A structural property for reduction of biochemical networks

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Abstract

Large-scale biochemical models are of increasing sizes due to the consideration of interacting organisms and tissues. Model reduction approaches that preserve the flux phenotypes can simplify the analysis and predictions of steady-state metabolic phenotypes. However, existing approaches either restrict functionality of reduced models or do not lead to significant decreases in the number of modelled metabolites. Here, we introduce an approach for model reduction based on the structural property of balancing of complexes that preserves the steady-state fluxes supported by the network and can be efficiently determined at genome scale. Using two large-scale mass-action kinetic models of *Escherichia coli* we show that our approach results in a substantial reduction of 99% of metabolites. Applications to genome-scale metabolic models across kingdoms of life result in up to 55% and 85% reduction in the number of metabolites when arbitrary and mass-action kinetics is assumed, respectively. We also show that growth predictions from the reduced models match those based on the original models. Since steady-state flux phenotypes from the original model are preserved in the reduced, the approach paves the way for analysing other metabolic phenotypes in large-scale biochemical networks.

Keywords

Metabolic networks, network reduction, constraint-based modeling

Introduction

Advances in phenotyping, quantitative genetics methods, and systems biology have helped characterize function of genes embedded in different types of biochemical networks (Fang et al., 2020; Silverbush and Sharan, 2019; Thompson et al., 2015). Generation of large-scale stoichiometric models, capturing the metabolism of individual cell types and their interactions in an organism or communities (Fang et al., 2020), has propelled the development of computational approaches for prediction and analysis of metabolic phenotypes (Bordbar et al., 2014). The sheer size of genome-scale metabolic networks indisputably leads to computational and numerical challenges when employing them to predict and analyse metabolic phenotypes, particularly when these networks are endowed with enzyme kinetics (Chindelevitch et al., 2014; Khodayari and Maranas, 2016; Stanford et al., 2013). Against this background we ask: Can large-scale biochemical models be reduced in an unbiased, i.e. fully automated fashion, while still guaranteeing that the steady-state flux phenotypes are preserved in the resulting models of smaller size?

There already exist several frameworks and theories to reduce biochemical models (Radulescu et al., 2012; Singh and Lercher, 2020). These approaches can be categorized based on different criteria: (i) whether they only employ the structure of the network (i.e. stoichiometry of biochemical reactions) (Clarke, 1992; Jonnalagadda and Srinivasan, 2014; Sambamoorthy and Raman, 2020; Singh and Lercher, 2020; Tefagh and Boyd, 2019) or also consider the kinetics of reaction fluxes (Danø et al., 2006; Feliu et al., 2019; Feliu and Wiuf, 2013, 2012; Radulescu et al., 2008; Rao et al., 2014; Roussel and Fraser, 2001; Sáez et al., 2017; Schmidt et al., 2008;

Sunnåker et al., 2011), (ii) whether they approximate or provide one-to-one correspondence of the steady-state properties between the original and reduced network (Erdrich et al., 2015; Feliu and Wiuf, 2013; Röhl and Bockmayr, 2017; Tefagh and Boyd, 2019), and (iii) whether the reduction process is fully automated, i.e. unbiased, or semi-automated (i.e. requires user input) (Singh and Lercher, 2020).

Reduction approaches rooted in the constraint-based modelling framework have been successfully employed to arrive at reduced models that approximate *steady-state flux properties* of large-scale metabolic networks. One group comprises approaches based on user-specified input, consisting of pre-selected metabolites, reactions, and functions (e.g. biomass production) that must be present or supported by the reduced model and, thus, result in reduced models biased by the user's input (Ataman et al., 2017; Erdrich et al., 2015; Röhl and Bockmayr, 2017). Other approaches in this group start with user-defined subsystems that are subsequently connected (and further refined) to obtain a minimal model that can fulfil a pre-specified function (Baroukh et al., 2014). In contrast, using ideas from reaction coupling (Burgard et al., 2004), a recent unbiased approach provides an efficient reduction of stoichiometric models by reaction removal, while ensuring one-to-one correspondence between the elementary flux modes of the original and reduced model (Tefagh and Boyd, 2019). Since these approaches do not consider kinetics of reaction flux, they remain silent about the effects that the reduction has on the concentrations of the remaining metabolites.

Approaches for reduction of models with mass action kinetics are particularly important to solve or approximate different reaction mechanisms (e.g. Michaelis-Menten, Hill) (Feliu et al., 2019; Pantea et al., 2014). They usually invoke the quasi-steady state assumption (QSSA), whereby the modelled components can be grouped into those with small concentrations, referred to as intermediates, and those with large concentrations (i.e. substrates and products), such that the network displays two (or more) timescales. Invoking QSSA implies that the

intermediates, that change on the fast time scale, are expressed as functions of the slow components (Feliu et al., 2019). Therefore, these intermediates are eliminated from the original network and, then, the reduced network, capturing the slow dynamics, is further analysed. Application of QSSA is not straightforward since it requires data on kinetic parameters that are challenging to obtain at a genome-scale level (Davidi et al., 2016). Therefore, such approaches cannot be analytically carried out (Pantea et al., 2014), and often involve approximations that lead to inaccuracies of estimations.

One unbiased technique to eliminate a component in mass action networks requires that the component appears only as a sole substrate or product in the reactions in which it participates (Feliu and Wiuf, 2013). Assuming steady state, the concentration of such a component can be readily expressed as a function of the concentrations of the remaining components. This approach guarantees correspondence between the conservation laws of the original and reduced network and the respective numbers of positive steady states (Feliu and Wiuf, 2013). This idea has been generalized to allow linear removal of some subsets of components that appear only with stoichiometry at most one in any reaction of a given network endowed with mass action kinetics (Sáez et al., 2017). Yet, structural conditions ensuring that the steady-state flux spaces of the reduced network are subset of the reduced network by removal of components of any stoichiometry in networks endowed with arbitrary kinetics remain elusive.

Here we identify such a structural property for model reduction and show that it can be efficiently computed and applied in genome-scale metabolic networks from organisms across the kingdoms of life. The condition allows consideration of biochemical constraints and can, therefore, be invoked with or without assumptions on optimized biological function. The key advantage of the structural condition is that it can be applied to large-scale biochemical networks endowed with mass action kinetics, and under some restrictions, to networks

endowed with arbitrary kinetics, while guaranteeing that the steady-state flux phenotypes of the original model are preserved in the reduced.

