Random sampling of elementary flux modes in large-scale metabolic networks

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ABSTRACT

Motivation: The description of a metabolic network in terms of elementary (flux) modes (EMs) provides an important framework for metabolic pathway analysis. However, their application to large networks has been hampered by the combinatorial explosion in the number of modes. In this work, we develop a method for generating random samples of EMs without computing the whole set.

Results: Our algorithm is an adaptation of the canonical basis approach, where we add an additional filtering step which, at each iteration, selects a random subset of the new combinations of modes. In order to obtain an unbiased sample, all candidates are assigned the same probability of getting selected. This approach avoids the exponential growth of the number of modes during computation, thus generating a random sample of the complete set of EMs within reasonable time. We generated samples of different sizes for a metabolic network of Escherichia coli, and observed that they preserve several properties of the full EM set. It is also shown that EM sampling can be used for rational strain design. A well distributed sample, that is representative of the complete set of EMs, should be suitable to most EM-based methods for analysis and optimization of metabolic networks.

Availability: Source code for a cross-platform implementation in Python is freely available at http://code.google.com/p/temsampler.

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 INTRODUCTION

The description of a metabolic network in terms of elementary (flux) modes (EMs) provides an important framework for metabolic pathway analysis (Schuster et al. 1999). Elementary mode analysis identifies all minimal functional pathways connecting substrates with biomass and products inherent to a metabolic network. EMs have been used to understand the cellular metabolism through analysis of the network structure, regulations and characterization of all possible phenotypes (Çakır et al. 2009; Schuster et al. 1999, 2006; Stelling et al. 2004). Examples of other recent applications of pathway analysis are in the determination of minimum medium requirements (Schilling and Palsson 2001) and in the development of reduced kinetic models (Biegler and Biegler 1999). They also play an essential role in the development of model-based metabolic engineering strategies for strain optimization by identification of suitable intervention targets (Hädicke and Klamt 2011, 2012; Trinh et al. 2003, 2009). A comprehensive review on elementary mode analysis and other applications of EMs can be found in (Trinh et al. 2009).

EMs are also closely related to the problem of identifying all transition invariants (t-invariants) in Petri net theory (Chuang 2009). In fact, if all reactions are irreversible, the set of EMs is equivalent to the minimal t-invariants of a Petri net. Thus, it is not surprising that the algorithms for computation of EMs and t-invariants have evolved closely (see Schuster et al. 2003 for a comparison of both concepts).

Despite recent improvements in the algorithms for computation of EMs (Klamt et al. 2002; Ferrer and Stelling 2008), their application to real world metabolic networks has been hampered by the combinatorial explosion in the number of modes as the size of the networks increase. The enumeration of the complete set of EMs for genome-scale networks has been infeasible so far, and perhaps even undesirable due to the hardly manageable number of modes that would be generated.

An attractive approach is the enumeration of a subset of pathways representing the complete system. Several approaches have been proposed hereto, though none of them provides a purely random sample of EMs. Current state of the art approaches typically enumerate EMs with a certain objective or constraint; like the enumeration of the shortest pathways (De Figueiredo et al. 2003; Rezola et al. 2011), the enumeration of pathways including a specific target reaction (Kloete et al. 2009), enumeration based on available measurements (Klamt et al. 2013; Soons et al. 2013), enumeration of all possible pathways through selected reactions that satisfy the steady-state flux of the entire network (elementary flux patterns) (Kloete et al. 2009), or decomposition of the network in modules (Schuster et al. 2004; Schwartz et al. 2009). These approaches do not represent the full solution space and hence a number of potentially interesting solutions may be missed.

One of the key requirements for successful understanding of the cellular metabolism based on EMs is the ability to enumerate a representative subset of modes. In this work, we develop a method for generating random samples of EMs without computing their
The EM sampler was implemented as an adaptation to the canonical basis approach by Schuster and Hilgetag. The algorithm begins with a matrix containing the transposed stoichiometric matrix augmented with the identity matrix. Then, for each metabolite, all the non-zero entries in the corresponding column are detected and replaced with all possible combinations that annul the respective entries. The combinatorial nature of the pairwise input/output reaction combination for each metabolite is the key to the exponential growth of the number of modes during the execution of the algorithm. Therefore, we add an additional filtering step which, at each iteration, selects only a subset of the possible combinations. This selection is based on a given probability function that randomly selects among the candidates. The algorithm is described as follows:

1. **Initialize** the matrix \( T = [S_j] \).

