Systems biology

NIHBA: a network interdiction approach for metabolic engineering design

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Abstract

Motivation: Flux balance analysis (FBA) based bilevel optimization has been a great success in redesigning metabolic networks for biochemical overproduction. To date, many computational approaches have been developed to solve the resulting bilevel optimization problems. However, most of them are of limited use due to biased optimality principle, poor scalability with the size of metabolic networks, potential numeric issues or low quantity of design solutions in a single run.

Results: Here, we have employed a network interdiction model free of growth optimality assumptions, a special case of bilevel optimization, for computational strain design and have developed a hybrid Benders algorithm (HBA) that deals with complicating binary variables in the model, thereby achieving high efficiency without numeric issues in search of best design strategies. More importantly, HBA can list solutions that meet users’ production requirements during the search, making it possible to obtain numerous design strategies at a small runtime overhead (typically ≈ 1 h, e.g. studied in this article).

Availability and implementation: Source code implemented in the MATLAB Cobratoolbox is freely available at https://github.com/chang88ye/NIHBA.

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

With the advance of genome-scale metabolic modelling (GSMM), the past decades have witnessed a significant number of computational tools for microbial metabolic engineering (Maia et al., 2016). These tools facilitate improved strain performance for the production of a variety of high-value biochemicals and biosynthetic precursors, including vanillin (Brochado et al., 2010), lycopene (Choi et al., 2016), malonyl-CoA (Xu et al., 2011) and alkane and alcohol (Fatma et al., 2018).

A large number of strain design tools are based on bilevel optimization. OptKnock (Burgard et al., 2003) is one of the earliest bilevel optimization-based tools. OptKnock maximizes target chemical production while assuming mutant strains at optimal growth in flux balance analysis (FBA). The resulting bilevel problem is solved through a reformulation that makes the inner level problem equivalent constraints under the condition of strong duality (Burgard et al., 2003). The OptKnock model was latter extended to improve target production via gene up/down-regulation (Pharkya and Maranas, 2006), cofactor specificity (King and Feist, 2014) or heterologous pathways (Pharkya et al., 2004), and to develop anti-cancer drugs by the identification of synthetic lethal genes (Pratapa et al., 2015). These studies demonstrate the great effectiveness of the bilevel optimization-based framework in metabolic engineering.

However, the bilevel optimization-based framework in literature has numerous limitations. The first one is the intensive computational cost in search of optimal solutions. Bilevel optimization is often reformulated into a mixed-integer linear programming (MILP) so as to be solved by exact MILP solvers. It can take up to a week to solve a MILP resulting from a medium-sized GSMM (Feist et al., 2010). Many practical strategies, such as model reduction and refinement of candidate knockout set (Feist et al., 2010), have been used to reduce the computational time but may miss the best design strategies due to reduced search space. GDBB (Egen and Lun, 2012) introduced a truncated branch and bound to speed up the search process. GDSLs used local search with multiple search paths to reduce the search space for each local MILP (Lun et al., 2009). While finding optimal solutions are computationally costly for exact solvers, other studies resorts to inexact methods, such as genetic algorithms (Patil et al., 2005; Rocha et al., 2010) and swarm intelligence (Choon et al., 2015). These methods, however, still scale poorly with the size of GSMM and are specially ineffective when a large number of genetic manipulations are allowed for target production, which is a
Network interdiction for metabolic engineering design

2 Results

2.1 NIHBA: using NI and benders decomposition

Evolutionary game theory for metabolic modelling has achieved great success, whereas the other opposing player (metabolic engineer) attempts to manipulate the metabolic network in order to maximally disrupt the first player’s activity. Therefore, the NI is a max–min problem in which the objective involves only the target production, avoiding the use of the widely assumed growth optimality. The NI is a special case of general bilevel problems. The solution to this NI problem is a novel hybrid algorithm based on Benders decomposition (Codato and Fischetti, 2006), aiming to address the other limitations mentioned previously. NIHBA, the proposed approach, has shown the ability to efficiently find a large number of growth-coupled design strategies with diverse production envelopes in a single run and to scale well with the size of allowable knockouts.

