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Capturing persistence of high-dimensional delayed complex balanced chemical reaction systems via decomposition of semilocking sets

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Abstract— **With the increasing complexity of time-delayed systems, the diversification of boundary types of chemical reaction systems poses a challenge for persistence analysis. This paper focuses on delayed complex balanced mass-action systems (DeCBMAS) and it derives that some boundaries of a DeCBMAS cannot contain an ω-limit point of some trajectory with positive initial conditions by using the method of semilocking set decomposition and the property of the facet, further expanding the range of persistence of DeCBMASs. These findings demonstrate the effectiveness of semilocking set decomposition to address the complex boundaries and offer insights into the persistence analysis.**

I. INTRODUCTION

Chemical reaction networks (CRNs) are widely used in system modeling and analysis in various fields, including biochemical processes [1], electricity [2], medicine [3] and even machine learning [4]. However, natural systems can be complex, which presents challenges for analysis. To address this, a common method of model reduction is to introduce time delays to replace complex intermediate processes [5]. Time delays can also be used induce gene switches in biological systems [6], model transport systems [7], and more. However, the introduction of time delays dramatically changes the dynamical properties of the system, making research on time-delayed CRNs essential.

The mass-action law is a widely used approach for characterizing reaction rates and intensities in chemical reaction networks. Such a network with mass-action kinetics is called a mass-action system. Due to the complex interactions between multiple species in such systems, the dynamics of mass-action systems can exhibit high levels of nonlinearity, posing challenges for their analysis. In response to this challenge, Chemical Reaction Network Theory (CRNT) has been developed over the past 40 years to investigate the relationship between the structure of a chemical reaction network and its dynamical properties, building on the pioneering work by Feinberg and Horn [8], [9]. More recently, [10] developed a dynamic model of a chemical reaction network with constant delays using the classical chain method, opening up new avenues of research on delayed CRNT [11], [12].

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Persistence is one of the critical topics of CRNT which refers to the non-extinction of species in a system and was first introduced in ecological systems. It plays a crucial role in the portrayal of biodiversity and system stability [13], characterizing the long-term dynamics of complex systems like animal populations [14], the spread of infectious diseases [15], and biochemical reaction systems [16]. For chemical reaction systems, persistence means that all species existing in the beginning will not be used up forever. From the perspective of dynamical systems and equations, persistence implies that the lower limit of the trajectory is larger than zero as time tends to infinity. Additionally, for bounded systems, we can use the relationship between the ω-limit set and the boundary to inscribe it, making persistence an important theoretical research topic [17]. Feinberg presented the "persistence conjecture," stating that all weakly reversible mass-action systems are persistent, making it another research hotspot. Another well-known conjecture is the "Global Asymptotic Stability (GAC) Conjecture," which states that all complex balanced systems are persistent. Although there has been a great deal of work around these two hypotheses [18], [19], [20] for non-delayed chemical reaction systems, the persistence analysis of delayed systems is just beginning. [21] derived that a conservative delayed chemical reaction system is persistent if some conservative relation between species in semilocking set exists. [22] focused on the delayed complex balanced system and obtained that a DeCBMAS system is persistent if the boundary to which semilocking set corresponds is a vertex or a facet of stoichiometric compatibility class, thus deriving the persistence of 2-dimensional (2d) DeCBMASs directly.

In this paper, we focus on studying the persistence of DeCBMASs with a stoichiometric subspace of dimension greater than 2d. In such systems, boundaries can be complex and extend beyond the facet or vertex cases. To address this complexity, we propose the semilocking set decomposition method as a potential tool. Using this method, we investigate the boundaries F_W, where W can be divided into several subsets $W^{(p)}$ such that each $F_{W^{(p)}}$ is a facet. We examine these boundaries from two perspectives: whether there are common elements between $W^{(p)}$ and the sufficient conditions of F_W exhibiting no ω-limit point of any trajectory starting from a positive point can be found. Thus deriving the persistence of DeCBMASs with such semilocking boundaries F_W directly. This method provides new possibilities for simplifying the persistence analysis of high-dimensional systems. The structure of the paper is as follows: Section II provides preliminaries on chemical reaction mass-action

systems with time delays and the fundamental concepts of persistence. In Section III, we derive the persistence of some higher-dimensional delayed complex balanced systems. Finally, we conclude in Section IV.