2. For each metabolite \( i \):
   - Let \( R = \{ j | T_{ij} \neq 0 \} \).
   - Delete all rows \( R \) from \( T \).
   - Let \( T_{new} = \{ \} \).
   - For each combination \( (R) \):
     - \( T = add(T_x, T_a) \).
     - \( rev(T_x) \).
     - \( sgn(T_x) \).
     - If \( \text{min}(T_x) < s_{new} \), append \( T \) to \( T_{new} \).
     - \( T_{new} = \text{filter}(T_{new}) \).
     - Append \( T_{new} \) to \( T \).

3. Get \( E \) from \( T = \{ 0, 1 \}^T \).

where \( S \) is the stoichiometric matrix, \( I \) is the identity matrix of size \( s \), and \( E \) is the elementary matrix. In order to find all possible row combinations, the following function is defined:

\[
\text{combinations}(R) = \{ (j, k) | j \in R, k \in \mathbb{R}, k \neq j \}.
\]

Function \( rev \) keeps track of the reversibility of the candidate modes so that reversible modes can be freely combined, and irreversible ones can only be combined in the appropriate direction. A candidate mode is reversible if it contains reversible reactions. In order to combine candidate modes such that column \( i \) is annihilated (i.e., metabolite \( i \) is balanced), it is important to make sure that they are combined in the proper direction. This is implemented by the following function:

\[
\text{add}(T_x, T_a) = \begin{cases} \begin{array}{l} T_x, & \text{if } \text{rev}(T_x) \land \text{rev}(T_a), \\ T_a, & \text{if } \text{rev}(T_a) \land \text{rev}(T_x), \\ T_x - T_a & \text{if } \text{rev}(T_a) \land \neg \text{rev}(T_x), \\ T_a - T_x & \text{if } \text{rev}(T_x) \land \neg \text{rev}(T_a), \\ T_x + |T_a| & \text{if } \neg \text{rev}(T_x) \land \neg \text{rev}(T_a). \end{array} \end{cases}
\]

For a mode to be elementary, it must have minimal support [Schuster et al., 2009]. There are two methods to check if a mode is elementary: the combinatorial test and the rank test [Ferrer and Stelling, 2009]. The combinatorial test compares the support vector of the new mode with the support of all modes computed at that point. However, this method is not appropriate in our case because we do not have the full set of elementary modes required for the test. On the other hand, the rank test is based only on the support vector of the candidate mode. Therefore, we opted to use this test in our implementation:

\[
\text{minimal}(e) \equiv \text{rank}(S_{new} - S_e) = |s(e) - 1|
\]

where \( s(e) = |j |e \neq 0 \rangle \) is the support of \( e \), and \( S_{new} - S_e \) is a submatrix of the stoichiometric matrix composed of the metabolites that have been processed so far, and the reactions that belong to the support of \( e \). We also verify if the new candidate mode contains any reversible reaction occurring in both directions simultaneously. In that case, the candidate can be discarded without performing the test.

The filtering step is the novelty of the method proposed in this work (Fig. 1). In order to prevent the exponential growth in the number of candidate modes, we randomly select a sample of the new candidate modes at each step. This is implemented by the following function:

\[
\text{filter}(T) = T_{[s_{new}]}(1\ldots s_{new} \Rightarrow s_{new})
\]

where \( N \) is the number of new candidate modes, \( X \sim \mathcal{U}(0, 1) \) and \( P \) is a given selection probability.