Results and Discussion

Balancing of complexes as a structural condition for network reduction

To illustrate the condition, we first introduce some key concepts from stoichiometric modelling of biochemical networks. A biochemical network is composed of reactions through which biochemical species acting as substrates are transformed into products. The biochemical network on Fig. 1a is composed of ten reactions that transform six species. The network structure is described by nodes that denote complexes, corresponding to the left- and right-hand sides of the considered reactions, and edges representing the reactions. Therefore, the network on Fig. 1a contains eight complexes connected by ten reactions. The incoming and outgoing neighbourhoods of a complex are given by the complexes to which it is directly connected via incoming and outgoing reactions, respectively. For instance, the incoming neighbourhood of complex 2B is composed of complexes D and F, and the outgoing neighbourhood comprises A+E and F. The stoichiometric matrix of the network, N, is then given by the product of the matrix, Y, describing the species composition of complexes and the incidence matrix, A, of the corresponding directed graph (Methods, Supplementary Fig. S1) (Müller and Regensburger, 2012; Neigenfind et al., 2013). In addition, the reactions are weighted by non-negative numbers which correspond to fluxes of a steady-state flux distribution, v, which satisfies $Nv = 0$. The steady-state condition implies that the concentrations of species are invariant in time, i.e. the species are *balanced*, whereby the production and consumption rates are the same.

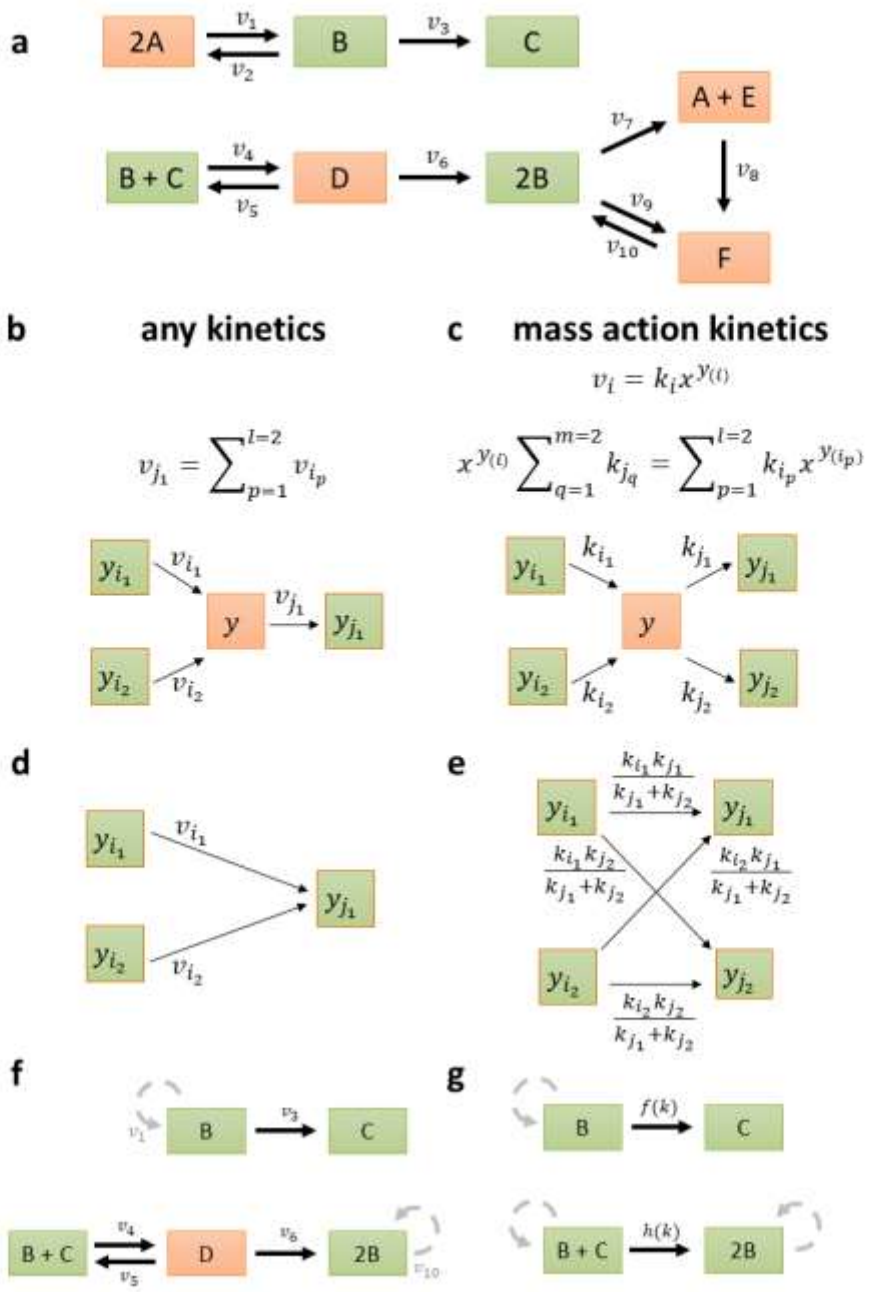

Figure 1. Balanced complexes for network reduction. (**a**) Toy example network borrowed from Shinar and Feinberg (2010), including six species, A – F, eight complexes, depicted as rectangles, and ten reactions, with rates v_1-v_{10}, each connecting two complexes. Balanced complexes are shown in orange, while non-balanced complexes are depicted in green. Balanced complexes 2A, A+E, and F have one outgoing reaction, while the balanced complex D has more than one outgoing reaction. Structural motif allowing removal of the balanced complex

y (**b**) with single outgoing reaction, for an arbitrary kinetics and (**c**) with multiple outgoing reactions, for mass action kinetics. Removal of the complex amounts to substitution of variables, either with respect to reaction rates v or monomials of species concentrations x^y, which can be represented by (**d**) network rewriting, for arbitrary kinetics and (**e**) additional scaling of reaction rate constants, with mass action kinetics. (**f**) Reduced network obtained by removing the balanced complexes 2A, A+E, and F; the loop reactions are shown in grey since they do not contribute to the stoichiometric matrix. (**g**) Reduced network obtained from the network in panel (**f**) after removal of the balanced complex D, assuming mass action. For simplicity, the rate constants are given as functions $f(k)$ and $h(k)$.

