consisting of three steps. The first step is called diversity search (lines 11–16 of Algorithm 1), which is used to find the direction for tuning the values of bounds. The second step is called quality search (lines 19–23 of Algorithm 1), which is used to search for better values of bounds for the diversity-selecting immune algorithm to find higher fitness values of  $\alpha$  associated with the bounds. The third step is crossover operation (lines 27–30). To find global optima without becoming trapped in a local optimum, the adaptive bound-searching algorithm performs diversity search or quality search. Subsequently, it continues to select the two best pairs of bounds to perform crossover until the stopping criterion is satisfied.

Fig. 2 illustrates the three steps involved in the adaptive bound-searching algorithm. During diversity search,  $\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\text{base}}) = [g^{\text{base}} \lambda^{\text{base}}]^{\top}$  is used to search for new  $\mathbf{b}^{\text{bounds}}$  values in a specific region (i.e., the dashed rectangular area in Fig. 2(a)). During quality search,  $\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\text{base}}) = [g^{\text{base}} \lambda^{\text{base}}]^{\top}$  and  $\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\text{best}}) = [g^{\text{best}} \lambda^{\text{best}}]^{\top}$  are used to search for a new  $\mathbf{b}^{\text{bounds}}$  value in a certain search direction. During the crossover operation, the previous  $\mathbf{b}^{\text{bounds}}$  values  $[g^{\text{best}} \lambda^{\text{best}}]^{\top}$  and  $[g^{\text{best}2} \lambda^{\text{best}2}]^{\top}$  are used to generate a new **b**<sup>bounds</sup> value.

The input parameter t of Algorithm 1 indicates the number of trials performed by the diversity-selecting immune algorithm. The term  $t^{\text{search-end}}$  is the maximum number of trials for which the same bounds **b**<sup>bounds</sup> are used in the diversity-selecting immune algorithm. Finally, the parameter  $t^{\text{NS-end}}$  reflects the maximum number of times that diversity search is conducted.

The inputs  $[g^{\theta}, \lambda^{\theta}]$  represent the current bounds (i.e.,  $\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\theta}) = [g^{\theta} \ \lambda^{\theta}]^{\top}$ ) where  $\theta$  represents the index of searching bounds. The values of the bounds are related to the values of the external variable  $\boldsymbol{\alpha}$ . The *m*th value of  $\boldsymbol{\alpha}^{\theta}$  in (16) can be recovered from a given vector  $\boldsymbol{\lambda}^{\text{pre}}$  of eigenvalues or generated in a pointwise manner over prescribed bounds  $[-g^{\theta}, g^{\theta}]$ . If a range  $[-\lambda^{\theta}, 0] \times [-\lambda^{\theta}, \lambda^{\theta}]$  is given, the initial  $\boldsymbol{\lambda}^{\text{pre}}$  vector can be randomly generated over the range as follows:

$$[\boldsymbol{\lambda}^{\text{pre}}]_m \in \{\sigma + j\omega : (\sigma, \omega) \in [-\lambda^{\theta}, 0] \times [-\lambda^{\theta}, \lambda^{\theta}]\}$$
(19)

where complex values of  $\lambda^{\text{pre}}$  occur in conjugate pairs. The parameter  $\alpha^{\theta}$  can be generated in accordance with the bounds defined as follows:

$$[\boldsymbol{\alpha}^{\theta}]_m \in [-g^{\theta}, g^{\theta}].$$
(20)

After applying the diversity-selecting immune algorithm under the initial bounds (i.e.,  $\mathbf{b}^{\text{bounds}}$   $([g^{\theta} \ \lambda^{\theta}]^{\top}) = [g^{\text{initial}} \lambda^{\text{initial}}]^{\top}$ ) for  $t^{\text{search-end}}$  trials, the average fitness value of  $\boldsymbol{\alpha}$  in the  $t^{\text{search-end}}$  trials is computed. Because the direction for the new bound search must be determined, a diversity search (lines 11–16) is performed to search for new bounds  $\mathbf{b}^{\text{bounds}}$   $([g^{\theta} \ \lambda^{\theta}]^{\top}) = [g^{\theta+1} \ \lambda^{\theta+1}]^{\top}$  in a region of the search space with the bounds  $[g^{\text{base}} \ \lambda^{\text{base}}]^{\top}$ . The bounds  $[g^{\text{base}} \ \lambda^{\text{base}}]^{\top}$  are equal to  $[g^{\text{initial}} \ \lambda^{\text{initial}}]^{\top}$  when the initial bounds are prescribed. In addition, the new bounds  $[g^{\theta+1} \ \lambda^{\theta+1}]^{\top}$  will be used by the diversity-selecting immune algorithm to compute new fitness and average fitness values of  $\boldsymbol{\alpha}$ .

# Algorithm 1 Adaptive Bound-Searching Algorithm

**Input:**  $t, \theta, A_{bds}, [g^{\theta}, \lambda^{\theta}], [g^{base}, \lambda^{base}], [g^{step}, \lambda^{step}]$  $[g^{\text{best}}, \lambda^{\text{best}}]$ **Output:**  $[g^{\theta+1}, \lambda^{\theta+1}]$ 1:  $t^{\rm NS} \leftarrow 0$ 2: if  $t < t^{\text{search-end}}$  then  $[g^{\theta+1}, \lambda^{\theta+1}] \leftarrow [g^{\theta}, \lambda^{\theta}]$ 3:  $[g^{\text{base}}, \lambda^{\text{base}}] \leftarrow [g^{\theta}, \lambda^{\theta}]$ 4:  $\theta \leftarrow \theta + 1$ 5: break 6: 7: else while  $t > t^{\text{search-end}}$  and  $t^{\text{NS}} < t^{\text{NS-end}}$  do 8:  $t^{\rm NS} \leftarrow t^{\rm NS} + 1$ 9: if  $[g^{\text{step}}, \lambda^{\text{step}}] = [0, 0]$  then 10: Perform diversity search in (21) to obtain 11: the candidate bound  $[g_c^{\theta+1}, \lambda_c^{\theta+1}]$  and calculate  $\rho([g_c^{\theta+1}, \lambda_c^{\theta+1}]^{\top})$  by using novelty functions in (22)-(24)if  $\rho([g_c^{\theta+1}, \lambda_c^{\theta+1}]^{\top}) > \rho^{\text{bds-min}}$  then 12: Set  $[g^{\theta+1}, \lambda^{\theta+1}] \leftarrow [g^{\theta+1}_c, \lambda^{\theta+1}_c]$ 13: 14:  $\theta \leftarrow \theta + 1$ break 15: end if 16: end if 17: if  $t^{NS} = t^{NS-end}$  then 18: Calculate new search direction  $[g_{new}^{step}, \lambda_{new}^{step}]$  using 19: (25) **if**  $[g_{\text{new}}^{\text{step}}, \lambda_{\text{new}}^{\text{step}}] \neq [0, 0]$  **then** quality search 20: Perform quality search in (26) to search 21: for  $[g^{\theta+1}, \lambda^{\theta+1}]$  and set  $[g^{\text{base}}, \lambda^{\text{base}}] \leftarrow [g^{\text{best}}, \lambda^{\text{best}}]$  and  $[g^{\text{step}}, \lambda^{\text{step}}] \leftarrow [g^{\text{step}}_{\text{new}}, \lambda^{\text{step}}_{\text{new}}]$  $\theta \leftarrow \theta + 1$ 22. break 23: else 24: Enlarge the search region by adjusting  $r^{NS}$ 25: Set  $t^{\rm NS} = 0$ 26: if  $r^{NS} > r^{max}$  then 27: Perform crossover operation in (27) to 28: obtain  $[g^{\theta+1}, \lambda^{\theta+1}]$  and set  $\theta \leftarrow \theta + 1$ break 29: end if 30: end if 31: end if 32: end while 33:  $t \leftarrow t + 1$ 34: 35: end if 36: %  $t^{\text{search-end}}$ ,  $t^{\text{NS-end}}$ ,  $\rho^{\text{bds-min}}$ , and  $r^{\text{max}}$  are preset parameters of Algorithm 1.