2.2 Case studies

Our case studies investigate the production of both native biochemicals (i.e. succinate and ethanol) closely linked to energy metabolism and a non-native secondary metabolism product (i.e. lycopene).

2.2.1 Succinate and ethanol production

NIHBA was tested on iML1515 (Monk et al., 2017), the largest Genome-scale metabolic (GEM) model for Escherichia coli, for the production of succinate and ethanol. For large models, Feist et al. (2007), by removing network arcs. We proposed a NI model for identifying gene-associated reaction knockouts, but up-down-regulation of genes can be considered in this model as well. The NI model is a special case of bilevel optimization. It was recast into a standard MILP problem (Fig. 1B) using a special reformulation approach (Section 4). The resulting MILP contains both complicating binary variables and easy continuous variables. It can be computationally intensive for a large size of binary variables and/or a high allowable number of knockouts, and likely to have numeric issues for exact solvers due to Big-M effects (Codato and Fischetti, 2006). We, therefore, resorted to Benders decomposition for this NI model. We proposed a hybrid Benders algorithm (HBA) with two novel techniques to solve the model efficiently and obtain as many design solutions as possible in a single run (Fig. 1C). The solutions from our approach, NIHBA, were then analysed in production envelopes (Fig. 1D), from which the most promising design solution can be selected for implementation.
\[
\Delta H(y, y') = \min \{c_P^T v \mid v \geq \frac{1}{2} (\hat{y} + \bar{y}) \}
\]

\[
\hat{y} + \bar{y} = 0.
\]

\[
Ax \leq (b - B\bar{y}) + \mu (b - B\hat{y})
\]

Fig. 1. A schematic workflow of the proposed NIHBA tool for strain design. (A) Illustration of network interdiction in strain design: host cells avoid overproducing a product (i.e. \(\min c_P v\)) whereas metabolic engineers interdict the host network to maximally impair the host’s activity (i.e. \(\max \min c_P v\)), where \(c_P\) is the coefficient vector for the product and \(v\) is a steady-state flux vector. (B) Mathematically modelling the network interdiction problem in strain design, followed by problem reformulation to obtain a standard MILP problem. (C) Hybrid Benders decomposition algorithm. The MILP is decomposed into a binary master problem and a linear slave problem, and Pareto-optimal cut generation and local branching are introduced to speed up the search of solutions. (D) Solutions that meet production requirements are stored and evaluated.
less than a third of the theoretical maximum production (TMP; Feist et al., 2010), which is computed by changing the FBA objective from growth maximization to target reaction flux maximization in iML1515. A slight relaxation of carbon number to 15 helps to identify a solution with around two-thirds of TMP, and succinate production reaches ~25 mmol/gDW/h (73% TMP) when no carbon number is constrained in candidate reactions. This indicates that some reactions with large carbon numbers are very important in redirecting flux towards succinate, although they may not carry high flux values. For example, both pyruvate dehydrogenase (PDH) and pyruvate formate lyase (PFL) acting on a high carbon compound, i.e. Acetyl-CoA, provide a good reaction flux value in wild-type pyruvate formate lyase (PFL) acting on a high carbon compound.

The growth rate (h⁻¹), minimum production (mmol/gDW/h) and maximum production (mmol/gDW/h) are from the solution with the highest minimum production rate.

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The growth rate (h⁻¹), minimum production (mmol/gDW/h) and maximum production (mmol/gDW/h) are from the solution with the highest minimum production rate.