An analogous condition on balancing can be defined for a single complex: Given a biochemical network, a complex is balanced in a set of steady-state flux distributions S if the sum of fluxes of its incoming and outgoing reactions is the same for every flux distribution in S. Clearly, complexes that act as sinks or sources, that only have incoming or outgoing reactions, respectively, cannot be balanced in a network without blocked reactions (i.e. reactions which carry no flux in every steady state the network supports). Further, a complex is considered *trivially balanced* if it includes a species that appears in no other complex in the network. This result is a consequence of the balancing of species due to the steady state assumption. A balanced complex that includes species all of which appear in other complexes are termed *non-trivially balanced*. For instance, complex C cannot be balanced as it is a sink, while D, A+E, and F are trivially balanced since species D, E, and F appear only in these complexes that have both incoming and outgoing reactions. Note that our definition of trivially balanced complexes extends the notion of an intermediate species in other reduction approaches (Feliu and Wiuf, 2013). Finally, 2A is a non-trivially balanced complex, since A appears in two complexes of which one, A+E, is trivially balanced.

For a set S of steady-state flux distributions, every balanced complex can be readily identified by constraint-based modelling (Methods). The approach amounts to determining that the minimum and maximum total fluxes around a complex are zero for all steady-state flux distributions in S. These conditions can be verified by linear programming that is efficient even for large-scale networks (Methods). The identification of balanced complexes can be further streamlined by easy screening of trivially balanced as well as sink and source complexes. Networks in which all complexes are balanced are termed complex balanced, and they can be identified by calculating the structural property of deficiency (Feinberg, 1987). Seminal theoretical results pinpoint that complex balanced networks do not exhibit exotic properties, like multistationarity and oscillations. However, it has not yet been addressed how one can identify individual balanced complexes and what the implications of their presence in the network are with respect to the capacity to exhibit particular phenotypic properties.

We next ask if balanced complexes are relevant for reduction of networks which are not complex balanced. To answer this question, we first consider the scenario with a network endowed with arbitrary kinetics. If a balanced complex has only one outgoing reaction, then the flux of this reaction can be expressed as a sum of the fluxes of incoming reactions. The balanced complex can then be safely removed since the flux of the outgoing reaction can be substituted with the respective sum of fluxes of the incoming reactions for the balanced complex. This is concomitant to introducing a bipartite directed clique, connecting each complex in the incoming neighbourhood with the complex in the outgoing neighbourhood (Fig. 1b,d). . Note that any loop edges introduced by this transformation can be removed, since they do not contribute to the balancing equations. For instance, A+E, F, and 2A can be removed as balanced complexes, resulting in the network on Fig. 1f; however, this cannot be done for the balanced complex D since it has more than one outgoing reaction. Since the removal of complexes in this way results in expressing one flux as a sum of others, the reduced network

is unique and does not depend on the order of removing the balanced complexes. A similar idea has been used in the unbiased efficient reduction of stoichiometric models (Tefagh and Boyd, 2019), however, based on the coupling of reactions around balanced species and without the rewiring of reactions.

Attempting to remove a balanced complex with more than one outgoing reaction fails in general; however, under the constraint that all outgoing reactions are fully coupled (i.e. their flux ratio in every steady state is a unique constant) all outgoing reaction fluxes collapse into one and the balanced complex can be removed. Interestingly, this constraint is trivially met for networks endowed with mass action kinetics, since the ratio of fluxes of reactions outgoing from any complex is given by the ratio of the respective rate constants. Importantly, this removal can be carried out even if values for the rate constants are not specified, since the ratio is ensured to be constant. Therefore, under mass action, a balanced complex can be removed by introducing a bipartite directed clique of reactions with rescaled kinetic constants (see Methods, Fig. 1c,e). For instance, the balanced complex D can be removed, like the other balanced complexes in the network, resulting in a mass action network with fewer complexes and species, and reactions with modified kinetic parameters, as shown in Fig. 1g.

The usage of balanced complexes to reduce networks with mass action kinetics generalizes the removal of trivially balanced complexes in which species appear with stoichiometry of one (Feliu and Wiuf, 2013). However, the proposed approach allows removal of species of any stoichiometry, provided they appear only in balanced complexes. It also provides a sound extension of a reduction approach in which complexes are--arbitrarily--assumed to be balanced (Rao et al., 2014) – and leads to biases in the model reduction. In our approach, the conservation laws in the original network hold in the reduced, but not necessarily vice versa (see Methods). Therefore, if the original network has at most one positive steady state for any rate constants and values for the conservation moieties, then the reduced model also has at most one positive

steady state for the rescaled rate constants (Feliu and Wiuf, 2013). Hence, analysis of the reduced model can help identify if multistationarity is precluded in the original, larger model if seminal conditions apply (Feinberg, 1987). Note that, the removal of balanced complexes may result in removal of species, but may lead to an increase in the number of reactions. Most importantly, the steady-state concentration of any removed species in the process of model reduction can be expressed as a function of the concentrations of the species in the reduced model (Supplementary Fig. S2).

Reduction of a large-scale kinetic model of *Escherichia coli* metabolism

To verify that the proposed approach could lead to reduction of metabolic networks endowed with mass action kinetics, we used the genome-scale (Khodayari and Maranas, 2016) and the so-called core (Khodayari et al., 2014) kinetic metabolic models of *E. coli*. The core model is composed of 828 species, 1474 irreversible reactions, and 1190 complexes, while the genome-scale model consist of 3002 species, 5237 irreversible reactions, and 4371 complexes. Relying solely on the structure of the network, we identified 484 and 1639 balanced complexes in the core and genome-scale kinetic models, respectively, of which 77.7% and 75.4% were trivially balanced. From the 484 and 1639 balanced complexes 23% and 26% had only one outgoing reaction. The removal of such balanced complexes led to a decrease in the number of species by ~14% in comparison to both investigated kinetic models. Both models consider elementary reaction steps and, therefore, model species can be of three types: metabolite, enzyme or metabolite-enzyme complex. We observed that ~95% of the species removed denoted species that represent metabolite-enzyme complexes. When considering the additional restriction due to mass action kinetics, we could apply the approach in a second round of reduction. This led to the identification of 694 and 2708 additional non-trivial balanced complexes in the core and genome-scale kinetic model, respectively. Removal of these balanced complexes led to ~99% decrease in the number species in comparison to the original model for the core as well as the

genome-scale model. Therefore, the approach does lead to a substantial reduction in the number of species even when only the structure of the network was employed.