The selection probability is a critical aspect of the algorithm. A low probability may cause the elimination of vital connections in the network, whereas a high probability may not prevent the combinatorial explosion. Ideally, one would want a high selection probability for low connectivity nodes, and a low selection probability at high connectivity nodes. Therefore, we opted to define the selection probability as a function of the number of candidate modes. Furthermore, we can observe that the selection of modes follows a binomial distribution with a given selection size equal to \( N \) \( P \). Hence, at each step we define \( P = \frac{N}{N + a} \), such that:

\[
\lim_{N \to \infty} P \approx \frac{K}{N + a} = K
\]

where \( K \) is a given constant that determines a maximum upper bound in the number of new candidate modes at each step.

2.2 Implementation

The algorithm was implemented in Python and uses the open libraries NumPy/SciPy [Jones et al., 2011] for numerical computations, and libSBML [Bolouri et al., 2008] (for reading SBML (Systems Biology Markup Language) model files. All tests were performed on an Intel Core 2 Duo 2.13 GHz processor with 3 GB RAM, running Linux Kernel 3.0 and Python 2.7.

2.3 Model

The algorithm was tested using a condensed genome-scale metabolic reconstruction of Escherichia coli [Bau et al., 2009]. The model contains 72 metabolites (52 internal, 20 external) and 95 reactions (75 internal, 20 drain). Glucose was set as the external carbon source and flux variability analysis (FVA) [Mahadevan and Schilling, 2003] was performed in order to detect blocked reactions, which were then removed from the model. The simplified model contains 68 metabolites and 87 reactions. The EMs for this model were calculated with efmmode [Ferrer and Stilling, 2009], resulting in a total of 102.74 EMs.

3 RESULTS

3.1 Sampling

The selection probability is controlled by the constant \( K \), the only adjustable parameter in the algorithm (see Section 2). Therefore, we performed several tests using different values for this parameter. For each value of \( K \), a total of 10 trials were run, and the individual samples were merged into a larger set. Additionally, we verified that all modes obtained are truly elementary modes contained within the full set of EMs for the tested model.
Random sampling of elementary flux modes

Fig. 1. The computation of elementary modes consists on iteratively removing all internal metabolites, and combining every pair of input/output reactions. For highly connected nodes, this results in a combinatorial explosion of new connections (expansion phase). To avoid the exponential growth along the iterations, caused by the accumulation of this effect, we add an additional filtering step that randomly samples the new combinations (contraction phase).

Table 1. Size of the EM samples obtained and respective computation times for different values of K

<table>
<thead>
<tr>
<th>K</th>
<th>No EMs</th>
<th>Time (s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>10^2</td>
<td>(1.1±0.6)×10^3</td>
<td>(9.5±4.9)×10^-1</td>
</tr>
<tr>
<td>10^3</td>
<td>(9.9±3.3)×10^3</td>
<td>(4.1±1.7)×10^1</td>
</tr>
<tr>
<td>10^4</td>
<td>(9.3±0.6)×10^2</td>
<td>(2.4±0.8)×10^3</td>
</tr>
<tr>
<td>10^5</td>
<td>(8.8±0.2)×10^3</td>
<td>(1.5±0.2)×10^5</td>
</tr>
</tbody>
</table>

The data represent the mean values and standard deviation for 10 trials per experiment.

The first test is the sample size and computation time as a function of K. By controlling the selection probability, it is expected that the resulting sample size will be affected and, consequently, the computation time as well. Results for these experiments are shown in Table 1. By performing linear regression of these values on a log–log scale, it is possible to observe that the number of modes obtained grows linearly with K, whereas the computation time grows nearly quadratically (Fig. 2).

In order to obtain a well-distributed sample it is important to guarantee that the reaction participation (i.e. the fraction of EMs in which a reaction participates) is preserved by the sampling procedure. Otherwise we would obtain a biased sample of the full EM set. We compared the reaction participation of the generated samples against the respective values in the full set of EMs (Fig. 3). It is possible to observe that for lower values of K, there is a weaker correlation between the reaction participation of the samples and the reaction participation of the full EM set. This is likely due to the fact that the sample size is too small to obtain a good coverage of the solution space. However, it is possible to observe that, as K increases, the Pearson correlation coefficient (r) also increases. For K = 10^5 we observe a high correlation (r = 0.986) between the reaction participation that is estimated by the sampling approach and the true values. In all cases, the dispersion seems to be homogeneous, showing no observable bias, hence the degree of correlation is only affected by the sample size.