Fig. 2. Result of NIHBA simulation for succinate production. Abbreviations of reactions are as follows: PDH, pyruvate dehydrogenase; PFL, pyruvate formate lyase; LDH-L, L-lactate dehydrogenase

Table 1. Succinate and ethanol production predicted by NIHBA with at most five knockouts for different sizes of candidate set

2.2.2 Lycopene biosynthesis

A heterologous lycopene biosynthesis pathway, as reported in Alper et al. (2005) and Choi et al. (2010), was added to the iML1515 model to predict lycopene production (Fig. 5). When eight
Fig. 3. Performance of NIHBA with different number of knockouts for succinate and ethanol production. (A) For succinate, the number of solutions achieving a certain percentage of the maximum theoretic production rate, and the minimum and maximum production rate of the best solution at optimal growth found for a different number of knockouts. (B) For ethanol, the number of solutions achieving a certain percentage of the maximum theoretic production rate, and the minimum and maximum production rate of the best solution at optimal growth found for a different number of knockouts (KOs). (C) The objective value of NIHBA against runtime for succinate production. (D) The objective value of NIHBA against runtime for ethanol production.

Fig. 4. Knockout distribution for succinate and ethanol production. (A) The percentage of solutions with at least one knockout from each subsystem for succinate production. (B) The percentage of solutions with at least one knockout from each subsystem for ethanol production. (C) The fraction of design solutions that have a specific knockout (only knockouts with at least a percentage 20% for either target products are displayed).
knockouts are allowed, running NIHBA on this expanded model generates a large number of solutions, with lycopene production rate ranging from 0.88 to 1.60 mmol/gDW/h (42–78% TMP) (see Supplementary Material A). Interestingly, most of the knockouts, e.g. PDH and PFL, are closely linked to pyruvate, which is a key upstream building block for lycopene biosynthesis. This suggests that increasing the availability of precursors could lead to high lycopene production. Apart from these, NIHBA also identified some non-intuitive knockouts, such as ribose-5-phosphate isomerase, glycine hydroxymethyltransferase (GHMT2r), phosphoenolpyruvate carboxylyase (PPC) and glutamate dehydrogenase (GLUDy). It is worth noting that the knockout of GLUDy, PPC, GHMT2r and PDH identified by NIHBA has also been predicted by other methods (Choi et al., 2010), but NIHBA shows more diverse combinations of these reactions as manipulation strategies. Additionally, although lycopene biosynthesis interferes less with cell growth, the simulation suggests NIHBA is still able to manipulate the metabolic network properly to lower growth capability (maximum growth rate) so that more substrate resources are available potentially for lycopene production. Reduced growth capability is undesired for a production strain, and thus, this is a strong growth-coupled design (Feist et al., 2010), but NIHBA shows more diverse combinations of these reactions as manipulation strategies.

2.3 Comparison with other tools

2.3.1 Comparison with minimization of metabolic adjustment

The minimization of metabolic adjustment (MOMA) (Segré et al., 2002) has demonstrated great success in predicting genetic deletion targets for improving production strains. Here, NIHBA is compared with MOMA in identifying at most five reaction knockouts for succinate production. For MOMA, a sequential approach (Alper et al., 2005) was used to identify multiple knockout solutions.

The best solutions (see Supplementary Material B) identified by MOMA and NIHBA are compared by their production envelopes, as shown in Figure 6. The production envelopes help us understand the production variability as growth increases. Figure 6 shows that the production strain designed by NIHBA has a significantly reduced maximum growth rate and the guaranteed lower bound of succinate production rate is > 5 mmol/gDW/h, regardless of growth rate. Thus, this is a strong growth-coupled design (Feist et al., 2010). In contrast, the MOMA solution shows slightly reduced maximum growth rate. However, the succinate production rate for the MOMA solution varies widely, and the guaranteed lower bound is zero. This implies, although the solution identified by MOMA guarantees minimal metabolic adjustment, the production rate can be zero in the resulting mutant strain.

This simulation demonstrates that a simple optimization principle, such as minimal metabolic adjustments in MOMA, cannot ensure that the resulting production strain yields improved biochemical production. In contrast, a more rigorous model like NIHBA considering the equilibrium between multiple players in metabolic engineering games clearly works better.