The reduced core kinetic model comprises: fumarate, succinate as well as ubiquinone-8 and ubiquinol-8, interconverted by fumarate reductase (FRD2) and succinate dehydrogenase (SUCDi) together with the related substrate-enzyme complexes (Fig.2). In the reduced genome-scale model extracellular pyruvate, acetate, and L-glucose as well as enzymes exchanging those metabolites with the environment extend the set of species around fumarate reductase and succinate dehydrogenase that are found in the reduced core kinetic model (Fig. 2). Therefore, the steady-state concentrations of all other metabolites in these kinetic models can be expressed as functions of the few species that are present in the reduced model.

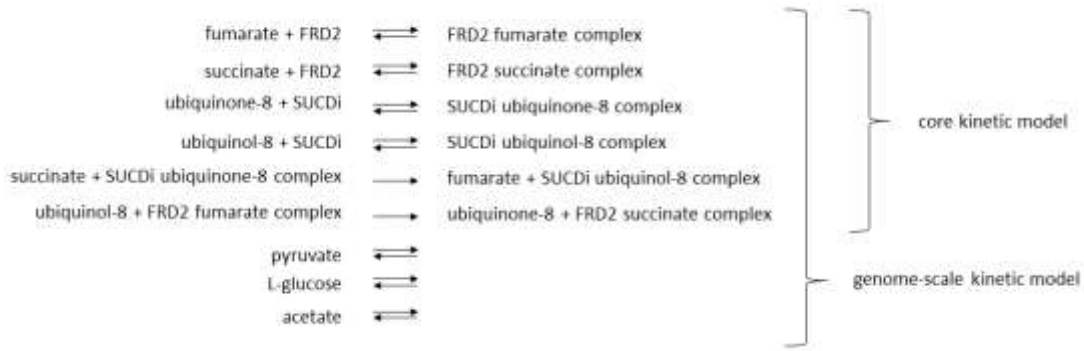

Figure 2. Illustration of the reduced core and genome-scale kinetic models obtained by reduction of a mass action kinetic model. The reduced core kinetic model comprises ten components and ten reactions, while the reduced genome scale kinetic model consists of 13 compounds and 16 reactions. (fumarate reductase - FRD2, succinate dehydrogenase - SUCDi). The concentration of the components present in the reduced networks can be used to model the concentration of all other components in the original networks.

Reduction of large-scale stoichiometric metabolic networks

Motivated by the findings from the reduction of the core and genome-scale kinetic models of *E. coli* metabolism, we next employed the proposed approach to inspect the reduction in the number of species in genome-scale metabolic models of different organisms. To this end, we used the metabolic networks of twelve organisms to compare and contrast the reductions for the following scenarios: (i) all reactions are assumed to be reversible in contrast to the case when irreversibility constraints, included in the original models, are used, (ii) all reactions follow arbitrary kinetics or their fluxes are described by mass action kinetics, (iii) balanced complexes are determined with respect to the set of steady-state flux distributions compatible with reversibility in comparison to steady-state flux distributions at optimal growth. Note that reversible reactions are split into two irreversible reactions before applying the approach.

With arbitrary kinetics of reaction fluxes, the general observation was that invoking irreversibility led to only a small increase (< 7%) in the number of removed species across all organisms (Fig. 3a, Supplementary Table S1). The model of *M. barkeri* is an exception to this finding, with 30% increase in species reduction when considering reaction irreversibility. In addition, imposing constraints on biomass had negligible additional effect on the balanced complexes in majority of the networks, except in the models of *P. putida* and *N. pharaonis*, for which there was an increase by 26 and 30% in the number of removed species, respectively (Fig. 3a). This finding demonstrated that the balanced complexes are a property of the network structure and steady-state constraint, rather than due to optimality conditions imposed.

