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# A stronger necessary condition for the multistationarity of chemical reaction networks

Sylvain Soliman

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**Abstract** Biochemical reaction networks grow bigger and bigger, fed by the high-throughput data provided by biologists and bred in open repositories of models allowing merging and evolution. Nevertheless, since the available data is still very far from permitting the identification of the increasing number of kinetic parameters of such models, the necessity of structural analyses for describing the dynamics of chemical networks appears stronger every day.

Using the structural information, notably from the stoichiometric matrix, of a biochemical reaction system, we state a more strict version of the famous Thomas' necessary condition for multistability. In particular, the obvious cases where Thomas' condition was trivially satisfied, mutual inhibition due to a multimolecular reaction and mutual activation due to a reversible reaction, can now easily be ruled out.

This more strict condition shall not be seen as some version of Thomas' circuit functionality for the continuous case but rather as related and complementary to the whole domain of the structural analysis of (bio)chemical reaction systems, as pioneered by Chemical Reaction Network Theory.

**Keywords** Jacobian matrix · Influence graph · Feedback circuit · Multistationarity · Chemical reaction network

**Mathematics Subject Classification (2000)** 92C42 · 34C10 · 34C23 ·

## 1 Introduction

In the last thirty years, the conjecture of Thomas (1981) on the necessary presence of a positive circuit for the occurrence of multistability has opened a whole field of research.

First on the mathematical side, since it has been proven under various forms, depending on the restrictions on the system: discrete (Richard and Comet 2007; Remy et al. 2008) or continuous (Plahte et al. 1995; Gouzé 1998; Snoussi 1998; Cinquin and Demongeot 2002; Soulé 2003).

But also based on the insight gained from it allowing better modeling and understanding of biochemical networks, especially in the emerging field of Systems Biology.

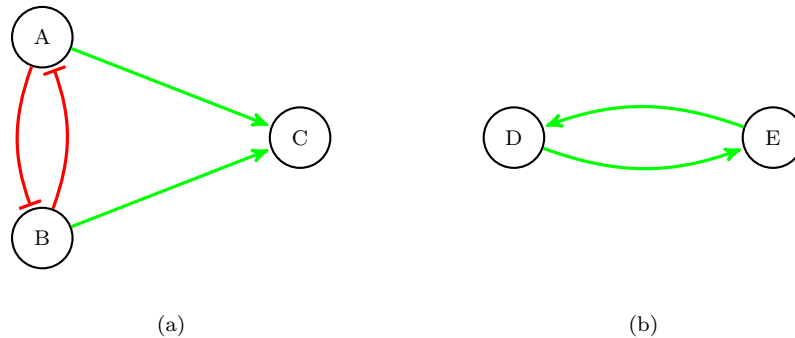
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However, if that second aspect is striking in the field of discrete modeling of gene regulatory networks, even the stronger versions of Thomas' necessary conditions published recently (Kaufman et al. 2007) did not have the same impact in the Ordinary Differential Equations (ODE) based modeling community.

This is mostly due to the fact that this necessary condition, the existence of a positive loop in the Jacobian of the ODE system, is almost always satisfied. Indeed, any binary reaction equipped with Mass-Action kinetics will lead to the mutual inhibition of the two substrates, and thus create such a loop (see Fig. 1a).

Even a reversible unary reaction can lead to satisfying the condition, since it induces a mutual activation of the two biochemical species (see Fig. 1b).



**Fig. 1** (a): mutual inhibition resulting from  $A + B \Rightarrow C$ . (b): mutual activation resulting from  $D \rightleftharpoons E$ . For clarity, self-loops have not been represented

Since many models are still being constructed based on ODEs, the community turned to other types of conditions, especially for purely Mass-Action or Non Auto-Catalytic (NAC) systems (Craciun et al. 2006; Craciun and Feinberg 2005).

Nevertheless, even using these conditions, Craciun and Feinberg (2006) state that enzyme kinetics like  $S + E \rightleftharpoons C \Rightarrow P + E$  promote cycles and thus might explain why such systems *might be far more prone than others to exhibit multiple equilibria*.