2.3.2 Comparison with bilevel optimization-based tools

For comparison, the NI problem was also solved using the OptKnock (Burgard et al., 2003) and GDLS (Lun et al., 2009) approaches with the Gurobi MILP solver (Gurobi Optimization, 2018), called NI-OptKnock and NI-GDLS, respectively. NI-GDLS used $M = 5$ search paths and a search size of $k = 3$ in order to get multiple solutions. For efficiency, parameters in the Gurobi solver was set according to Egen and Lun (2012).

For succinate, when at most five knockouts are allowed, NIHBA found a large number of solutions whereas both NI-OptKnock and NI-GDLS failed to find a feasible solution. The failure is mainly due to numeric issues in Big-M formulation, which existed even although we switched to indicator constraints or CPLEX12.8 for MILP. This demonstrates that HBA overcomes such numeric issues. For readability, we only show a small number of selected solutions from NIHBA in the production envelope (Fig. 7A). As seen, NIHBA can obtain diverse solutions forming a good representative of the trade-off between cell growth and succinate production. Interestingly, NIHBA identified a strong growth-coupled design (non-zero production at no growth), despite its slightly suboptimal production rate at the maximum growth.

For ethanol, all the algorithms found feasible solutions with at most five knockouts, and all contain a solution with the maximum production rate, as illustrated in Figure 7B-D (a small portion of solutions from NIHBA are displayed for readability). This shows that NIHBA has comparable performance in terms of optimality. Despite three solutions found from NI-GDLS, one of them is not growth coupled and the other two have the same production envelope, from which little can be gained about the trade-off between cell growth and target production. In contrast, NIHBA found many solutions with diverse production envelopes, among which strong growth-coupled designs exist.

3 Discussion

The implications of bilevel optimization for identifying genetic manipulations has been found very helpful for metabolic engineering. Most existing bilevel-based tools assume that cells always grow optimally, a biased optimization principle that is found incorrect for mutants or certain microorganisms in some studies (Schuetz et al., 2012; Segré et al., 2002). As a consequence, design strategies found by these tools may be biologically infeasible in spite of highest production rates at optimal growth. In addition, these tools involve
solving a bilevel problem through big-M reformulation to a standard MILP that is suitable for exact solvers of commercial software like Gurobi and CPLEX. However, the resulting MILP is often large due to the genome scale of metabolic networks, and exact solution to MILP can be computationally prohibitive, particularly when a large design space (or numerous genetic manipulations) is allowed. Furthermore, big-M formulation produces a weak MILP, leading to numeric issues such that no feasible solutions can be found. This article have proposed to address biased assumptions from the point of view of game theory, leading to a network interdiction problem (NIP). The NIP is not handled using popular exact solvers, instead it is solved through an efficient hybrid Benders decomposition algorithm to lower computational costs and overcome numeric issues.

The proposed approach, NIHBA, has shown its ability to obtain a large number of growth-coupled design strategies with diverse production phenotypes and achieve optimal production rates within an hour or so, regardless of the size of design space (the maximum allowable number of knockouts).

NIHBA uses a game theoretic framework to model the interaction (somehow competitive) between host cells and metabolic engineers. This framework assumes that host cells have a few objectives. These objectives are not necessarily to optimality individually but reach a trade-off between them. In this sense, NIHBA is different from traditional FBA approaches which often require a single biologically rigorous optimality objective, such as optimal growth or maximum energy generation (Schuetz et al., 2012). Therefore, design strategies found by NIHBA do not necessarily yield the best production at optimal growth. Instead, they guarantee non-zero production when the cell achieves a minimal required growth rate to sustain growth (Feist et al., 2010). NIHBA employs an HBA, HBA, to solve the NIP. Our case studies have demonstrated numerous advantages of this algorithm. First, it is free of numeric issues, making it much more stable than exact MILP solvers in top-ranked optimization platforms, e.g. Gurobi and CPLEX. Second, it can be considered a parameter-free algorithm as opposed to other methods like GDLS that requires a setting of multiple parameters, although NIHBA uses a parameter $\mu$ for identifying Pareto optimal cuts. In practice, NIHBA is not sensitive until a value of $\mu < 10^{-6}$ is used. Third, it is computationally efficient such that 1 h on average is sufficient for NIHBA to identify high-production solutions, and the runtime for a high-production rate does not scale with the number of knockouts, which is not the case for existing methods. Last, it obtains numerous growth-coupled solutions in a single run. This is important as it not only helps understand the trade-off between target production and cell growth but also provides the possibility to examine and test multiple solutions, from which the most promising design can be chosen for experimental implementation.