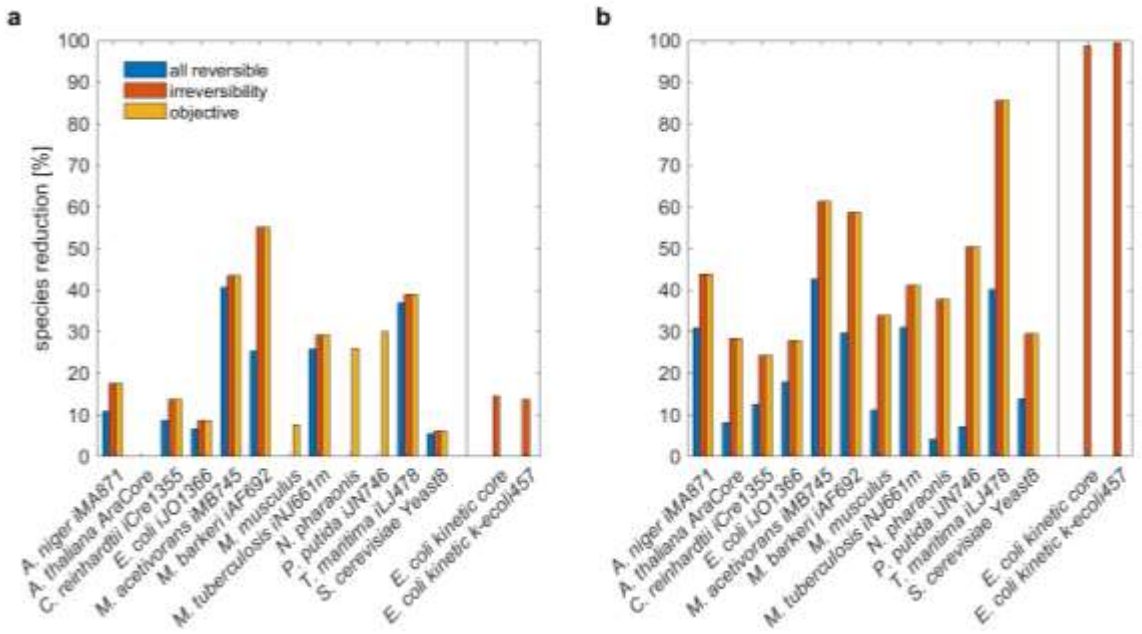

Figure 3. Reduction of genome-scale metabolic networks. Genome-scale metabolic models of twelve organisms from all kingdoms of life are used in the reduction (**a**) with arbitrary kinetics and (**b**) assuming mass action kinetics. The analysis also includes two large, mass-action kinetic models of *E.* coli. Shown is the percentage of reduction in the number of species with respect to the original model.

Consideration of mass action kinetics led to an increase in model reduction of, on average, 26% in comparison to the case of arbitrary kinetics when all reactions are considered reversible (Fig. 3a, b). In contrast to the case of arbitrary kinetics, the assumptions of reaction irreversibility has a large effect on the reduction in the number of species in comparison to the case when all reactions are assumed to be reversible (Fig. 3b). On average, we observed 23% increase in species reduction when reaction irreversibility is considered. Finally, imposing constraints on biomass had no effect on the balanced complexes and, thus, on the number of removed species, when mass action was considered (Fig. 3b).

Altogether, when irreversibility for reactions in the original model was considered, the proposed approach led to no reduction in the number of species in the *Arabidopsis thaliana* core, *M. musculus*, *N. paharaonis* and *P. putida* model and reached up to 55.1% reduction in the model of *M. barkeri*. On average we observed 18% of species being removed across all considered networks. Instead, when mass action kinetics was considered, we found a reduction between 24.3% for *E. coli* to 85.7% in *T. maritima*, with an average of 44% across the considered models. These results demonstrated that substantial reduction in the number of removed species is possible, while ensuring that the key network properties at steady state are matched between the original and reduced network. In addition, the reduction eliminated up to 17 (12%) species which enter complexes with stoichiometry larger than one (Supplementary Table S2), which is not possible with the existing approaches.

Next, we investigate compartment-wise species reduction in models across kingdoms, considering reaction irreversibility and mass action kinetics. The general observation was that models comprising extracellular space show large reduction for this compartment. The reduction ranged from 26% for *N. pharaonis* to 100% in *T. maritima* (Supplementary Table S3). On average, the reduction over the ten models including extracellular space as a compartment was 65.5%. The average reduction for the cytoplasmic part of bacterial and archaea models was 49%. Compartmented models of *S. cerevisiae*, *C. reinhardtii* and *A. thaliana* showed largest reduction in mitochondria, chloroplast and cytosol, respectively (Supplementary Table S3).

Using the two genome-scale metabolic models of *E. coli* and *S. cerevisiae* we compared the set of metabolites in the original and reduced models using Jaccard similarity. The original models show Jaccard similarity of 0.27. Also the reduced models have Jaccard similarity of 0.26 for the set of metabolites. A similar observation was made comparing bacterial models of *E. coli*, *M. tuberculosis*, and *N. pharaonis* for which at least 95% of the metabolite names could be

translated to a common name space. Here, we found Jaccard similarity across the set of metabolites of 0.19 for the original models and 0.16 in the reduced models.

Growth predictions from reduced models

To showcase the benefit of the reduction approach, we considered the reduced models that still include the metabolites (i.e. species) participating in the biomass reactions from the original model (with specified irreversibility). This allows us to compare the simulated growth between the original and reduced models. The resulting reduced models included 4% fewer metabolites in the model of *A. thaliana* to 28% in the model of *M. musculus* (Fig. 4b). Our findings demonstrate that optimal growth predicted by the original models are exact match for those of the reduced models (Fig. 4a). Thus, this analysis showcases that the proposed property can be used to remove some well-defined balanced complexes (e.g. those that do not include the building blocks of biomass) without affecting growth phenotypes, thus, allowing more targeted applications.

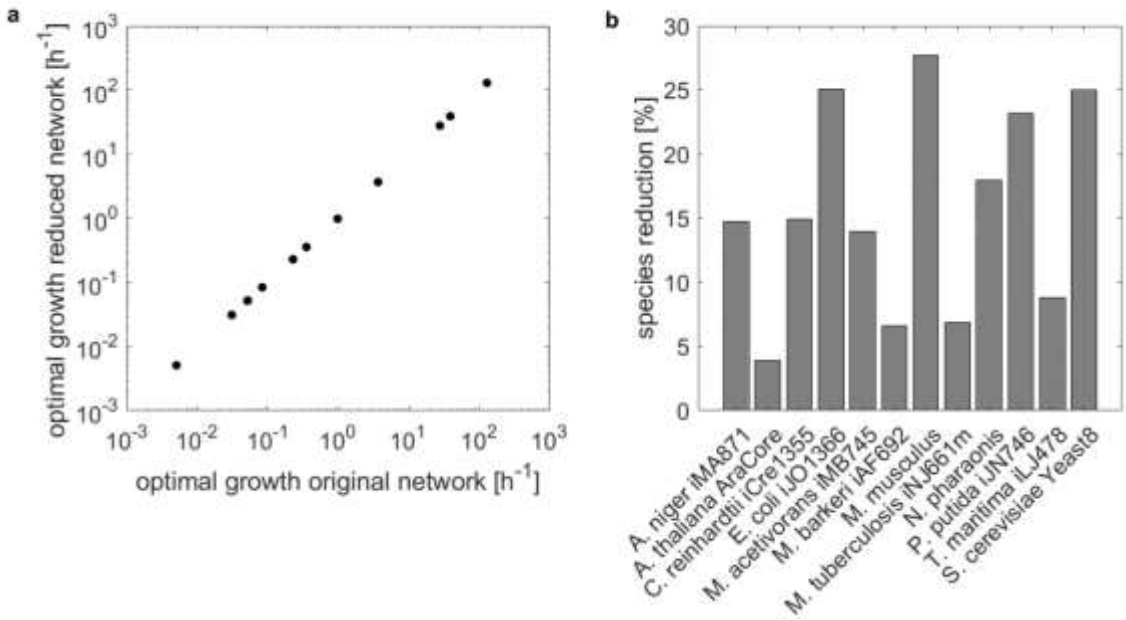

Figure 4. Growth prediction in original and reduced models. For direct comparison it is ensured that metabolites that comprise the biomass reaction in the original model remain in the

reduced model. (**a**) Optimal growth estimated from the original and reduced models assuming arbitrary kinetics. (**b**) Model reduction on the level of metabolites.