In this article, after some preliminaries, we give necessary conditions for multistability, not restricted to Mass-Action or NAC chemical reaction systems, stronger than Thomas', and local as in Soulé (2003). They show that enzyme kinetics of the above form—Fig. 1 or enzyme kinetics *à la* (Craciun and Feinberg 2006)—do not by themselves create multistability-inducing cycles.

Our approach is based on the Directed Species Reaction (DSR) graph as defined in Kaltenbach (2012) and the related analysis of terms appearing in the Jacobian's determinant. It is *local*, i.e., the existence of a positive loop can be verified for a given point of the phase space. Note that since the local version of Thomas' conjecture for oscillations has been proven false by Richard and Comet (2011), there is no direct generalization of our work to the existence of limit cycles, even using Hurwitz determinants as analogous to principal minors for Hopf bifurcations.

## 2 Jacobian characterization of multistability

Following Soulé (2003) we will use the Gale and Nikaido (1965) univalence theorem and its refinements.

We consider a differentiable map  $F$  from  $\mathbb{R}^n$  to itself and study the corresponding system  $\dot{x} = F(x)$ . Its *Jacobian* matrix, noted  $J$ , is defined as usual as follows:

$$J_{ij}(x) = \partial f_i / \partial x_j(x)$$

The *influence graph* associated to  $J$  at each point  $x$  is the labelled directed graph with vertices  $\{x_i \mid 1 \leq i \leq n\}$ ; an arc  $(x_i, x_j)$  if  $J_{ij}$  is not null, and the sign of  $J_{ij}$  as label.

The graphs depicted in Fig. 1 are influence graphs where the labels are represented as colors and arrow tips: green and pointy tip for a positive sign, red and T-tip for a negative sign.

A *Hamiltonian Hooping* (or *nucleus*) of  $J$  is a disjoint collection of cycles of its influence graph, covering all  $n$  vertices.

### Theorem 1 (Soulé 2003)

*Let  $F$  be any differentiable map from  $\mathbb{R}^n$  to itself, with Jacobian matrix  $J$ . If  $F$  has two nondegenerate zeroes in some open  $\Omega$  then there exists a in  $\Omega$  such that some principal minor of  $-J(a)$  is negative.*

Using the Leibniz formula for determinants that defines them in terms of permutations of the indices of the matrix, and the link between those and hamiltonian hoopings, one then obtains the classical necessary condition on the existence of some  $a$  such that there is a positive circuit in  $J(a)$ .

Note that this result can be extended to the case where  $\Omega$  is the (closed) positive orthant, when some additional, but commonly accepted in the Systems Biology community, conditions are met. This is the case for instance if  $F$  is the function associated with the dynamics of a chemical reaction system with only Mass-Action kinetics (Craciun and Feinberg 2005), or if one is only interested in multistability associated to Saddle-node bifurcations.

## 3 Directed Species-Reaction graph

Let us now consider a (bio)chemical reaction system with  $n$  species  $S_1, \dots, S_n$  and  $m$  reactions  $R_1, \dots, R_m$ . Using notations from Kaltenbach (2012) we write:

$$R_j = \sum_{i=1}^n y_{ij} S_i \longrightarrow \sum_{i=1}^n y'_{ij} S_i$$

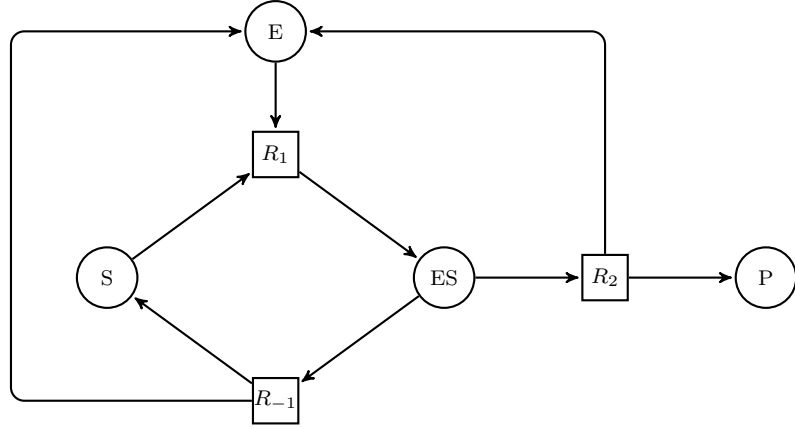
The  $y$  and  $y'$  represent the stoichiometric coefficients of the reactants and products of the reaction.