Fig. 2(a) illustrates the diversity search. The parameters  $g^{\theta+1}$  and  $\lambda^{\theta+1}$  are computed using the following equations:

$$g^{\theta+1} = g^{\text{base}} + g^{\text{random}}$$
$$\lambda^{\theta+1} = \lambda^{\text{base}} + \lambda^{\text{random}}$$
(21)

where  $g^{\text{random}}$  is a random number selected from

$$(-g^{\text{base}}r^{\text{NS}}, g^{\text{base}}r^{\text{NS}}) \setminus \{0\}$$

and  $\lambda^{random}$  is a random number selected from

$$(-\lambda^{\text{base}}r^{\text{NS}}, \lambda^{\text{base}}r^{\text{NS}}) \setminus \{0\}.$$

The variable  $r^{NS}$  determines the size of the search region.

The novelty function  $\rho(\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\theta+1}))$  is computed as follows:

$$\rho(\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\theta+1})) = \rho([g^{\theta+1} \lambda^{\theta+1}]^{\top})$$
$$= \frac{1}{|\mathcal{A}|} \sum_{l=1}^{|\mathcal{A}|} \text{dist}(\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\theta+1}), \mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}_{l})).$$
(22)

The term dist( $\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\theta+1})$ ,  $\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}_l)$ ) is computed using the following equation:

dist(
$$\mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}^{\theta+1}), \mathbf{b}^{\text{bounds}}(\boldsymbol{\alpha}_{l})$$
)  
=  $\sqrt{(\frac{\lambda^{\theta}}{g^{\theta}})^{2}(g_{l} - g^{\theta+1})^{2} + (\lambda_{l} - \lambda^{\theta+1})^{2}}$ (23)

where  $(\frac{\lambda^{\theta}}{g^{\theta}})^2$  is used for rank-normalizing the value of  $(g_l - g^{\theta+1})^2$ .

If the candidate new **b**<sup>bounds</sup>  $([g_c^{\theta+1} \lambda_c^{\theta+1}]^{\top})$  value is sufficiently novel, i.e.,  $\rho([g^{\theta+1} \lambda^{\theta+1}]^{\top})$  is higher than a threshold  $\rho^{\text{bds-min}}$  expressed as:

$$\rho^{\rm bds-min} = \lambda^{\rm base} r^{\rm NS} \tag{24}$$

then we set  $\mathbf{b}^{\text{bounds}} ([g^{\theta+1} \ \lambda^{\theta+1}]^{\top}) = [g_c^{\theta+1} \ \lambda_c^{\theta+1}]^{\top}$  and terminate Algorithm 1.

If the new candidate bounds  $[g_c^{\theta+1} \lambda_c^{\theta+1}]^{\top}$  with high novelty cannot be found through diversity search in the search region (i.e., the dashed rectangular area in Fig. 2(a)),  $t^{\text{NS}}$ becomes equal to  $t^{\text{NS-end}}$ . If  $t^{\text{NS}}$  is equal to  $t^{\text{NS-end}}$  and if an average fitness value higher than the initial average fitness value has been found in the previous trials (i.e., better bounds  $[g^{\text{best}} \lambda^{\text{best}}]^{\top}$  that correspond to a better average fitness value have been found), the directions for quality search are determined. The term  $\mathbf{b}^{\text{bounds}} ([g^{\text{best}} \lambda^{\text{best}}]^{\top}) \in \mathcal{A}_{\text{bds}}$  corresponds to the best average fitness value  $f^{\text{best}}$  where  $\mathcal{A}_{\text{bds}}$  is a set storing a few  $\mathbf{b}^{\text{bounds}} ([g \lambda]^{\top})$  values. Each  $[g \lambda]^{\top}$  value corresponds to an average fitness value of  $\boldsymbol{\alpha}$ . The search directions  $g^{\text{step}}$ and  $\lambda^{\text{step}}$  are determined using the following equations:

$$g^{\text{step}} = g^{\text{best}} - g^{\text{base}}$$
$$\lambda^{\text{step}} = \lambda^{\text{best}} - \lambda^{\text{base}}.$$
 (25)

The vector  $[g^{\text{step}} \lambda^{\text{step}}]^{\top}$  is represented by a yellow arrow in Fig. 2(b). Quality search is performed in line 21 of Algorithm 1.

On the basis of the search directions in (25),  $g^{\theta+1}$  and  $\lambda^{\theta+1}$  are generated as follows:

$$g^{\theta+1} = g^{\text{best}} + g^{\text{step}}$$
$$\lambda^{\theta+1} = \lambda^{\text{best}} + \lambda^{\text{step}}.$$
 (26)

The dashed arrow in Fig. 2(b) represents the same vector as the yellow arrow in Fig. 2(b). After performing quality search by using (26),  $[g^{\text{base}} \lambda^{\text{base}}]^{\top}$  is updated (i.e.,  $[g^{\text{base}} \lambda^{\text{base}}]^{\top} = [g^{\text{best}} \lambda^{\text{best}}]^{\top}$ ), and the current **b**<sup>bounds</sup> values are updated in line 21 of Algorithm 1. Quality search might be performed for many trials if a larger average fitness value can be found along a search direction.

If a larger average fitness value cannot be found along a search direction (i.e.,  $[g^{\text{base}} \lambda^{\text{base}}]^{\top}$  is equal to  $[g^{\text{best}} \lambda^{\text{best}}]^{\top}$ ), the diversity search is conducted in a larger search region (line 11 of Algorithm 1) by increasing the value of  $r^{\text{NS}}$  in (21) after performing quality search or diversity search. In this case, the  $\rho^{\text{bds-min}}$  in (24) is also assigned a new value.