Conclusion

The constraint-based modelling framework provides a powerful suite of approaches to study the genotype-to-phenotype mapping not only in a single cell, but also across multiple unicellular organisms in a microbial community and interconnected tissues in a multi-cellular organism. However, these advanced applications are associated to increases in the model size which lead to computational and numerical issues in predicting phenotypes of interest. Here, we proposed a fully automated (i.e. unbiased) approach for reduction of models with arbitrary or mass action kinetics. The approach is based on identifying balanced complexes which contain either a single outgoing reaction, in the case of arbitrary kinetics, or more than one outgoing reaction, for mass action kinetics. We also show that the structural condition can be efficiently identified in large-scale networks. Moreover, such balanced complexes can be safely removed from the network as their removal translates into identification of substitution of variables which preserves the steady-state flux distributions of the original model. In addition, the variable substitution can be graphically represented by rewriting the network, leading to a reduced network, and can be carried out without knowledge of kinetic parameters (in the case of mass action kinetics). Most importantly, if a species appears only in balanced complexes, it can be removed from the network and, under the assumption of mass action kinetic, its steady-state concentration can be represented as functions of the steady-state concentrations of the metabolites that remain in the reduced network.

Our extensive analysis of genome-scale kinetic models endowed with mass action show that more than 99% of the metabolites can be removed following the proposed reduction. In addition, since the approach is constraint-based, it also allows us to examine if reaction

reversibility or assumption on cellular tasks (e.g. growth) that are optimized have an effect on the size of the reduced model, in terms of number of species. The analysis with genome-scale metabolic models across kingdoms of life show that reaction reversibility and assumption of kinetics have the largest effect on the size of the reduced models, leading to up to 85% reduction in the number of species. Nevertheless, we show that if the reduction is performed such that no metabolite participating in the biomass reaction is removed, the reduced model is not affected with respect to predicted growth phenotypes.

Since the proposed approach is based on a property that can be efficiently determined even in large-scale networks, it provides the means for reduction of multi-tissue and microbial community models. Moreover, it opens the possibility to study the relationship of key properties, such as robustness and multistationarity, between the original and reduced models. However, these applications will have to ensure imposing additional constraints on the removal of the balanced complexes that do not affect the conservation laws in the network. Finally, our approach opens the possibility for unbiased model reduction by seeking to identify other types of structural motifs in large-scale metabolic networks.

Methods

Models and their processing

The genome-scale metabolic models of twelve organisms (Supplementary Table S1), were obtained from their original publications (Andersen et al., 2008; Arnold and Nikoloski, 2014; Benedict et al., 2012; Fang et al., 2010; Feist et al., 2006; Gonzalez et al., 2010; Imam et al., 2015; Lu et al., 2019; Nogales et al., 2008; Orth et al., 2011; Quek and Nielsen, 2008; Zhang et al., 2009). The blocked reactions, reactions with absolute flux values less than 10^{-9} $mmol/gDW/h$, in the metabolic network were determined by Flux Variability Analysis (Gudmundsson and Thiele, 2010) and were removed from the original models. Each reversible

reaction was split into two irreversible reactions. Two cases for the irreversible reactions originally declared in the model were considered: (1) all were treated as reversible (and were split, as aforementioned) or (2) were maintained as irreversible. The lower bounds for the irreversible reactions were set to zero, while the upper bounds were fixed to the maximum of the upper bounds in the original model. Optimum biomass was determined per Flux Balance Analysis (Orth et al., 2010) with the assumed reaction reversibility.

Identification of balanced complexes

Let Y denote the non-negative matrix of complexes, with rows denoting species and columns representing complexes. The entry y_{ij} denotes the stoichiometry with which species i enters the complex j. Let A denote the incidence matrix of the directed graph with nodes representing complexes and edges denoting reactions. The rows of A denote the complexes and its column stand for the reactions. Since the graph is directed, each column of A has precisely one -1 and one 1 entry, corresponding to the substrate and product complexes of the respective reaction. The stoichiometric matrix is then given by $N = YA$.

The sum of fluxes around the complex i is given by the ith entry of the vector Av, denoted by $[Av]_i$. A complex is balanced in the set of flux distributions $S = \{v | Nv = 0, v_{min} \leq v \leq v_{max}\}$ if for every $v \in S$, it holds that $[Av]_i = 0$. This condition can be verified by determining that the minimum and maximum values of $[Av]_i$ equal to 0 for each complex i, separately. The latter can be ensured by solving two linear programs:

$min/\max[Av]_i$

s.t.

$YAv = Nv = 0$

$v_{min} \leq v \leq v_{max}$.

Removal of balanced complexes

Suppose that the complex y is balanced and that it participates in l incoming and m outgoing reactions as a product and substrate complex, respectively. Let $y_{i_1},\dots y_{i_l}$ and $y_{j_1},\dots y_{j_m}$ denote the substrate and product complexes of the l incoming and m outgoing reactions.

Let us assume that $m = 1$, i.e., the complex y is incident on only one outgoing reaction. Due to the balancing of y, $v_{j_1} = \sum_{p=1}^{l} v_{i_p}$. The removal of the complex y without affecting the steady-state fluxes entails: (i) removal of the $l + 1$ reactions incident on y from the original network and (ii) insertion of l reactions with a substrate complex from $y_{i_1},\dots y_{i_l}$ and a product complex y_{j_1}. This amounts to substituting every occurrence of v_{j_1} by $\sum_{p=1}^{l} v_{i_p}$, preserving steady-state flux solutions (i.e. the reduced network includes all steady-state flux solutions of the original).