Furthermore, we analyzed the EM samples regarding their distribution within the flux solution space. For that matter, we plotted the EMs distribution within the phenotypic phase plane for oxygen uptake and cellular growth normalized by glucose uptake (Edwards et al., 2002). Figure 4 shows the distribution for the full set compared with the samples for different values of K. It can be observed that the samples are unbiased relatively to the full set, and that the coverage of the solution space improves with the size of the samples.

We also evaluated how the sampling procedure affects the pathway length distribution (Fig. 5). It is possible to observe that the full EM set has a skewed Gaussian-like distribution with a maximum frequency of pathways with 50 reactions. However, we observe that as K decreases, the distribution shifts towards smaller pathway lengths. This is not surprising since the EMs with larger support vectors will undergo more sampling steps. Nonetheless, it is observed that for K = 10^5, the distribution of the sample is considerably close to the distribution of the full set.

3.2 Case study: rational strain design

One of the applications of elementary mode analysis is the rational design of mutant strains for industrial production of chemical compounds (Hädicke and Klamt, 2010, 2011; Trinh et al., 2008). The enumeration of the EMs of a metabolic network, allows the...
Fig. 3. Reaction participation in the full EM set versus the participation in samples of different sizes, and the respective Pearson correlation coefficients ($r$).

In order to understand if the utilization of EM samples is appropriate for rational strain design, we compared the knockout strategy obtained with the full EM set, using the method of Trinh et al. (2008), against the strategies obtained with different samples ($K = 10^5$). Succinate production was used as the case study, all experiments were constrained to a maximum of 8 knockouts, and only strategies with viable biomass production were allowed. In order to have an estimate of the production rate for each case, we used the method of minimization of metabolic adjustment (MOMA) to predict the flux distribution of the mutants Segrè et al. (2002).

The results are presented in Table 2. It is possible to observe that the knockout strategies found for the samples differ from that of the full EM set (see Supplementary Fig. S1 for a clustering analysis). Nonetheless, all the knockouts predicted with the full set appear frequently in the other knockout strategies. Also, the succinate production rates estimated with MOMA are high in most cases. Only in one case (Sample 8) there was no production, although it predicted 4 knockouts common to the full EM set.

4 DISCUSSION

4.1 Sampling quality

The main goal of this work is the creation of a sampling approach for computing EMs in large-scale networks without computing their whole set. For that matter, it is important to guarantee that the sampling approach provides a uniform coverage of the complete solution space. Our method is controlled by a single parameter that influences the number of computed EMs, by adjusting the selection probability during the execution of the algorithm. Our results show that the sample size obtained is directly proportional to $K$.

For most EM-based applications, it is important to obtain a sample that preserves the reaction participation (the fraction of EMs in which a reaction participates). The results show that the sampling is unbiased in that aspect. However, the correlation of the estimated values with the true values is affected by the size of the sample. The larger the sample size, the better will be the correlation obtained. This is also reflected in the analysis of the phenotypic phase plane for oxygen uptake and cellular growth. The samples present an unbiased representation of the solution space, although the coverage obtained will depend on the sample size.

Regarding the pathway length distribution of the EMs, the results show that there can be a bias towards smaller pathway lengths for low values of $K$. The importance of this bias depends on the application for which the sample will be used. One may argue that shorter pathways are more efficient, hence more likely to carry higher fluxes. For a large value of $K$, we can observe that the bias is not significant. However, for larger networks, the demands in terms of computational time and memory may not allow for arbitrarily large values of $K$ and the effect may become more significant. One way to compensate for such effect would be to give larger selection probabilities to modes with larger support vectors. In that case, additional testing is required in order to check if that artificial selection would cause any bias in other properties of the samples.
Comparison of the optimal knockout strategies for succinate production for the full EM set and different EM samples

Table 2.