Finally, if the region for the diversity search reaches a prescribed size, i.e.,  $r^{\text{NS}}$  is higher than a prescribed threshold  $r^{\text{max}}$ , and better bounds corresponding to a higher average fitness value cannot be found after performing a quality search or diversity search, the crossover operation is performed to generate new bounds  $[g^{\theta+1} \ \lambda^{\theta+1}]^{\text{T}}$ . This operation can be expressed by the following equations:

$$g^{\theta+1} = \xi^{\text{bounds}} g^{\text{best}} + (1 - \xi^{\text{bounds}}) g^{\text{best}2}$$
$$\lambda^{\theta+1} = \xi^{\text{bounds}} \lambda^{\text{best}} + (1 - \xi^{\text{bounds}}) \lambda^{\text{best}2}$$
(27)

where  $\xi^{\text{bounds}}$  is a random number selected from the range (0, 1) and  $[g^{\text{best}2} \lambda^{\text{best}2}]^{\top} \in \mathcal{A}_{\text{bds}}$  represents the second-best bounds that correspond to the second-highest average fitness value of  $\boldsymbol{\alpha}$ . Fig. 2(c) illustrates the crossover operation.

In this case,  $\mathbf{b}^{\text{bounds}}$   $([g^{\theta} \ \lambda^{\theta}]^{\top})$  can be used by the diversity-selecting immune algorithm to compute new fitness values of  $\boldsymbol{\alpha}$  that are associated with  $\mathbf{b}^{\text{bounds}}$   $([g^{\theta} \ \lambda^{\theta}]^{\top})$ , and  $[g^{\theta} \ \lambda^{\theta}]^{\top}$  is copied to archive  $\mathcal{A}_{\text{bds}}$ .

# D. PROPOSED DIVERSITY-SELECTING IMMUNE ALGORITHM

Motivated by the HMOIA [21] for generating and updating  $\alpha$ , we developed a diversity-selecting immune algorithm based on QD. This algorithm employs the concept of QD to determine the external variables, that is, it searches for behaviors  $\alpha$  that correspond to high fitness values. Algorithm 2 presents the pseudocode of the developed diversity-selecting immune algorithm. In line 2 of Algorithm 2, the population is initialized with the nominal population size  $N_{\text{nom}}$  as follows:

$$\{\boldsymbol{\alpha}_1, \boldsymbol{\alpha}_2, \ldots, \boldsymbol{\alpha}_{N_{\text{nom}}}\}$$

During the evolutionary process of the artificial immune system [33], the population size changes over iterations but remains smaller than the maximum population size  $N_{\text{max}}$ .

The values of  $\alpha$  can be recovered from a given vector of eigenvalues  $\lambda^{\text{pre}}$ . This vector can be determined using a trust-region Levenberg–Marquardt method [21], [34], which can

## Algorithm 2 Diversity-Selecting Immune Algorithm

- **Input:**  $[g^{\theta} \lambda^{\theta}]^{\top}$  for the bounds on the entries of behaviors  $\alpha$ , empty archive  $\mathcal{A}_{bvr}$
- **Output:** Best behavior  $\alpha$  and the fitness value  $f^{BMI}$
- 1: Use  $[g^{\theta} \lambda^{\theta}]^{\top}$  for prescribing bounds on the entries of behaviors  $\boldsymbol{\alpha}$
- 2: Initialize the population  $\mathcal{A}_{pop}$  with the nominal population size  $N_{nom}$  and set the maximum population size be  $N_{max}$
- 3: Copy all the behaviors  $\alpha \in \mathcal{A}_{pop}$  to  $\mathcal{A}_{bvr}$
- 4: Compute the fitness function in (31)
- 5:  $t^{\text{immune}} \leftarrow 1$
- 6: while  $t^{\text{immune}} \leq t^{\text{immune-max}} \mathbf{do}$
- 7: Perform hypermutation operation in (32) and (33)
- 8: Repeat hypermutation operation with probability  $\epsilon$  until high-novelty  $\alpha$  has been found by using (34).
- 9: Copy the new behaviors  $\alpha$  to  $\mathcal{A}_{bvr}$
- 10: Compute the fitness function in (31)
- 11: Update the population  $\mathcal{A}_{pop}$
- 12:  $t^{\text{immune}} \leftarrow t^{\text{immune}} + 1$
- 13: end while
- 14: Select the feasible  $\alpha$  with the highest fitness value

be used to solve the pole placement problem:

$$\mathbf{F}^*(\boldsymbol{\lambda}^{\text{pre}}) = \arg\min_{\mathbf{F}} \frac{1}{2} ||\text{eig}(\mathbf{A}_{\mathbf{F}}) - \boldsymbol{\lambda}^{\text{pre}}||_2^2 \qquad (28)$$

where eig( $\mathbf{A}_{\mathbf{F}}$ ) is the vector of eigenvalues of  $\mathbf{A}_{\mathbf{F}} \in \mathcal{R}^{n_x \times n_x}$ and  $\boldsymbol{\lambda}^{\text{pre}}$  is a prescribed vector of poles (or eigenvalues).

When large bounds are assigned, the search spaces in (19) and (20) are divided into several subspaces to improve the search efficiency:

 $[-\kappa_{s}\lambda^{\theta}, 0] \times [-\kappa_{s}\lambda^{\theta}, \kappa_{s}\lambda^{\theta}]$ 

and

$$[-\kappa_s g^{\theta}, \kappa_s g^{\theta}]$$

where  $\kappa_s \in (0, 1]$  for s = 1, 2, ..., S. The parameter *S* is the number of subspaces. Values of  $\alpha$  can be recovered using the following expression:

$$[\boldsymbol{\lambda}^{\text{pre}}]_m \in \{\sigma + j\omega : (\sigma, \omega) \in [-\kappa_s \lambda^{\theta}, 0] \times [-\kappa_s \lambda^{\theta}, \kappa_s \lambda^{\theta}]\}.$$
(29)

Alternatively,  $\alpha$  values can be generated in a pointwise manner through the following expression:

$$[\boldsymbol{\alpha}]_m \in [-\kappa_s g^{\theta}, \kappa_s g^{\theta}]. \tag{30}$$

After prescribing bounds for the behaviors and initializing the population, all behaviors  $\alpha$  in the population are copied to the empty archive  $\mathcal{A}_{bvr}$  in line 3 of Algorithm 2.