Let us now assume that $m \geq 1$ and that the network is endowed with mass action kinetics. The flux of a reaction i with complex $y_{(i)}$ as a substrate is given by $v_i = k_i x^{y_{(i)}}$, where $x^{y_{(i)}} = \prod_j x_j{}^{y_{ji}}$ and y_{ji} denotes the stoichiometric coefficient of species j in the complex $y_{(i)}$. Due to complex balancing, then, $x^{y_{(i)}} \sum_{q=1}^{m} k_{j_q} = \sum_{p=1}^{l} k_{i_p} x^{y_{(i_p)}}$. The removal of the complex $y_{(i)}$ without affecting the steady-state values x^{y_i} of the complexes entails: (i) removal of the $l + m$ reactions incident on $y_{(i)}$ from the original network and (ii) insertion of ml reactions with a substrate complex from $y_{(i_1)},\dots y_{(i_l)}$ and a product complex from $y_{(j_1)},\dots y_{(j_m)}$. The rate constant of the reaction with $y_{(i_p)}$ and $y_{(j_q)}$ as substrate and product complexes, respectively, is given by $\frac{k_{i_p} k_{j_q}}{\sum_{q=1}^{m} k_{j_q}}$. This amounts to substituting every occurrence of $x^{y_{(i)}}$ by $\sum_{p=1}^{l} \frac{k_{i_p}}{\sum_{q=1}^{m} k_{j_q}} x^{y_{(i_p)}}$ in $NK\varphi(x) = 0$, preserving the steady-state flux solutions with respect to $\varphi(x)$ (rather than fluxes, in the case for arbitrary kinetics, above). Note that $\varphi(x)$ is a vector

collecting x^y over all complexes, while K is the matrix with as many rows as reactions and as many columns as complexes, whose entry k_{ij} corresponds to the rate constant of the reaction i having complex j as a substrate or zero, otherwise.

Correspondence of conservation laws

The removal of a balanced complex corresponds structurally to substituting of any directed path of two reactions, $N_{.i}$ and $N_{.j}$, on which the balanced complex is the middle node, with another reaction, given by reaction vector $N_{.i} + N_{.j}$. Clearly, $N_{.i} + N_{.j} \in \mathrm{span}(\{N_{.i}, N_{.j}\})$. It follows that every new reaction in the reduced network lies in the column span of N. Denoting the stoichiometry matrix for the reduced network by $\underline{N}$, $\mathrm{im}(\underline{N}) \subseteq \mathrm{im}(N)$ yields $\ker(N^T) \subseteq \ker(\underline{N}^T)$.Therefore, for every conservation law, $\lambda^T x = \theta$ that satisfies $\lambda \in \ker(N^T)$, one also has $\lambda \in \ker(\underline{N}^T)$, which means the conservation law is preserved in the reduced network. . However, a conservation law $\mu^T x = \theta$ in the reduced network may not necessarily correspond to one of the original network, unless further constraints are imposed on the balanced complexes being removed.

Growth predictions

We calculate optimal growth rates by flux balance analysis (FBA) in models with considered irreversibility and compare the estimated growth rates before and after removal of balanced complexes. Blocked reactions are removed from the original network and each reversible reaction is split into two irreversible reactions. To avoid cases where no biomass production is ensured in the original model after removal of blocked reactions due to numerical issues, we set the lower bound of the biomass reaction to 5% of the optimal biomass obtained from the model including blocked reactions. In addition, we ensure that the biomass reaction, whose flux is optimized during FBA, is still included in the reduced model. Therefore, we only remove

balanced complexes that do not include metabolites (i.e. species) participating in the biomass reactions from the original model.

Data access

The approach is implemented and available together with all data needed to reproduce the findings at https://github.com/ankueken/network_reduction_by_balanced_complexes.

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Author contributions

Conceptualization: Z.N., data collection: A.K., formal analysis: A.K., investigation: A.K., Z.N., software: A.K., P.W., validation: A.K., writing – original draft: Z.N., writing – reviewing and editing: A.K., P.W., D.L., Z.N.

Competing interests

Authors declare no competing interests.

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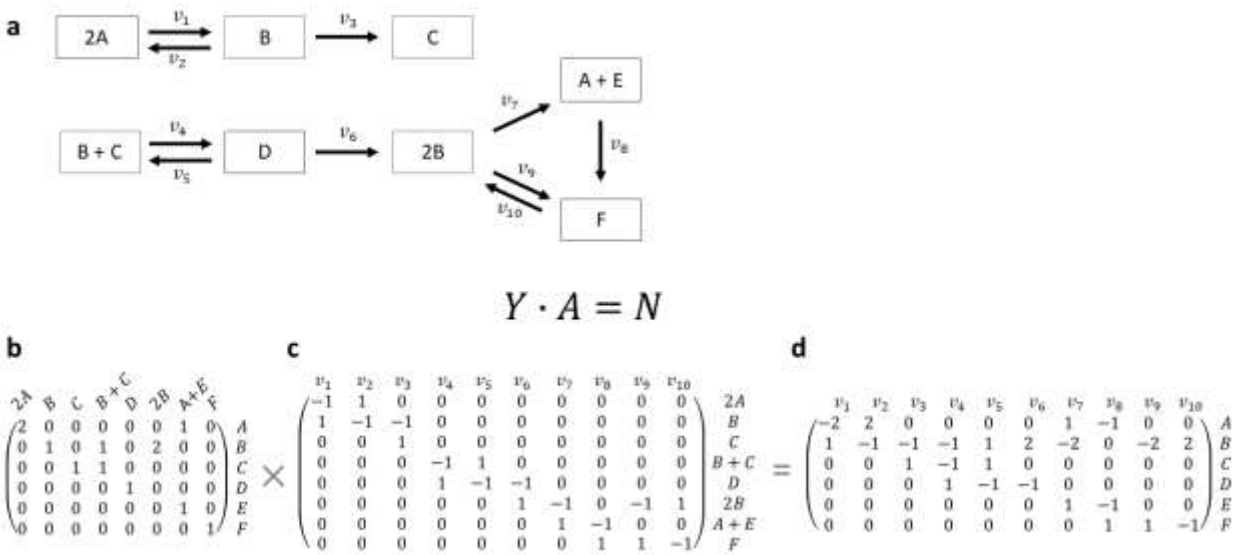
Supplementary Information for