Notations: $\bar{\mathscr{C}}^+ = C([-\tau_{\max}, 0]; \mathbb{R}^n_{\geq 0})$ is the space of non-negative function vectors defined on the interval $[-\tau_{\max}, 0]$, $\mathscr{C}^+ = C([-\tau_{\max}, 0]; \mathbb{R}^n_{>0})$ is the corresponding positive function vectors; $x^\psi(t)$ denotes the trajectory starting from $\psi \in \mathscr{C}$ and $x^\psi_t \in \mathscr{C}^+$ is a function on the trajectory $x^\psi(t)$ which is defined as $x^\psi(t+s), s \in [-\tau_{\max}, 0]$; nd network means n-dimensional network where n is the dimension of the stoichiometric subspace of the CRN.

II. PRELIMINARIES

Some background information on delayed chemical reaction systems and persistence should be provided first.

$\mathcal{N} = (S, C, R)$ can express each chemical reaction network (CRN) where $S = \{X_1, X_2, ..., X_n\}$ is the set of n species participating in some reactions of $R = \{R_1, ..., R_r\}$. Each reaction R_i is of the following form:

$$R_i: \quad \sum_{j=1}^{n} z_{ji} X_j \longrightarrow \sum_{j=1}^{n} z'_{ji} X_j, \tag{1}$$

where the stoichiometric coefficients $z_{ji}, z'_{ji} \in \mathbb{R}^n_{\geq 0}$ are non-negative integers, and the vectors $z_{\cdot i} = (z_{1i}, ..., z_{ni})^\top$ and $z'_{\cdot i} = (z'_{1i}, ..., z'_{ni})^\top$ are the corresponding reactant complex and product complex of R_i in the complex set C, respectively. A CRN can be also viewed as a directed graph with vertices to represent complexes while directed edges to correspond to reactions. A connected component of the graph is called a **linkage class**.

Each reaction vector $z'_{\cdot i} - z_{\cdot i}$ represents the change in concentrations of each species when the reaction R_i takes place. All of the reaction vectors span a **stoichiometric subspace** $\mathscr{S}$ of the network, defined as

$$\mathscr{S} = \operatorname{span}\{z'_{\cdot i} - z_{\cdot i} | i = 1, ..., r\}. \tag{2}$$

$\mathscr{S}^\perp = \{a \in \mathbb{R}^n | a^\top z = 0, \text{ for all } z \in \mathscr{S}\}$ is the orthogonal complement of $\mathscr{S}$.

mass-action law is a very prevalent used assumption of the reaction rate of R_i, which can be expressed by

$$\delta_i(x) = k_i x^{z_{\cdot i}} \triangleq k_i \prod_{j=1}^{n} x_j^{z_{ji}}, \tag{3}$$

where $x = (x_1, ..., x_n)^\top$ is the state vector with each concentration variable $x_j \in \mathbb{R}_{\geq 0}$ of species X_j, and each $k_i \geq 0$ is the reaction rate constant of the R_i. The dynamics of a **mass-action system** can be expressed as

$$\dot{x}(t) = \sum_{i=1}^{r} k_i x(t)^{z_{\cdot i}} (z'_{\cdot i} - z_{\cdot i}), \quad t \geq 0. \tag{4}$$

When time delays are introduced into the reactions, the dynamics of corresponding DeMASs are totally different [23], [10]. The time delay in a chemical reaction can cause a lag in the generation of the product, while the consumption of the reactant occurs instantaneously. This process can be reflected in the dynamics of the **delayed mass-action system** [23], [10]:

$$\dot{x}(t) = \sum_{i=1}^{r} k_i [x(t - \tau_i)^{z_{\cdot i}} z'_{\cdot i} - x(t)^{z_{\cdot i}} z_{\cdot i}], \quad t \geq 0. \tag{5}$$

where each constant $\tau_i \geq 0$ for $i = 1, \cdots, r$ denotes the time delay of the i-th reaction. A delayed mass-action system can be described as $\mathcal{M} = (S, C, R, k, \tau)$. Further define $\tau_{\max} = \max\{\tau_1, \cdots, \tau_r\}$, then the solution space of the delayed system (5) can be expressed as $\bar{\mathscr{C}}^+$. When $\tau_i = 0$ for $i = 1, \cdots, r$, the system (5) reduces to (4). Each trajectory of the system can only appear in a part of the solution space, and it cannot cover the entire solution space. Therefore [10] decompose the phase space $\bar{\mathscr{C}}^+$ into several equivalent classes called the **non-negative stoichiometric compatibility class** (SCC). Each trajectory $x^\psi(t)$ is forward invariant relative to SCC, namely, $x^\psi(t)$ with positive initial condition $\psi \in \mathscr{C}^+$ will always be in a $\mathcal{P}_\psi$ containing ψ where $\mathcal{P}_\psi$ of a DeMAS is defined as:

$$\mathcal{P}_\psi = \{\phi \in \bar{\mathscr{C}}_+ \mid c_a(\phi) = c_a(\psi) \text{ for all } a \in \mathscr{S}^\perp\}, \tag{6}$$

and the functional $c_a : \bar{\mathscr{C}}^+ \to \mathbb{R}$ is defined by

$$c_a(\phi) = a^\top \left[\phi(0) + \sum_{i=1}^{r} \left(k_i \int_{-\tau_i}^{0} \phi(s)^{z_{\cdot i}} ds\right) z_{\cdot i}\right]. \tag{7}$$

$\bar{x} \in \mathbb{R}^n_{>0}$ is a **positive equilibrium** of $\mathcal{M}$ if it satisfies $\dot{x}$ equals to zero at $\bar{x}$. $\bar{x}$ is further a **complex balanced equilibrium** if for any complex $\eta \in \mathbb{Z}^n_{\geq 0}$ in the $\mathcal{M}$, it satisfies:

$$\sum_{i:\ z_{\cdot i} = \eta} k_i \bar{x}^{z_{\cdot i}} = \sum_{i:\ z'_{\cdot i} = \eta} k_i \bar{x}^{z_{\cdot i}}. \tag{8}$$

It actually reaches a balance between the inflow and outflow of each complex at a complex balanced equilibrium $\bar{x}$.

Complex balanced system is a chemical reaction system whose each equilibrium is a complex balanced equilibrium. There are lots of good dynamical properties of Delayed complex balanced systems (DeCBMAS), the existence and the uniqueness of a positive equilibrium in each positive SCC, and the local asymptotic stability of each $\bar{x} \in \mathbb{R}^n_{>0}$ [23].

Persistence plays an important role in the long-term dynamical analysis of mass-action systems and has a clear biological significance. Some definitions and results of persistence of DeMASs have been proposed [21].

Definition 1 (Persistence) *A DeMAS $\mathcal{M}$ is said to be persistent if each trajectory $x^\psi(t) \in \mathbb{R}^n \geq 0$ starting from $\psi \in \mathscr{C}^+$ satisfies*

$$\liminf_{t \to \infty} x_j^\psi(t) > 0 \quad \textit{for each species} \quad X_j \in \mathcal{S}.$$

Persistence can also be derived by diagnosing the relationship between ω-limit sets and boundaries for bounded DeMASs.

Definition 2 (ω-limit set) *For each trajectory $x^{\psi}(t)$ starting from $\psi \in \bar{\mathscr{C}}^{+}$, the ω-limit set of each trajectory $x^{\psi}(t)$ is a positive invariant set of the trajectory defined as*

$$\omega(\psi) := \{\theta \in \bar{\mathscr{C}}^{+} \mid x^{\psi}_{t_N} \to \theta, \text{ for some time sequence } t_N \to \infty \text{ with } t_N \in \mathbb{R}\}.$$

where $x^{\psi}_{t_N} \triangleq x^{\psi}(t_N + s), s = [-\tau_{\max}, 0]$.

Definition 3 (persistence for bounded systems) *A bounded DeMAS $\mathcal{M}$ is persistent if*

$$\omega(\psi) \bigcap \left(\bigcup_{W} L_W \right) = \varnothing, \quad \forall\ \psi \in \mathscr{C}^{+}, \tag{9}$$

where

$$L_W = \left\{ \phi \in \bar{\mathscr{C}}^{+} \middle|^{\phi_j(s)=0,\ X_j \in W,}_{\phi_j(s)\neq 0,\ X_j \notin W,} \ \forall s \in [-\tau_{\max}, 0] \right\}, \tag{10}$$

is called a boundary of $\bar{\mathscr{C}}^{+}$. Further, $F_W = L_W \cap \mathcal{P}_{\psi}$ is one of the boundaries of $\mathcal{P}_{\psi}$.

The above definition reveals that each boundary can be determined by a subset of $\mathcal{S}$ denoted as W and persistence means no ω-limit point of each trajectory with a positive initial point on each boundary F_W. Some boundaries have already been excluded the possibility of having ω-limit points, such as the non-semilocking boundary and facet whose definitions are presented as follows.