The rate law associated with reaction  $R_j$  will be written  $v_j$ . This defines a dynamical system in the sense of previous section:  $\dot{x} = F(x)$  where  $x_i$  is the concentration of species  $S_i$  and

$$f_i(x) = \sum_j v_j(x) \cdot (y'_{ij} - y_{ij})$$

This kind of systems encompasses most of the Systems Biology models developed nowadays. One can notice for instance that the Systems Biology Markup Language (SBML) of Hucka et al. (2008) can be translated to such reactions by splitting reversible reactions into forward and backward reactions and by including modifiers on both sides of the reaction (they are not affected by it, but do affect it).

Such a system can be represented naturally in a graphical form as a bipartite graph for species and reactions, as depicted in Fig. 2. Arcs can also be labelled with the  $y$  and  $y'$  in a Petri-net-like manner.



**Fig. 2** Bipartite graph representation of the enzymatic reaction:  $S + E \rightleftharpoons ES \Rightarrow E + P$ . Arcs being all labelled with 1, this label is not shown.

Using the same bipartite vertices but different arcs and labels, it is possible to represent the Directed Species-Reaction (DSR) graph of Kaltenbach (2012). The arcs are now defined and labelled as follows:

$$\lambda(S_i, R_j) = \frac{\partial v_j}{\partial x_i}$$

$$\lambda(R_j, S_i) = y'_{ij} - y_{ij}$$

If the label  $\lambda$  is zero, then there is no arc.  $\lambda$  is extended to paths (resp. subgraphs) as the product of the labels of all arcs in the path (resp. subgraph). For a path  $P$ , we shall write  $\lambda_{SR}(P)$  (resp.  $\lambda_{RS}(P)$ ) for the product of labels considering only species to reaction (resp. reaction to species) arcs.

Intuitively, the  $\lambda_{SR}$  represent the contribution of species to each reaction rate, whereas the  $\lambda_{RS}$  describe the stoichiometric effect of reactions on each species.

Fig. 3 shows the DSR graph for the same chemical reaction network as Fig. 2.

Lemma 6.2 of (Kaltenbach 2012) gives a decomposition of the Jacobian in terms of the set  $\mathcal{H}$  of the hamiltonian hoopings over species, i.e., covering each species exactly once, of the DSR graph:

$$\det(J) = \sum_{H \in \mathcal{H}} \sigma(H) \lambda(H) \quad (1)$$

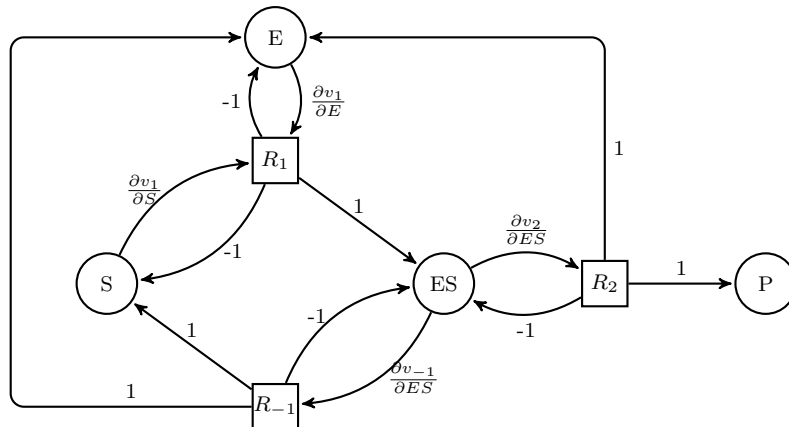
where  $\sigma$  is the *sign* of the species-hooping, defined as usual.

Since the DSR graph can of course be restricted to only certain species, the same lemma can be used for any principal minor of the original determinant.