In lines 4 and 10 of Algorithm 2, the fitness function (objective function)  $\mathcal{F}$  of  $\boldsymbol{\alpha}$  in (16) is computed using

#### TABLE 1. Spectral abscissa optimization.

Problem	F∈	$\mathcal{R}^{n_u  imes n_y}$	1		Results of ex	isting metho	ds, $\alpha_0(\mathbf{A_F})$			Results of ODOM,
Name	$n_{\mu}$	$  n_{v}$	HIFOO	LMIRank	PENBMI	CCDM	ICAM	MRVs	Mean	$\alpha_0(\mathbf{A_F})$
AC1	3	3	-0.2061	-8.4766	-7.0758	-0.8535	-0.7814	-18.0761	-5.9116	-52.2891
AC4	1	2	-0.0500	-0.0500	-0.0500	-0.0500	-0.0500	-0.05	-0.05	-0.05
AC5	2	2	-0.7746	-1.8001	-2.0438	-0.7389	-0.7389	-2.4051	-1.4169	-2.4159
AC7	1	2	-0.0322	-0.0204	0.0896	-0.0673	-0.0502	-0.0747	-0.0259	-0.0872
AC8	1	5	-0.1968	-0.4447	0.4447	-0.0755	-0.0640	-0.4447	-0.1302	-0.4447
AC9	4	5	-0.3389	-0.5230	-0.4450	-0.3256	-0.3926	-2.0823	-0.6846	-2.3951
AC11	2	4	-0.0003	-5.0577	X	-3.0244	-3.1573	-16.9018	-5.6283	-138.8328
AC12	3	4	-10.8645	-9.9658	-1.8757	-0.3414	-0.2948	-18.3236	-6.9443	-52.5179
HE1	2	1	-0.2457	-0.2071	-0.2468	-0.2202	-0.2134	-0.2446	-0.2296	-0.2462
HE3	4	6	-0.4621	-2.3009	-0.4063	-0.8702	-0.8380	-1.7847	-1.1104	-3.2928
HE4	4	6	-0.7446	-1.9221	-0.0909	-0.8647	-0.8375	-3.0567	-1.2528	-3.0968
HE5	4	2	-0.1823	X	-0.2932	-0.0587	-0.0609	-1.1953	-0.3581	-1.0151
HE6	4	6	-0.0050	-0.0050	-0.0050	-0.0050	-0.0050	-0.005	-0.005	-0.005
REA1	2	3	-16.3918	-5.9736	-1.7984	-3.8599	-2.8932	-19.3041	-8.3702	-199.4919
REA2	2	2	-7.0152	-10.0292	-3.5928	-2.1778	-1.9514	-19.4238	-7.3650	-29.6645
REA3	1	3	-0.0207	-0.0207	-0.0207	-0.0207	-0.0207	-0.0207	-0.0207	-0.0207
DIS2	2	2	-6.8510	-10.1207	-8.3289	-8.4540	-8.3419	-19.4340	-10.2551	-68.9765
DIS4	4	6	-36.7203	-0.5420	-92.2842	-8.0989	-5.4467	-16.0222	-26.5191	-185.1219
WEC1	3	4	-8.9927	-8.7350	-0.9657	-0.8779	-0.8568	-11.9629	-5.3985	-21.6390
IH	11	10	-0.5000	-0.5000	-0.5000	-0.5000	-0.5000	-0.1576	-0.4429	-0.3516
CSE1	2	10	-0.4509	-0.4844	-0.4490	-0.2360	-0.2949	-0.3489	-0.3774	-0.4372
TF1	2	4	X	x	-0.0618	-0.1544	-0.0704	-0.2688	-0.1389	-0.2573
TF2	2	3	X	x	-1.0e-5	-1.0e-5	-1.0e-5	-1.0e-5	-1.0e-5	-1.0e-5
TF3	2	3	X	X	-0.0032	-0.0031	-0.0032	-0.0032	-0.0032	-0.0032
NN1	1	2	-3.0458	-4.4021	-4.3358	-0.8746	0.1769	-5.89	-3.0619	-5.8928
NN5	1	2	-0.0942	-0.0057	-0.0942	-0.0913	-0.0490	-0.094	-0.0714	-0.0939
NN9	3	2	-2.0789	-0.7048	x	-0.0279	0.0991	-17.8516	-4.1128	-25.8536
NN13	2	2	-3.2513	-4.5310	-9.0741	-3.4318	-0.2783	-13.6061	-5.6954	-13.6067
NN15	2	2	-6.9983	-11.0743	-0.0278	-0.8353	-1.0409	-10.9821	-5.1598	-10.9741
NN17	2	1	-0.6110	-0.5130	x	-0.6008	-0.5991	-0.6107	-0.5869	-0.6107

The letter "x" means that no solution was found.

deterministic algorithms. Because a minimization problem is formulated, the fitness value  $f^{BMI}$  is obtained as follows:

$$f^{\rm BMI}(\boldsymbol{\alpha}) = -\mathcal{F}(\boldsymbol{\alpha}). \tag{31}$$

If  $f^{\text{BMI}}(\boldsymbol{\alpha})$  is higher than  $f^{\text{BMI-best}}$ ,  $f^{\text{BMI-best}}$  is set as  $f^{\text{BMI}}(\boldsymbol{\alpha})$ . The parameter  $f^{\text{BMI-best}}$  is the approximate optimal fitness value associated with the BMI problem.

In lines 7 and 8 of Algorithm 2,  $\alpha \in \mathcal{A}_{pop}$  and  $\tilde{\alpha}$  are randomly generated using (29) or (30). Thus, a new behavior  $\alpha^{new}$  can be generated by performing the hypermutation operation over  $\alpha$  and  $\tilde{\alpha}$ . This operation is expressed as follows:

$$\boldsymbol{\alpha}^{\text{new}} = \begin{cases} \boldsymbol{\xi}^{\text{immune}} \boldsymbol{\alpha} + (1 - \boldsymbol{\xi}^{\text{immune}}) \tilde{\boldsymbol{\alpha}}, & rand() > \epsilon \\ \boldsymbol{\alpha}^{\text{random}}, & \text{otherwise} \end{cases}$$
(32)

where

$$[\boldsymbol{\alpha}^{\text{random}}]_m = \begin{cases} [\tilde{\boldsymbol{\alpha}}]_m, & \text{rand}() > \epsilon \\ [\boldsymbol{\alpha}]_m, & \text{otherwise.} \end{cases}$$
(33)

In (32),  $\xi^{\text{immune}}$  is a random number selected from the range (0, 1), and  $rand() \in (0, 1)$  is a random number generator. The hypermutation operation expressed in (32) is performed  $\lfloor N_{\text{max}}/|\mathcal{A}_{\text{pop}}| \rfloor$  times, where  $\lfloor \cdot \rfloor$  represents the floor function, and  $|\mathcal{A}_{\text{pop}}|$  represents the population size.