In computational strain design, a model reduction procedure (Feist et al., 2010) is often employed to reduce the search space for computational efficiency. One important step in this strategy is to exclude reactions acting on high-carbon metabolites. Many existing strain design tools rely on a predefined carbon number to reduce the number of candidates so that the resulting MILP has fewer binary variables (Feist et al., 2010). As a result, optimal solutions may be eliminated. This work has observed this issue in the case study of succinate production. Accordingly, NIHBA suggests to discard the high-carbon reaction reduction step. In this sense, NIHBA is more likely to identify optimal solutions compared with other strain
design tools. It should be noted that the relaxation of search space can lead to increased runtime of MILP solvers. However, this has been alleviated by an efficient HBA in NIHBA.

The proposed HBA is not limited to NIPs. It can be applied to any bilevel or single-level optimization problems that have complicating mixed-integer variables. Although promising, HBA needs improvements on convergence at late stages for optimality proof. Like other exact solvers, an appropriate optimality gap or time limit may alleviate excessive exploration but cannot determine the optimality of solutions. Further improvements can be made along this direction to enhance the convergence of HBA. It is also noteworthy that multiple solutions by HBA are not searched in a systematic way. They may not form a perfect representative of the trade-off between target production and cell growth. Therefore, more investigations are required to extract limited but well-diversified solutions in the search process of HBA.

Despite numerous solutions found by NIHBA, the selection of promising solutions poses a new challenge to decision-makers. It is therefore important to have a good solution ranking approach. Solutions may be roughly ranked according to the frequency of individual knockouts in addition to their subsystem distribution or by a scoring system with manual settings (Schneider and Klamt, 2019). Thus, a more systematic solution ranking is desirable. Another limitation of this work is the use of constraint-based models. While constraint-based models make it possible to investigate large-scale metabolic networks, they do not capture the dynamic nature of biologic systems. Further investigations are needed to make NIHBA applicable to dynamic models or hybrid models (Kim et al., 2018) for better metabolic engineering applications.

4 Materials and methods

4.1 Flux balance analysis
A metabolic network of m metabolites and n reactions has a stoichiometric matrix S that is formed by stoichiometric coefficients of the reactions. Let J be a set of n reactions and vj the reaction rate of j ∈ J. Sv represents the concentration change rates of the m metabolites. FBA aims at optimizing a linear biological objective cv when the system is at steady state (i.e. the concentration change rate is zero for all the metabolites) and v is subject to thermodynamic constraints:

\[
\max_v \quad cv \\
\text{s.t.} \quad \begin{cases} 
Sv = 0 \\
lb_j \leq v_j \leq ub_j, j \in J
\end{cases}
\] (1)

where lbj and ubj are the lower and upper flux bounds of reaction j, respectively. c is a weight vector specifying the degree of importance to the biological objective.

4.2 Network interdiction-based strain design and reformulation
NI for strain design considers metabolic engineers as interdictors or adversaries who attempt to maximally disrupt host cells’ activity that biochemicals of interest are not overproduced due to homoostasis. The strain design task can, therefore, be formulated as a max-min problem:

\[
\max_{y \in Y} \min_v \quad cv, \\
\text{s.t.} \quad Sv = 0, \\
lb_j (1 - y_j) \leq v_j \leq ub_j (1 - y_j), j \in J, \\
lb_j \leq v_j \leq ub_j, j \notin J \setminus J_f
\] (2a)

where \(c_v\) is a coefficient vector for the target biochemical. That is, \(c_v\) is a vector of zeros except for the \(P\)-th element (the index of the target biochemical reaction) which is set to one.