<table>
<thead>
<tr>
<th>Test</th>
<th>No Total EMs (succ)</th>
<th>Reaction knockouts</th>
<th>No EMs (succ)</th>
<th>Est. rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Full EM set</td>
<td>100273 (48602)</td>
<td>ACALD, G4PDH2r, GLUDy, LDHi, D, NADTRHD, PFL, PYK, SUCDi</td>
<td>406 (320)</td>
<td>6.997</td>
</tr>
<tr>
<td>Sample 1</td>
<td>8745 (3962)</td>
<td>ACALD, GLUSy, ICL, LDHi, D, PFL, PGL, SUCDi, THD2</td>
<td>59 (34)</td>
<td>3.797</td>
</tr>
<tr>
<td>Sample 2</td>
<td>9001 (3979)</td>
<td>ACALD, GLUSy, ICL, LDHi, D, ME2, PFL, PGL, SUCDi</td>
<td>69 (30)</td>
<td>3.397</td>
</tr>
<tr>
<td>Sample 3</td>
<td>8607 (4011)</td>
<td>ACALD, ATPS4r, GLUDy, ME1, PFL, PYK, SUCDi, TKT2</td>
<td>50 (37)</td>
<td>4.455</td>
</tr>
<tr>
<td>Sample 4</td>
<td>8682 (3838)</td>
<td>ACALD, ACKr, GLUDy, ICL, LDHi, D, PFL, PGL, SUCDi</td>
<td>48 (42)</td>
<td>6.647</td>
</tr>
<tr>
<td>Sample 5</td>
<td>8489 (3553)</td>
<td>ACALD, ACKr, GLUSy, LDHi, D, PFL, PGL, SUCDi, THD2</td>
<td>76 (52)</td>
<td>3.473</td>
</tr>
<tr>
<td>Sample 6</td>
<td>8453 (3574)</td>
<td>ATPS4r, GLUSy, ME1, NADTRHD, PFL, PYK, SUCDi, TALA</td>
<td>44 (36)</td>
<td>2.044</td>
</tr>
<tr>
<td>Sample 7</td>
<td>9056 (4080)</td>
<td>ACALD, GLUSy, ME1, PFL, PGL, SUCDi, THD2</td>
<td>81 (55)</td>
<td>3.473</td>
</tr>
<tr>
<td>Sample 8</td>
<td>8877 (4228)</td>
<td>ACALD, ATPS4r, FBP, G4PDH2r, GLUSy, ME1, NADTRHD, PFL</td>
<td>38 (10)</td>
<td>0.000</td>
</tr>
<tr>
<td>Sample 9</td>
<td>8647 (4007)</td>
<td>ACALD, G4PDH2r, GLUSy, ME2, NADTRHD, PFL, PYK, SUCDi</td>
<td>41 (30)</td>
<td>6.899</td>
</tr>
<tr>
<td>Sample 10</td>
<td>9097 (4129)</td>
<td>ACALD, ATPS4r, GLUSy, LDHi, D, NADTRHD, PFL, SUCDi, TALA</td>
<td>41 (31)</td>
<td>0.207</td>
</tr>
</tbody>
</table>

Total number of EMs (succinate producing). Optimal reaction knockout; Number of remaining EMs (succinate producing); Estimated production rate (mmol/gDW/h) computed from MOMA.

We tested our approach with a case study of rational strain design for succinate production in E. coli. The results have shown that, using an EM sample, it is possible to predict most of the best potential reaction knockouts, and to obtain close to optimal solutions. The utilization of heuristic methods to search for satisfactory solutions, is a common approach in metabolic engineering for large metabolic networks, when an exhaustive search becomes prohibitive (Patil et al. 2009).

4.2 Performance

We implemented our sampling method as an adaptation to the canonical basis approach (Schuster and Hilgetag, 1993). This approach has a very simple and intuitive topological interpretation in terms of the graph of the metabolic network (Fig. 1). However, it is very inefficient compared to the more recent nullspace approach (Klamt et al. 2006). There are very efficient implementations of this approach (e.g. using bit pattern trees (Ferrier and Stelling 2008)). The efmmtool software, which implements these state-of-the-art methods (Ferrier and Stelling 2008), is able to compute the full set of approximately a hundred thousand EMs in the order of seconds to minutes. Our implementation of the canonical basis approach, on the other hand, takes within minutes to hours to compute a few thousand EMs. In our tests, we used a condensed genome-scale reconstruction of E. coli (Orth et al. 2008), which is a simplified version of the full genome-scale model (Feist et al. 2007). In order to apply our method to the full model, it will be necessary to analyze how this approach can be reformulated as a modification to the nullspace approach and integrated into the most recent implementations (Ferrier and Stelling 2008).