In line 8 of Algorithm 2, if NS is performed with the probability  $\epsilon$ , the diversity-selecting immune algorithm can avoid finding many behaviors with low novelty. The novelty of a new behavior  $\alpha$  can be computed using the following

equation:

$$\rho(\mathbf{b}^{\text{immune}}(\boldsymbol{\alpha})) = \frac{1}{k} \sum_{l=1}^{k} ||\mathbf{b}^{\text{immune}}(\boldsymbol{\alpha}) - \mathbf{b}^{\text{immune}}(\boldsymbol{\alpha}_{l})||_{2}$$
(34)

where  $\mathbf{b}^{\text{immune}}(\boldsymbol{\alpha}) = \boldsymbol{\alpha} \in \mathcal{R}^{n_u n_y}$  and  $\mathbf{b}^{\text{immune}}(\boldsymbol{\alpha}_l)$  is the *l*thnearest neighbor of  $\mathbf{b}^{\text{immune}}(\boldsymbol{\alpha})$  in the archive with respect to the  $L_2$  norm. If a novel  $\boldsymbol{\alpha}$  value cannot be found for a few trials, the novelty threshold  $\rho^{\text{bvr-min}}$  is decreased.

After the hypermutation operation is performed, new behaviors are generated. If  $rand() < \epsilon$  and the novelty of the new behavior  $\alpha$  is higher than  $\rho^{\text{bvr-min}}$ , the new behavior  $\alpha$  is copied to the archive  $\mathcal{A}_{\text{bvr}}$ , and the fitness value of  $\alpha$  is computed; otherwise, the hypermutation operation is performed until the aforementioned conditions are met.

To maintain a manageable population size and ensure feasibility, the population is updated (line 11 of Algorithm 2) by removing some infeasible behaviors. Eventually, the feasible behavior with the highest fitness value in the population is selected (line 14 of Algorithm 2) as the solution to the BMI problem.

## E. EXAMPLE OF USING QDOM

Consider the spectral abscissa of  $\mathbf{A}_{\mathbf{F}}$  in (5). The spectral abscissa optimization problem can be defined as (6). The controller gain matrix  $F \in \mathcal{R}^{n_u \times n_y}$  can be transformed into an  $n_u n_y \times 1$  vector (i.e.,  $\boldsymbol{\alpha}$ ) for solving the spectral abscissa optimization problem.

The QDOM algorithm can be decomposed into three components, namely the adaptive bound-searching algorithm

#### TABLE 2. H2 optimization.

Problem	$\mathbf{F} \in \mathcal{R}^{n_{u} \times n_{y}}$			Results of QDOM,				
Name	$n_u$	$n_{\rm v}$	HIFOO	PENBMI	CCDM	MRVs	Mean	$  G_{cl}  _2$
AC1	3	3	0.025	0.0061	0.054	0.015	0.0250	0.0141
AC2	3	3	0.0257	0.0075	0.054	0.01566	0.0257	0.0114
AC3	2	4	2.0964	2.0823	2.1117	2.1206	2.1028	2.0996
AC4	1	2	11.0269	х	11.0269	11.0269	11.0269	11.0269
AC6	2	4	2.8648	2.8648	2.8664	3.026	2.9055	3.0285
AC7	1	2	0.0172	0.0162	0.0176	0.0162	0.0168	0.0162
AC8	1	5	0.633	0.7403	0.6395	0.6321	0.6612	0.6339
AC12	3	4	0.0022	0.0106	0.0992	0.0627	0.0437	0.0672
AC15	2	3	1.5458	1.4811	1.5181	1.6564	1.5504	1.5730
AC16	2	4	1.4769	1.4016	1.4427	1.4641	1.4463	1.4568
AC17	1	2	1.5364	1.5347	1.5507	1.5392	1.5403	1.5348
HE2	2	2	3.4362	3.4362	4.7406	3.7494	3.8406	3.8179
HE3	4	6	0.0197	0.0071	0.1596	0.0333	0.0549	0.0272
HE4	4	6	6.6436	6.5785	7.1242	15.7738	9.0300	14.3825
REA1	2	3	0.9442	0.9422	1.0622	0.9593	0.9770	0.9600
REA2	2	2	1.0339	1.0229	1.1989	1.0261	1.0705	1.0240
DIS1	4	4	0.6705	0.1174	0.7427	0.51	0.5102	0.4553
DIS2	2	2	0.4013	0.37	0.3819	0.372	0.3813	0.3703
DIS3	4	4	0.9527	0.9434	1.0322	0.997	0.9813	1.0076
DIS4	4	6	1.0117	0.9696	1.0276	1.0644	1.0183	1.0512
WEC1	3	4	7.394	8.1032	12.9093	12.1017	10.1271	11.1693
WEC2	3	4	6.7908	7.6502	12.2102	13.2889	9.9850	11.6239
AGS	2	2	6.9737	6.9737	6.9838	7.1807	7.0280	7.0669
BDT1	3	3	0.0024	X	0.0017	3.52e-05	0.0014	3.1192e-05
MFP	3	2	6.9724	6.9724	7.0354	7.0556	7.0090	7.0297
PSM	2	3	0.033	0.0007	0.1753	0.0217	0.0577	0.0137
EB2	1	1	0.064	0.0084	0.1604	0.0832	0.0790	0.0271
EB3	1	1	0.0732	0.0072	0.0079	0.0846	0.0432	0.0397
TF1	2	4	0.0945	X	0.1599	0.1949	0.1498	0.2005
TF2	2	3	11.1803	X	11.1803	11.1803	11.1803	11.1803
TF3	2	3	0.1943	0.1424	0.2565	0.2568	0.2125	0.2766
NN2	1	1	1.1892	1.1892	1.1892	1.1892	1.1892	1.1892
NN4	2	3	1.8341	1.8335	1.859	1.8945	1.8553	1.9049
NN8	2	2	1.5152	1.5117	1.5725	1.5241	1.5309	1.5182
NN11	3	5	0.1178	0.079	0.1263	0.0972	0.1051	0.0904
NN13	2	2	26.1012	26.1314	62.3995	30.1629	36.1988	30.0894
NN14	2	2	26.1448	26.1314	62.3995	29.6438	36.0799	29.5450
NN15	2	2	0.0245	x	0.021	0.0034	0.0163	0.0014
NN16	4	4	0.1195	0.1195	0.1195	0.1208	0.1198	0.1220
NN17	2	1	3.253	3.2404	3.3329	3.2554	3.2704	3.2511

The letter "x" means that no solution was found.

(Algorithm 1), diversity-selecting immune algorithm (Algorithm 2), and average fitness value update process.