\[
y \in \{0, 1\}^J \land \sum_j y_j < K \quad (K \text{ is the maximum allowable number of knockouts}), \\
y_j \text{ indicates the reaction } j \text{ is inactive (} v_j = 0\text{) if } y_j = 1 \text{ and active otherwise. } \bar{J} \text{ is a subset of } J, \text{ containing candidate knockout reactions.}
\]

Observing that in the follower problem \(v_j | y_j = 0\) always holds for all \(j \in \bar{J}\), we can eliminate all the flux constraints imposed by \(y_j\), i.e. Equation (2c), by rephrasing the inner objective function in a Lagrangian manner:

\[
\min \quad c_v v + \sum_{j \in \bar{J}} M_j v_j y_j, \\
\text{s.t.} \quad Sv = 0, \\
\text{lb}_j \leq v_j \leq \text{ub}_j, j \in \bar{J}
\] (3a)

where \(M_j\) is a large positive Lagrange multiplier and \(M = (M_1, \ldots, M_J)\). The reformulated follower problem is equivalent to the original problem in the sense that they have the same optimal value provided that \(M_j\) is sufficiently large for all \(j \in \bar{J}\) such that \(v_j = 0\) when \(y_j = 1\). The value of \(M\) used in this work is around 100 (e.g. randomly drawn from [90,110]).

The reformulated follower function (3a) can be linearized by adding auxiliary variables \(u_j = \max(v_j, -v_j)\). As a result, we have the reformulated bi-level framework:

\[
\max_{y \in Y} \quad cv, \\
\text{s.t.} \quad \min_{y,u} \quad c_v v + \sum_{j \in \bar{J}} M_j u_j y_j, \\
\text{s.t.} \quad Sv = 0, \\
u_j \geq v_j, u_j \geq -v_j, j \in \bar{J}, \\
\text{lb}_j \leq v_j \leq \text{ub}_j, j \in \bar{J}
\] (4a)

\[
\text{s.t.} \quad Sv = 0, \\
u_j \geq v_j, u_j \geq -v_j, j \in \bar{J}, \\
\text{lb}_j \leq v_j \leq \text{ub}_j, j \in \bar{J}
\] (4c)

4.3 Hybrid benders algorithm
The bi-level problem (4) is reformulated to a standard MILP by applying LP duality to the follower problem (4b–4c). For simplicity, the resulting MILP is written in the following compact form

\[
\max_{x, y} \quad c \bar{x} \\
\text{s.t.} \quad \sum_{j \in \bar{J}} y_j \leq K \\
\bar{S} \bar{x} = 0 \\
\bar{A} \bar{x} + \bar{B} y \leq \bar{b}
\] (5a)

\[
\bar{S} = [S, 0_{m \times n_{\bar{J}}} ], \text{ and}
\bar{A} = \begin{bmatrix} -I & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
1 & 0 & -I & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & S^T & I & -I & 1 & -1 & -1 & 0 & 0 & 0 \\
c_v & 0 & 0 & -\text{lb}_j^T & \text{ub}_j^T & 1 & 1 & 0 & 0 & 0 \\
\end{bmatrix}, \bar{B} = \begin{bmatrix} \text{diag}(U) \end{bmatrix}, \bar{b} = \begin{bmatrix} 0 \end{bmatrix}
\] (5b)

\[
\bar{A} = \begin{bmatrix} -I & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
1 & 0 & -I & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
1 & 0 & -I & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & S^T & I & -I & 1 & -1 & -1 & 0 & 0 & 0 \\
c_v & 0 & 0 & -\text{lb}_j^T & \text{ub}_j^T & 1 & 1 & 0 & 0 & 0 \\
\end{bmatrix}, \bar{B} = \begin{bmatrix} \text{diag}(M) \end{bmatrix}, \bar{b} = \begin{bmatrix} 0 \end{bmatrix}
\] (5d)

where \(U\) is a vector of maximum absolute flux for each reaction, i.e. \(U_j = \max(|\text{lb}_j|, |\text{ub}_j|), \forall j \in \bar{J}\).