Fig. 5. Comparison of the pathway length distribution of the full set of EMs against the distribution for samples at different values of K and the correlation coefficient (r) between the original frequency distribution and the latter
of methods with pre-computation such as the lazy rank updating method proposed by [Ferrez and Stelling, 2008].

Our results show that the computational time grows nearly quadratically with the size of the sample. Therefore, it would seem advantageous to use a divide-and-conquer strategy to compute a sample of size N by appending together P independent samples of size N/P. However, in order to obtain smaller sample sizes, one has to decrease the selection probability (by adjusting K), which affects the quality of the samples regarding the pathway length distribution. Note that it is possible to take advantage of multiple CPUs to run several samples in parallel and combine the samples into one larger set. However, it must be kept in mind that this does not provide the same sampling quality as a sample of the same size obtained with a higher selection probability.

One of the advantages of elementary mode analysis, when compared with methods based on flux balance analysis, is the fact that the EM set needs to be computed only once. Once the EM set is computed, the analysis and optimization of the metabolic network is quite straightforward. On the other hand, bi-level optimization frameworks require expensive computational time at every evaluation [Burgard et al., 2001; Paul et al., 2001]. Therefore, even if the computation of an EM sample, large enough to obtain an unbiased coverage of the solution space, is highly time consuming at the genome-scale, this effort is compensated on the long term.

5 CONCLUSION

As more data are collected, metabolic models keep constantly growing in size. This increases the challenge for EM-based analysis of metabolic networks, as the number of EMs grows exponentially with the network size. For that matter, the development of EM sampling approaches will become increasingly important. This work is a contribution in that direction. We developed a method that prevents the combinatorial explosion of the number of EMs during computation, by adding a filtering step that randomly samples among the candidate modes at each iteration. Unlike other methods for obtaining reduced sets of EMs [De Figueiredo et al., 2009; Jungers et al., 2010b; Kaleta et al., 2010a; Rezola et al., 2011; Riba et al., 2010], our approach does not use any objective functions or experimental flux constraints. EFMEvolver [Kaleta et al., 2009b] is the approach most similar to ours. It samples the EMs that contain a target reaction, rather than the whole solution space. It uses linear programming (LP) to find a single EM, and a genetic algorithm (GA) to search different solutions. It has the advantage that the procedure can be stopped after a desired number of modes have been collected, whereas our approach only yields valid EMs after completion. On the downside, it requires tuning the parameters for the GA and selection of a proper fitness function, whereas or method is tunable by a single parameter. Our method can show a bias towards smaller EM pathway lengths after a desired number of modes have been collected, whereas our method proposed by (Terzer and Stelling, 2008).

Our method can show a bias towards smaller EM pathway lengths fitness function, whereas or method is tunable by a single parameter. It has the advantage that the procedure can be stopped before the whole solution space is sampled. It uses linear programming (LP) to obtain reduced sets of EMs (De Figueiredo et al., 2009, 2010). Our results show that the computational time grows nearly quadratically with the size of the sample. Therefore, it would seem advantageous to use a divide-and-conquer strategy to compute a sample of size N by appending together P independent samples of size N/P. However, in order to obtain smaller sample sizes, one has to decrease the selection probability (by adjusting K), which affects the quality of the samples regarding the pathway length distribution. Note that it is possible to take advantage of multiple CPUs to run several samples in parallel and combine the samples into one larger set. However, it must be kept in mind that this does not provide the same sampling quality as a sample of the same size obtained with a higher selection probability.

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Conflict of Interest: none declared.

REFERENCES

Paul,K. et al. (2005) Evolutionary programming as a platform for in silico metabolic engineering. BMC Bioinformatics, 6, 308.
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