Algorithm 1 is used to generate the searching bound  $[g^{\theta} \lambda^{\theta}]^{\top}$  of  $\alpha$ . Then, Algorithm 2 randomly searches for  $\alpha$  in the given bound  $[g^{\theta} \lambda^{\theta}]^{\top}$ . To determine which candidate  $\alpha$  would be better, we solve the spectral abscissa problem in (8) for examining the fitness value  $f^{\text{BMI}}$  in (31) and calculating the average fitness value  $f^{\text{mean}}$  in (17).

For a given bounds  $[g^{\theta} \lambda^{\theta}]^{\top}$ , when the maximum number of trials  $t^{\text{search-end}}$  is reached, QDOM performs the average fitness update by comparing the mean fitness value  $f^{\text{mean}}$  of the current trial and the currently best average fitness value  $f^{\text{best}}$ . If  $f^{\text{mean}}$  is larger than  $f^{\text{best}}$ , we replace  $f^{\text{best}}$  by  $f^{\text{mean}}$ . The bound  $[g^{\theta} \lambda^{\theta}]^{\top}$  associated with  $\alpha$  coupled with the maximum fitness value is defined as the best bound  $[g^{\text{best}} \lambda^{\text{best}}]^{\top}$ . To help the adaptive bound-searching algorithm dynamically adjust the searching bound, the best bound  $[g^{\text{best}} \lambda^{\text{best}}]^{\top}$ and second best bound  $[g^{\text{best2}} \lambda^{\text{best2}}]^{\top}$  are saved in archive  $\mathcal{A}_{\text{bds}}$ .

Let trial index t = 1,  $t^{\text{search}} = 0$ ,  $t^{\text{search-end}} = 15$ , searching bound index  $\theta = 1$  and initial searching bound  $[g^1 \ \lambda^1]^{\top} = [g^{\text{initial}} \ \lambda^{\text{initial}}]^{\top}$ . At the beginning, we preset  $[g^{\text{base}}, \lambda^{\text{base}}] = [0, 0], [g^{\text{step}}, \lambda^{\text{step}}] = [0, 0], [g^{\text{best}}, \lambda^{\text{best}}] = [0, 0].$  Since t < 15, QDOM directly performs Algorithm 2 in the searching bound  $[g^{\text{initial}} \lambda^{\text{initial}}]^{\top}$  until  $t \ge 15$  where  $[g^{\text{initial}} \lambda^{\text{initial}}]^{\top} = [g^{\theta} \lambda^{\theta}]^{\top}$  for  $\theta = 1, 2, ..., 15$ .

Owing to  $t^{\text{serarch-end}} = 15$ , Algorithm 2 generates 15 feasible solutions. Thus, we can calculate  $f^{\text{mean}}$  and  $f^{\text{best}}$  and save  $[g^{\text{best}}, \lambda^{\text{best}}]$  and  $[g^{\text{best}2}, \lambda^{\text{best}2}]$  in archive  $\mathcal{A}_{\text{bds}}$ . The searching bound for t > 15 can then be updated on the basis of  $\mathcal{A}_{\text{bds}}$ . Once the average fitness value update process is accomplished, we set t = t + 1 and  $t^{\text{serarch}} = 0$ .

When  $t \ge 15$ , Algorithm 1 dynamically adjusts the searching region by using one of the following methods: diversity search, quality search, and crossover operation. Recall that  $t^{NS}$  and  $t^{NS-end}$  represent the iteration index and the end value of Algorithm 1 in searching for the high novelty bounds, respectively. Suppose that  $t^{NS-end} = 60$ .

For  $t \ge 15$ ,  $t^{\text{NS}} < 60$  and  $[g^{\text{step}}, \lambda^{\text{step}}] = [0, 0]$ , Algorithm 1 performs the diversity search in lines 11–16 of Algorithm 1 and updates the search bound as  $[g^{\theta+1} \lambda^{\theta+1}]^{\top}$ . If  $t \ge 15$ , and  $t^{\text{NS}} = 60$ , Algorithm 1 calculates new search direction  $[g_{\text{new}}^{\text{step}}, \lambda_{\text{new}}^{\text{step}}] \neq [0, 0]$ , perform the quality search in lines 19–23 of Algorithm 1 and

#### **TABLE 3.** $H_{\infty}$ optimization.

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$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$
AC3         2         4         4.7021         x         3.4859         3.9206         4.0362         3.82           AC4         1         2         0.9355         x         69.9900         69.99         46.9718         69.           AC6         2         4         4.1140         x         4.1954         4.8138         4.3744         4.67
AC4         1         2         0.9355         x         69.9900         69.99         46.9718         69.           AC6         2         4         4.1140         x         4.1954         4.8138         4.3744         4.67
AC6 2 4 4.1140 x 4.1954 4.8138 4.3744 4.67
AC7 1 2 0.0651 0.3810 0.0548 0.0315 0.1331 0.03
AC8 1 5 2.0050 x 3.0520 1.4305 2.1625 1.41
AC9 4 5 1.0048 x 0.9237 3.2926 1.7404 2.97
AC11 2 4 3.5603 x 3.0104 3.1158 3.2288 2.94
AC12 3 4 0.3160 x 2.3025 1.3532 1.3239 1.23
AC15 2 3 15.2074 427.4106 15.1995 17.1925 118.7525 16.55
AC16 2 4 15.4969 x 14.9881 15.8600 15.4483 15.51
AC17 1 2 6.6124 x 6.6373 6.6124 6.6207 6.61
HE1 2 1 0.1540 1.5258 0.1807 0.1538 0.5036 0.15
HE2 2 2 4.4931 x 6.7846 4.3681 5.2153 4.4
HE3 4 6 0.8545 1.6843 0.9243 0.8570 1.0800 0.85
HE4 4 6 23.3448 x 22.8713 46.5677 30.9279 42.31
HE5 4 2 8.8952 x 37.3906 20.8784 22.3881 19.40
REA1 2 3 0.8975 x 0.8815 0.8836 0.8875 0.8
REA2 2 2 1.1881 x 1.4188 1.1471 1.2513 1.15
REA3 1 3 74.2513 74.446 74.5478 74.2513 74.3741 74.25
DISI 4 4 4.1716 x 4.1943 4.3197 4.2285 4.26
DIS2 2 2 1.0548 1.7423 1.1546 1.0604 1.2530 1.06
DIS3 4 4 1.0816 x 1.1382 1.2727 1.1642 1.20
DIS4 4 6 0.7465 x 0.7498 0.9486 0.8150 0.89
TG1 2 2 12.8462 x 12.9336 14.2157 13.3318 14.19
AGS 2 2 8.1732 188.0315 8.1732 10.0239 53.6005 10.41
WEC2 3 4 4.2726 32.9935 6.6082 7.8382 12.9281 6.86
WEC3 3 4 4.4497 200.1467 6.8402 7.2021 54.6597 7.33
BDT1 3 3 0.2664 x 0.8562 0.2662 0.4629 0.26
MFP 3 2 31.5899 x 31.6079 33.9193 32.3724 33.21
IH 11 10 1.9797 x 1.1858 30.1004 11.0886 7.59
CSE1 2 10 0.0201 x 0.0220 0.0198 0.0206 0.01
PSM 2 3 0.9202 x 0.9227 0.9202 0.9210 0.92
EB1 1 1 3.1225 39.9526 2.0276 1.888 11.7477 1.89
EB2 1 1 2.0201 39.9547 0.8148 0.8142 10.9010 0.81
EB3 1 1 2.0575 3995311.074 0.8153 0.8143 998828.7 0.81
NN1 1 2 13.9782 14.6882 18.4813 15.5294 15.6693 14.19
NN2 1 1 2.2216 x 2.2216 2.2038 2.2157 2.22
NN4 2 3 1.3627 x 1.3802 1.4327 1.3919 1.39
NN8 2 2 2.8871 78281181.15 2.9345 2.9193 19570297 5 2.92
NN9 3 2 28,9083 x 32,1222 30,7173 30,5826 30,76
NILL 3 5 01037 x 01566 01075 01226 010
NN15         2         2         0.1037         X         0.1000         0.1075         0.1220         0.10
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$
NN17 2 1 11.2182 x 11.2381 11.2042 11.2202 11.20