Now thanks to the fact that  $\lambda(H) = \lambda_{SR}(H) \lambda_{RS}(H)$ , Kaltenbach (2012) groups all hoopings having the same species to reaction arcs using an equivalence relation noted  $\sim$  and obtains:

**Theorem 2 (Kaltenbach 2012)**

$$\det(J) = \sum_{[H] \in \mathcal{H}/\sim} \Lambda([H]) \lambda_{SR}(H)$$



**Fig. 3** DSR graph of the same enzymatic reaction:  $S + E \rightleftharpoons ES \Rightarrow E + P$ .

where  $\Lambda$  is defined as:

$$\Lambda([H]) = \sum_{H' \in [H]} \sigma(H') \lambda_{RS}(H')$$

It is important to notice that, in its original formulation this theorem has a second part and is only stated for systems such that  $\forall i, j, \partial v_i / \partial x_j \geq 0$ , i.e., the  $\lambda_{SR}$  are always non-negative. These systems are called NAC (Non AutoCatalytic) by Kaltenbach, but the hypothesis does not match the stronger and more usual definition of NAC systems (see for instance (Banaji et al. 2007)) that forbids the production of some species to depend on its concentration. It rather matches the definition of *monotonicity* of Fages and Soliman (2008b,a) and allows the restriction of the sign of an element in the above sum to the different components of  $\Lambda$ .

Nevertheless, since we will only use the decomposition given above and whose proof does not rely on this hypothesis, we will use the theorem in its full generality.

#### 4 Strengthening Thomas' conjecture

Considering Thm. 1 and applying Thm. 2 to each sub-DSR-graph corresponding to a principal minor of  $-J$ , one can see that a necessary condition for multistability is that some term of the sum is negative. This again states the usual condition about the existence of a positive cycle in the influence graph of  $J$ .

We will now examine the consequences of the decomposition of this sum more precisely. In particular, we will show that many negative terms can actually be proven to cancel out with other positive terms, leaving us with more specific negative terms (and thus positive circuits) to look for.

**Definition 1** The restriction of the system to a hooping  $H$  (noted  $|_H$ ) is the system where reactions  $\{R_i \mid i \in I\}$  not appearing in  $H$  are omitted.

Since each species appears exactly once in any (species-hamiltonian-)hooping, there is one reaction associated to each species by following the outgoing arc of that species. Note however that the same reaction can appear several times, as associated with several different species.

This definition is naturally extended to any function or graph defined by the biochemical system.

As noticed by Kaltenbach in the proof of one of the lemmas preceding Thm. 2,  $\Lambda$  can be computed directly from the stoichiometric matrix  $Y' - Y$  of the biochemical system. This observation is useful in proving our first lemma:

**Lemma 1** *Let  $H$  be a species-hamiltonian-hooping, if  $Y' - Y|_H$  is not of full rank, then  $\Lambda([H]) = 0$ .*

*Proof* As per Lemma 6.6 of Kaltenbach (2012) we have  $\Lambda([H])$  proportional to  $\det(Y' - Y|_H)$ , now, if that matrix is not of full rank, its determinant is 0.  $\square$

This allows us to state our main results:

**Theorem 3** *Let  $F$  be any differentiable map from  $\mathbb{R}^n$  to itself corresponding to a biochemical reaction system. If  $F$  has two nondegenerate zeroes in some open  $\Omega$  then there exists a in  $\Omega$  such that:*

1.  $-J(a)$  contains a positive circuit  $C$ ;
2.  $C$  is subcycle of some hooping  $H$  with  $Y' - Y|_H$  of full rank.

*Proof* Because we share the same hypotheses, we can use Thm. 1 to obtain  $a$  and the corresponding negative principal minor. It is then possible to apply Thm. 2 to decompose that minor according to the DSR graph as a sum of terms for each hamiltonian hooping equivalence class, and this sum must contain a negative term.

Since only positive circuits will lead to negative terms in the usual determinant decomposition, we can now prove the proposition *ab absurdam*. If all negative terms appear only in some  $\Lambda([H])$  such that the restriction of the stoichiometric matrix to  $H$  is not of full rank, they will be cancelled out by other terms, following Lemma 1. This would lead to a contradiction.  $\square$

Note that the first property, as usual, can be checked on the labelled influence graph, and that the second only cares about the reactions involved in subcycles of  $H$ . Thus, one can augment the usual labelling of the influence graph to contain not only the sign but also the reaction used for each arc and obtain enough information. Fig. 4 demonstrates this on the same example as Fig. 2.

Remark that  $H$  might not be *hamiltonian* since it is hamiltonian in a subgraph corresponding to the principal minor that is negative.

Let us now apply this theorem to some common cases.