The single-level reformulation (5) can be solved, like OptKnock, by modern MILP solvers. However, the big-M terms in (5) lead to a week LP relaxation (Codato and Fischetti, 2006), therefore, causing difficulties for MILP solvers. Besides, the model size of (6) increases rapidly for large metabolic networks, and as a result, a large-scale MILP has to be solved.
Benders decomposition avoids these drawbacks as it can deal with complicating binary variables and easy continuous variables separately. Like Benders decomposition (Codato and Fischetti, 2006), our HBA decomposes (5) into a binary integer programming master problem (MP) (7) and an LP slave problem (SP) (8) for fixed $y = \bar{y}$:

$$\text{MP : } z = \max_{y,z} \quad z \quad (7a)$$

subject to

$$\sum_{y \in F} y_i < K \quad (7b)$$

$$z \leq (b - By)^T \pi^o \quad \forall y \in O \quad (7c)$$

Benders cuts

$$y_i \in \{0, 1\}, z \geq 0; \quad (7d)$$

$$\text{SP : } \bar{z} = \max_x \quad \bar{c}x \quad (8a)$$

subject to

$$Ax \leq b - By \quad \{\pi\} \quad (8b)$$

where $O$ and $F$ are sets that correspond to the extreme points $\pi^o$ and extreme rays $\pi^f$ of the dual of SP, respectively. In each iteration, the Benders decomposition algorithm derives the dual vector $\pi$ from the SP (8) for $y = \bar{y}$ which is the solution to the MP in the previous iteration. In practice, a Benders cut is obtained by solving the dual of (8) rather than the primal. Two scenarios exist when solving the dual of (8): if the optimal value of the dual of SP is bounded, it means the SP is feasible, then an optimality cut $z \leq (b - By)^T \pi^o \quad \forall y \in O$ generated from the extreme point $\pi^o$ is added to the MP; if it is unbounded, it means the SP is infeasible, then a feasibility cut $(b - By)^T \pi^f \geq 0$ generated from the extreme ray $\pi^f$ is added to the MP to avoid unboundedness of the dual of SP in future iterations.

The classic Benders decomposition is not able to generate effective Benders cuts rapidly for our strain design problem, and therefore, requires a huge of iterations (consequently long computation time) before it converges. Here, we introduce an HBA with two strategies to speed up the convergence process.

Figure 8 shows a simplified flowchart of HBA. An implementation of the algorithm in MATLAB can be found in https://github.com/chang88ye/NHBA.

4.3.1 Pareto optimal cuts

Let $\pi^o$ be the dual vector of $\pi$ corresponding to (8), a standard Benders optimality cut is:

$$\text{Cut(}\pi^o\text{)} : z \leq (b - By)^T \pi^o \quad (9)$$

Since $\pi^o$ may not be unique, it is important to select an effective cut $\text{Cut(}\pi^o\text{)}$. Magnanti and Wong (1981) proposed to use Pareto optimal cuts to improve convergence. $\text{Cut(}\pi^o\text{)}$ is said to be Pareto optimal if no other $\text{Cut(}\pi^o\text{)}$ exists such that $(b - By)^T \pi^o < (b - By)^T \pi^o$ for any $y \in Y$ and at least one $y \in Y$ enables a strict inequality. There are a few methods available for identifying a Pareto optimal cut, but most of them have to solve the SP (8) twice, which may increase computational time significantly.

We turn to the approach of Sherali and Lunday (2013) where a Pareto optimal cut can be generated by solving only once in each iteration a slightly different SP:

$$\text{SP : } z = \max_x \quad \bar{c}x \quad (10a)$$

subject to

$$\bar{x} = 0 \quad [\lambda] \quad (10b)$$

$$Ax \leq (b - By) + \mu(b - By) \quad \{\pi\} \quad (10c)$$

where $\mu$ is a sufficiently positive value and $\bar{y}$ is a core point in the relative interior of the convex hull of $Y$. In this paper, $\bar{y}$ is updated by $0.5(\bar{y} + y)$ whenever a new feasible $y = \bar{y}$ is produced in the iteration of Benders decompositions. $\mu$ is not calculated as in Sherali and Lunday (2013) but rather fixed to $1e-8$ after multiple trials.