The letter "x" means that no solution was found.

# TABLE 4. Additional problems in spectral abscissa, $H_2$ and $H_\infty$ optimization.

Problem	<b>F</b> ∈	$\mathcal{R}^{n_u \times n_y}$	Results of MRVs,	Results of QDOM,
Name	$n_u$	$n_y$	$\alpha_0(\mathbf{A_F})$	$\alpha_0(\mathbf{A_F})$
AC18	2	2	-1.9248	-1.8694
DIS5	2	2	-2.7044	-2.7022
PAS	1	3	-2.05e-05	-1.4845e-04
NN12	2	2	-2.4761	-2.4637
Problem	$\mathbf{F} \in \mathcal{R}^{n_u \times n_y}$		Results of MRVs,	Results of QDOM,
Name	$n_u$	$  n_y$	$  G_{cl}  _2$	$  G_{cl}  _2$
AC18	2	2	20.0248	20.1650
DIS5	2	2	0.0013	6.6857e-04
NN12	2	2	8.6989	8.3609
Problem	$\mathbf{F} \in \mathcal{R}^{n_{\mathcal{U}} \times n_{\mathcal{Y}}}$		Results of MRVs,	Results of QDOM,
Name	$n_u$	$n_y$	$  G_{cl}  _{\infty}$	$  G_{cl}  _{\infty}$
AC18	2	2	10.8088	10.6846
DIS5	2	2	28.7928	28.8127
NN12	2	2	22.4556	17.7232

update  $[g^{\text{step}}, \lambda^{\text{step}}]$ ,  $[g^{\text{best}}, \lambda^{\text{best}}]$  and the new search bound  $[g^{\theta+1} \lambda^{\theta+1}]^{\top}$ . However, if  $[g^{\text{step}}_{new}, \lambda^{\text{step}}_{new}] = [0, 0]$ , we enlarge

the search region  $[g^{\theta+1} \lambda^{\theta+1}]^{\top}$  by adjusting  $r^{NS}$  in (21) and do diversity search again. Once  $r^{NS}$  is larger than  $r^{max}$ , we perform the crossover operation in (27) to obtain new search bound  $[g^{\theta+1} \lambda^{\theta+1}]^{\top}$ .

QDOM continuously runs Algorithms 1 and 2, and updates the average fitness value until  $t = T^{\text{max}}$ .

# **IV. NUMERICAL EXAMPLES**

This section presents the results obtained from applying various BMI solution methods to solve optimal control problems, namely spectral abscissa,  $H_2$ , and  $H_\infty$  optimization problems. The BMI solution methods employed were HIFOO [16], [17], [18], LMIRank [19], PENBMI [20], CCDM [7], ICAM [8], MRVs [21], and the proposed QDOM. Except for the QDOM and MRVs, the remaining methods are local optimization methods. We used various models from the constraint matrix-optimization problem library [9]–including aircraft (AC) models, helicopter (HE) models, reactor (REA)



Performance Comparison of Spectral Abscissa

FIGURE 3. Normalized spectral abscissa (the smaller the better). (a) QDOM and the existing methods. (b) QDOM and the benchmark values.



Performance Comparison of H

FIGURE 4. Normalized H<sub>2</sub> norm (the smaller the better). (a) QDOM and the existing methods. (b) QDOM and the benchmark values.

models, decentralized interconnected system (DIS) models, wind energy conversion (WEC) models, terrain-following (TF) models, and academic test problems (NNs)–to assess the performance of the proposed QDOM.

For spectral abscissa optimization,  $H_2$  optimization, and  $H_{\infty}$  optimization, (7), (13), and (14) were solved, respectively. The MATLAB routine norm (*sys*, *p*) with the discussed system *sys* =  $G_{cl}$  and *p* = 2 were used for computing the

 $H_2$  norm. The term  $\mathbf{B}_1 \mathbf{B}_1^{\top}$  in (13) was replaced with  $\mathbf{B}_1 \mathbf{B}_1^{\top} + 10^{-5}\mathbf{I}$  if  $\mathbf{B}_1 \mathbf{B}_1^{\top}$  was not positive definite. The MATLAB routine norm (*sys*, *p*) with the discussed system *sys* =  $G_{cl}$  and  $p = \infty$  were used for computing the  $H_{\infty}$  norm.

#### A. PARAMETER SETTING OF QDOM

In the spectral abscissa optimization,  $H_2$  optimization, and  $H_{\infty}$  optimization problems, we used the following



#### Performance Comparison of H

FIGURE 5. Normalized  $H_\infty$  norm (the smaller the better). (a) QDOM and the existing methods. (b) QDOM and the benchmark values.

parameters:  $t^{\text{search-end}} = 10$  and  $T^{\max} = 150$  (Fig. 1). In [21], the bounds of the entries of controller gain matrices were set as follows:  $[\mathbf{F}]_{ij} \in [-50, 50]$ , where *i* is the row index, *j* is the column index, and the eigenvalues of matrix  $\mathbf{A}_{\mathbf{F}}$  were randomly generated so that eig{ $\mathbf{A}_{\mathbf{F}}$ }  $\in \{\sigma + j\omega :$  $(\sigma, \omega) \in [-20, 0] \times [-20, 20]$ }. We set  $g^{\text{initial}} = 50$  and  $\lambda^{\text{initial}} = 20$ . When each  $\alpha$  value in the population was generated, 3 subspaces were used, and  $\kappa_s$  in (29) and (30) was set as  $\kappa_1 = 1$ ,  $\kappa_2 = 0.5$ , and  $\kappa_3 = 0.1$ . The parameters used for Algorithm 1 were as follows:  $t^{\text{NS-end}} = 50$ ,  $r^{\text{NS}} = 0.5$ , and  $r^{\max} = 1$ , and  $\rho^{\text{bvr-min}} = 0.1g^{\theta}$ . Moreover, the parameters for Algorithm 2 were as follows: k = 10,  $\epsilon = 0.5$ ,  $t^{\text{immune-max}} = 20$ ,  $N_{\text{nom}} = 40$ , and  $N_{\text{max}} = 160$  [21].