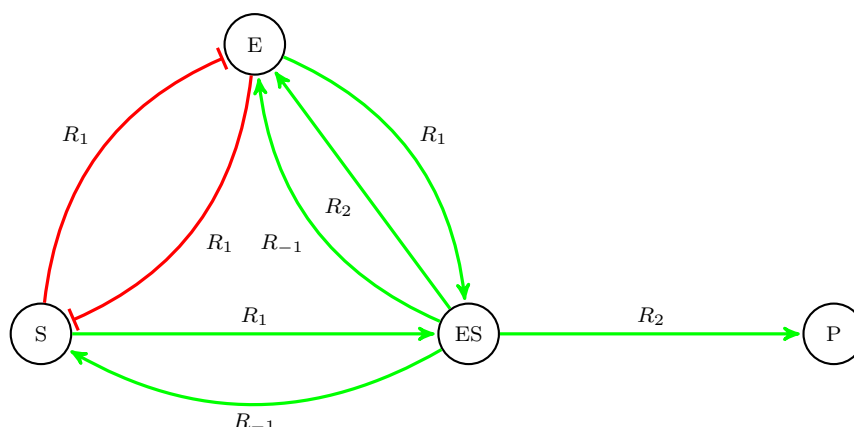
**Theorem 4** *A necessary condition for the multistability of a biochemical reaction system is that there exists a positive cycle in the influence graph associated to its Jacobian, using at most once each reaction.*

*Proof* This is a direct consequence of Thm. 3 since a matrix with two identical columns is clearly singular.

It is immediate to check that the mutual inhibition resulting from bimolecular reactions—like that between **E** and **S** in our running example or between **A** and **B** in Fig. 1—cannot fulfill these necessary conditions, since the same reaction— $R_1$  in Fig. 4—will be repeated twice.

**Corollary 1** *A necessary condition for the multistability of a biochemical reaction system is that there exists a positive cycle in the influence graph associated to its Jacobian, not using both forward and backward directions of any reversible reaction.*

*Proof* This is once again an immediate consequence of Thm. 3 since a matrix with two opposite columns is clearly singular.



**Fig. 4** Influence graph of  $S + E \rightleftharpoons ES \Rightarrow E + P$ . Arcs are labelled by their sign, as usual, but also by the unique reaction involved in order to obtain precisely the same species-species paths as in Fig. 3. Note for instance that there are two positive arcs from ES to E. Self-loops are omitted for clarity as in Fig. 1.

One can thus remark that the mutual activation resulting from reversible reactions—like that between ES and S in our running example or between D and E in Fig. 1—cannot fulfill these necessary conditions.

Note that this corollary corresponds to Lemma 6.9 from (Kaltenbach 2012) but with a much simpler proof involving no rewiring of the influence graph.

## 5 Conclusion

Using the structural information, notably from the stoichiometric matrix, of a biochemical system, we have been able to state a more strict version of the famous Thomas' necessary condition for multistability.

Of course, since we have made no hypothesis on the kinetic rate functions, one can easily represent any dynamical system as such biochemical reactions. Typically one would then have one reaction for each variable with rate corresponding to its derivative. In this case the supplementary hypothesis of our theorems collapse, leaving us with the usual conditions. However for more usual biochemical systems it brings a concrete difference, as illustrated by Thm. 4 or Cor. 1.

In particular, the obvious cases where Thomas' condition was trivially satisfied, as illustrated by Fig. 1 and Fig. 4, can now easily be ruled out.

The results are local (i.e., the cycle does exist for some  $a$  in the phase space) since they rely on local theorems as was the case in Soulé (2003). Since the other Thomas' condition, on oscillations, is not (Richard and Comet 2011) one cannot directly apply the same reasoning we used to Hurwitz Determinants. It might still be worth investigating, for instance when the signs of the influences in the labelled influence graph are known to be constant.

The same locality argument makes it difficult to interpret our stronger condition as some version of Thomas' circuit functionality for the continuous case. It is rather related and complementary to the whole domain of the structural analysis of (bio)chemical reaction systems, as pioneered by Chemical Reaction Network Theory. As such, we believe that our stronger necessary condition is enough to make circuit analysis a more worthwhile tool in the arsenal of the structural analyst of biochemical systems.



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