4.3.2 Local branching

Another technique we used for accelerating the convergence of Benders decomposition is local branching, which is particularly effective when problems have binary variables (Baena et al., 2018; Rei et al., 2009). Suppose $y'$ is a feasible solution in $Y$, the idea behind local branching is to divide the feasible region of $\bar{y}$ into two subregions by the Hamming distance between $y$ and $y'$:

$$\Delta_H(y, y') = \sum_{\forall y \neq y'} y_i + \sum_{\forall y_i < 1}(1 - y_i).$$

In every iteration of Benders decomposition, the MP (7) is solved in the subregion $\Delta_H(y, y') < r$ (where $r$ is a positive integer and the maximum is the cardinality $|y|$ of $y$). This leads to two scenarios: there is either a feasible or infeasible $y$ in the subregion $\Delta_H(y, y') < r$. If a feasible solution $\bar{y}$ is obtained, Benders cuts are generated by solving (10) with $y$. If not, it means the value of $r$ may be too small, and $\Delta_H(y, y') > r + 1$ is added to the MP (7) to stop re-exploration in the neighbourhood of $y'$ with the radius $r$. $r$ is then increased by one at a time until $\Delta_H(y, y') < r$ renders the MP (7) feasible. Note that $\bar{y}$ has to be updated by $\bar{y}$ if $y$ gives (7) an objective value worse than that of the SP (8), implying that no better solution can be obtained from the neighbourhood of $y'$.

4.4 Additional improvement strategies

HBA involves solving the MP (7) and SP (8) in a repeated manner. For efficiency, the following two strategies are used:

- Terminating the MP program prior to optimality. Suboptimal solutions to the MP are sufficient to generate valid Benders cuts. Therefore, the MP is terminated when a MIP Gap of $1 + 300/(\text{iter}^{0.5} + 1)$ (where $\text{iter}$ is the iteration counter) is reached.
- Reversing local branching whenever the $z$ value of the MP is worse than $\bar{z}$ value of the SP. $\bar{z}$ estimates the upper bound of the problem (2). $\bar{z} < z$ indicates the global optimum does not exist.
in the corresponding local branching and a reverse local branching should, therefore, be used.

4.5 Model reduction and candidate selection

The truncation of model size and candidate knockout set has great computational benefits. GEM models can be significantly simplified by compressing linear reactions and removing dead end reactions (those carrying zero fluxes). Likewise, many reactions can be excluded from consideration with a priori knowledge that, for example, they are vital for cell growth or their knockout is not likely to improve target production. We followed the model reduction procedure by Lun et al. (2009) and candidate selection procedure by Feist et al. (2010), resulting in a candidate set of 150–350 reactions for different target products from the latest E. coli GEM iML1515 (Monk et al., 2017) where the maximum uptake rates for glucose and oxygen are all 20 mmol/gDW/h.

4.6 Computation implementation

First of all, all the NI models were transformed into MILPs using duality theory (Burgard et al., 2003). Then, the resulting MILPs were implemented in MATLAB 2018b to be compatible with the Cobra Toolbox 3.0 (Heirendt et al., 2019) where we carried out simulations. All the MILPs were solved by Gurobi 7.5 (Gurobi Optimization, 2018) with both Heuristics and MIPFocus were set to 1 as suggested by Egen and Lun (2012). A time limit of 2h was applied to each MILP while performing computations on Ubuntu 16.04 LTS with an Intel® Core™ i5 Quad Core processor.

Data and software availability

The data and software used and the tool developed are all available online:

- GEM model: iML1515 from BIGG database (bigg.ucsd.edu).
- Simulation software: Cobra toolbox 3.0 (https://opencobra.github.io/).
- NIHBA: https://github.com/chang88ye/NIHBA.

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References