The value of  $t^{\text{NS-end}}$  represents the number of times that Algorithm 1 searches for the high novelty bounds. If we set the value of  $t^{NS-end}$  too large, then much time is required to perform the while loop. On the other hand, if we set the value of  $t^{\text{NS-end}}$  too small, one may not obtain a high novelty bound but a bound that simply satisfies the novelty constraints. t<sup>search-end</sup> represents the number of times for using the same bound  $[g^{\theta} \lambda^{\theta}]^{\top}$  to solve the BMI problem. Setting  $t^{\text{search-end}}$ too large may spend more time in calculating fitness values. If a small number is set, it can be difficult to accurately evaluate whether the given bound yields good solutions when solving the BMI problems.  $r^{NS}$  is used to determine the search region of the diversity search operation. Since the number of candidates bound is proportional to the search region, setting the value of  $r^{NS}$  too large can cause Algorithm 1 to spend a lot of time in the novelty test. However, a small value of  $r^{NS}$  may prohibit Algorithm 1 from obtaining a high novelty bound.  $r^{\max}$  is a threshold that controls the size of searching region.  $\rho^{\text{bvr-min}}$  is used to measure the novelty of the candidate behavior  $\boldsymbol{\alpha}$ . Setting a higher value  $\rho^{\text{bvr-min}}$  makes the novelty candidate behavior  $\boldsymbol{\alpha}$  difficult to obtain.  $t^{\text{immune-max}}$  is the iteration number of hypermutation operation. Since computing the fitness value of given bound  $[g^{\theta} \lambda^{\theta}]^{\top}$  usually couples with a higher computational burden, setting a higher  $t^{\text{immune-max}}$  value can significantly prolong the computation time. Finally, larger  $N_{\text{nom}}$  and  $N_{\text{max}}$  yield higher computational complexity of hypermutation operation.

#### **B. NUMERICAL RESULTS**

Tables 1–3 present the performance of the QDOM and other BMI solution methods in spectral abscissa optimization,  $H_2$  optimization, and  $H_{\infty}$  optimization, respectively. The mean values in Tables 1–3 indicate the average values of solutions obtained using the existing BMI solution methods. Because the method exhibiting the highest performance may be different in different problems, we compared the results obtained using the QDOM with the mean values to verify the effectiveness of the QDOM. The QDOM is considered to outperform most of the existing BMI solution methods if its results are lower than the mean values displayed in Tables 1–3.

For the performance levels achieved by existing methods when BMI problems were solved, the normalized mean values (denoted by  $\mu$ ) of the spectral abscissa,  $H_2$ , and  $H_{\infty}$  benchmark optimization problems were within the intervals [0, 0.9], [0.2174, 0.9], and [0.2, 0.9], respectively and the normalized standard deviation values (denoted by  $\sigma$ ) were within the intervals [0, 0.7319], [0.3775, 0.6501], and [0.3649, 0.6325], respectively. We used the value  $\mu - 0.5\sigma$  as our benchmark value to determine whether the obtained solution is a relatively better solution. A solution whose performance is lower than the benchmark value can be regarded as a relatively better solution.

According to the results presented in Tables 1–3 and Figs. 3–5, the solutions obtained by QDOM in spectral abscissa,  $H_2$ , and  $H_{\infty}$  optimization problems were 96.6%, 27.5%, and 52.17% lower than the benchmark value, respectively. In the order of spectral abscissa,  $H_2$ , and  $H_{\infty}$  optimization problems, for HIFOO, it was approximately 26.67%, 42.5%, and 73.91%, respectively; for PENBMI, it was 36.67%, 80%, and 1%, respectively; for CCDM, it was 20%, 15%, and 47.83%, respectively; for MRVs, it was 70%, 10%, and 45.65%, respectively.

Clearly, QDOM outperformed CCDM and MRVs in all BMI optimization problems. In spectral abscissa optimization problems, QDOM had an absolute advantage over the other methods. Although the PENBMI had 80% lower than the benchmark value in  $H_2$  optimization problems, it performed worst when solving  $H_{\infty}$  optimization problems. In addition, out of all  $H_2$  benchmark systems, five of them (12.5%) were not solvable by PENLMI. We conclude that PENBMI was less stable than the other methods. By using QDOM in solving  $H_2$  optimization problems, it yielded 42.5% solutions near the benchmark value with a distance of less than  $0.2\sigma$ . QDOM performed similarly to HIFOO in solving  $H_2$ optimization problems.

HIFOO had 80% lower than the benchmark value in  $H_{\infty}$  optimization problems, but it found difficulty solving spectral abscissa problems. By using QDOM to solve  $H_{\infty}$  optimization problems, 62.5% solutions near the benchmark value with a distance of less than  $0.2\sigma$  were attained. QDOM presented an acceptable level of performance in solving  $H_{\infty}$  optimization problems.

The aforementioned results imply that most existing BMI solution methods may find only local optima and cannot obtain a globally optimal solution. Since the QDOM merges the adaptive bound-searching algorithm and diversity-selecting immune algorithm, it can avoid being trapped in a local optimum while searching for better solutions by dynamically adjusting the searching region and searching for feasible solutions. Thus, excellent levels of performance can be achieved by the proposed QDOM as compared with existing methods.

#### **V. CONCLUSION**

This paper proposes a BMI solution method, namely a QDOM, that can design controller gain matrices for solving spectral abscissa optimization,  $H_2$  optimization, and  $H_{\infty}$  optimization problems. To find the global optimum and avoid entrapment in a local optimum when solving BMI problems, the QDOM implements the proposed adaptive bound-searching algorithm and diversity-selecting immune algorithm. By using the adaptive bound-searching algorithm, appropriate bound values can be found for the decision

variables in different problems. The diversity-selecting immune algorithm uses the concept of QD to find the best decision variables within a large search space while avoiding becoming trapped in a local optimum. We conducted simulations to compare the performance of the proposed QDOM and existing BMI solution methods. The proposed QDOM outperformed the existing BMI solution methods in solving several benchmark BMI problems. Our simulation results show that the proposed QDOM was more likely to find the global optimum than the compared BMI solution methods.

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