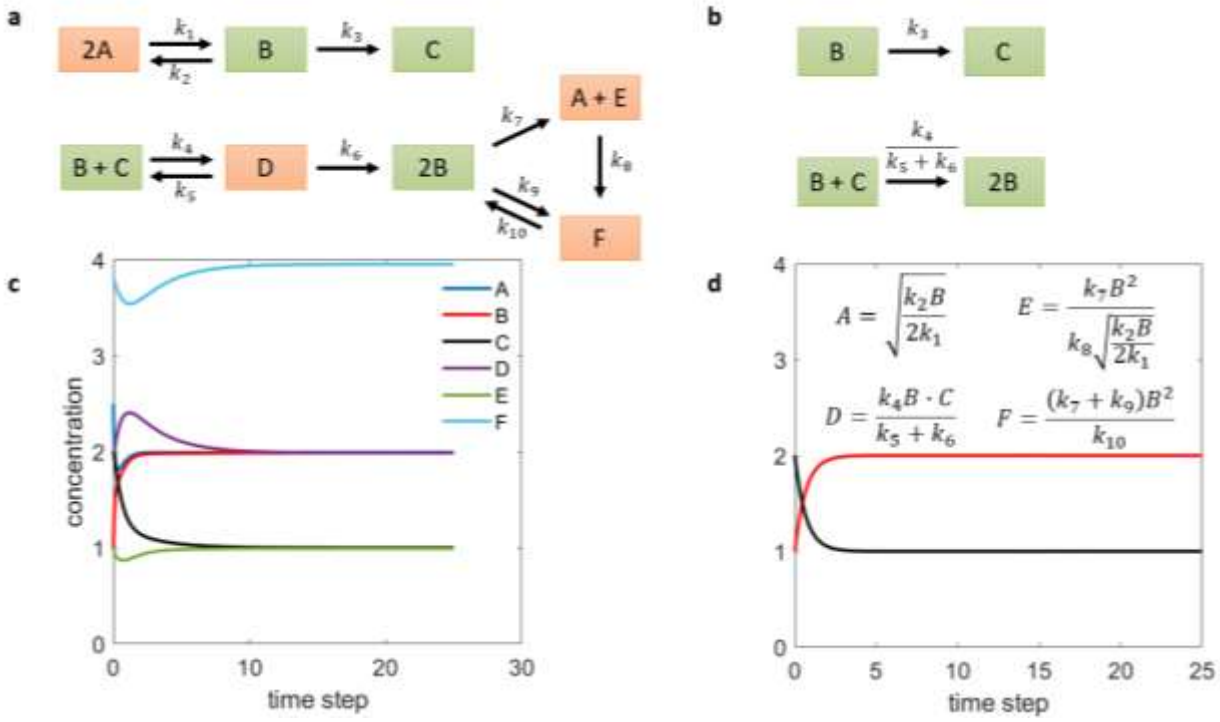
"A structural property for reduction of biochemical networks"

Anika Küken, Philipp Wendering, Damoun Langary, Zoran Nikoloski

Supplementary Figure



Supplementary Figure S1. Decomposition of the stoichiometric matrix. (**a**) Example network borrowed from Shinar and Feinberg (2010), including six species, A – F, eight complexes, depicted as rectangles, and ten reactions, with rates v_1-v_{10}, each connecting two complexes. (**b**) Species-complex matrix Y, where rows correspond to species and column correspond to complexes. Each entry indicates the molarity with which a species participates in a complex. (**c**) Incidence matrix A of the directed graph given in (**a**). (**d**) Stoichiometric matrix N, where rows correspond to species, columns correspond to reactions, and each entry indicates the molarity with which a species is produced (positive values) or consumed (negative values) by a reaction. The stoichiometric matrix of the network is given by by the product of species-complex matrix and incidence matrix, $N = Y \cdot A$.



Supplementary Figure S2. Concentration of removed species can be expressed as function of species in the reduced network. (**a**) Original network including six species, A – F, eight complexes, depicted as rectangles, and ten reactions, with rates v_1-v_{10}, each connecting two complexes. (**b**) Reduced network obtained by removing the balanced complexes 2A, A+E, F and D, assuming mass action. (**c**) Simulation of steady-state concentrations for species A – F in the original network using rate constants $k = (1, 2, 0.5, 1, 0.5, 0.5, 0.25, 0.5, 0.25, 0.5)$ and initial concentrations $x = (2.5, 1, 2, 2, 1, 3.8)$. (**d**) Simulation of steady-state concentrations for species B and C in the reduced network using rate constants $k = (0.5, 1)$ and initial concentrations $x = (1, 2)$, like for the original network simulation. Parameters k for the reduced network relate to parameters in the original network as shown in panel (b). Both networks simulate the same steady-state concentrations for species B and C. Concentrations of removed species A, D, E and F can be calculated as functions of species B and C present in the reduced network assuming mass action (see equations in (d)).

Supplementary Table legends

Supplementary Table S1. Overview results of balanced complex removal. The table provides an overview about the number of balanced complexes identified and removed per iteration as well as the type of the balanced complexes (trivial or non-trivial). Moreover, details about the number of species, complexes and reactions in original and reduced models are shown. During analysis three different scenarios were considered (1) every reaction is considered reversible, (2) reaction irreversibility considered, (3) objective (i.e. biomass) optimized. (**a**) Results obtained for the assumption of any kinetics. (**b**) Results obtained for the assumption of mass action kinetics. (**c**) Overview of total model reduction (%) in terms of model species for the different scenarios and assumptions about kinetics (related to Figure 2).

Supplementary Table S2. Overview of species with stoichiometry larger than one removed from networks during network reduction. Reaction irreversibility was considered and networks reduced according to the reduction motif of (**a**) any kinetics and (**b**) mass-action kinetics. Metabolite names are provided the way declared in the original publication.

Supplementary Table S3. Compartment-specific analysis. Shown are the numbers of metabolites in the original and reduced models for networks of twelve organisms across kingdoms of life.