Definition 4 (semilocking boundary) *For a CRN $\mathcal{N}$, a non-empty subset $W \subset \mathcal{S}$ is a **semilocking set** if for each reaction $z_{\cdot i} \to z'_{\cdot i}$ with some $z'_{ji} > 0, X_j \in W$, there must exist some species $X_{j'} \in W$ such that $z_{j'i} > 0$. And the corresponding face F_W is called a semilocking boundary.*

Facet is defined from the view of the dimension of the projected space on W^c.

Definition 5 (facet) *For a DeMAS $\mathcal{M}$, F_W is a facet of the SCC $\mathcal{P}_{\psi}$ of $\mathcal{M}$ if $\dim \mathscr{S}|_{W^c} = \dim \mathscr{S} - 1$.*

Remark 1 *It is easy to verify that the above definition shares the same meaning as Definition 4.1 in [22] but with a more concise expression.*

III. MAIN RESULTS

The goal of persistence analysis in chemical reaction networks is to determine whether the points on the semilocking boundary F_W have the potential to be ω-limit points of some trajectory with a positive initial condition. Among all the boundaries, the "facet" is a special case, and we have investigated whether ω-limit points exist on facets for any DeCBMAS [22]. This result is formally stated in the following theorem.

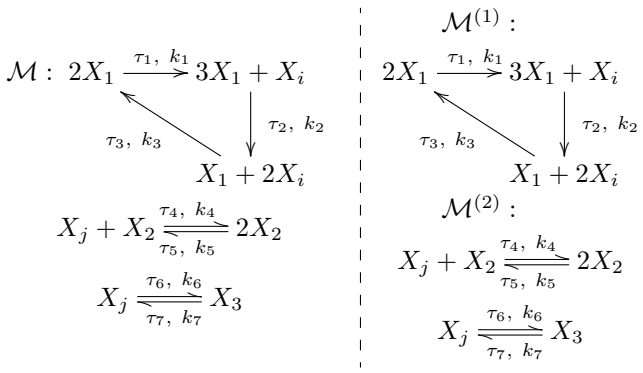
Theorem 1 ([22]) *Given a DeCBMAS (S, C, R, k, τ) of (5), for any semilocking set $W \subset S$, if F_W defined by Definition 3 is either empty or a facet of the SCC $\mathcal{P}_{\psi}$, this DeCBMAS is persistent.*

As the complexity of chemical reaction networks increases, the dimension of the chemical stoichiometric space also increases, leading to a diversification of semilocking boundaries. In this paper, we conduct further analysis of the properties of other types of boundaries by decomposing the corresponding semilocking sets.

A. Semilocking sets composed of independent subsets

In this subsection, we focus on a semilocking set W of a delayed chemical reaction mass-action system $\mathcal{M} = \{S, C, R, k, \tau\}$ that can be decomposed into several independent subsets $W^{(p)}$, where each $F_{W^{(p)}}$ is a facet of $\mathcal{M}$. Here, independent means that any two subsets have no common species, and any two species in different subsets have no interactions, i.e. they cannot participate in one reaction. We present an example to illustrate this case.

Example 1 *Consider the following delayed system $\mathcal{M}$*



$\mathcal{M}$ is a 4d DeCBMAS. And the subset $W = \{X_1,\ X_2\}$ is a semilocking set with its boundary L_W in the following form

$$L_W = \{\psi \in \bar{\mathscr{C}}^{+} | \psi(s) = (0, 0, \psi_3(s), \psi_i(s), \psi_j(s))^{\top}, s \in [-\tau_{\max}, 0], \psi_3(s) > 0, \psi_i(s) > 0, \psi_j(s) > 0\}.$$

Vectors $(0, 0, 0, 1, 0)$ and $(0, 0, 1, 0, -1)$ are both in the stoichiometric subspace $\mathscr{S}$, which means $\dim \mathscr{S}|_{W^c} = 2$, thus F_W is not a facet of $\mathcal{M}$. However, we can decompose W into two independent subsets $W^{(1)} = \{X_1\}$ and $W^{(2)} = \{X_2\}$ with X_1, X_2 not involved in the same reaction. Moreover, the boundaries $F_{W^{(1)}}$ and $F_{W^{(2)}}$ are both facets of $\mathcal{M}$.

There are two cases to consider:

1) *X_i and X_j are not the same species. In this case, the subsets $\mathcal{M}^{(1)}$ and $\mathcal{M}^{(2)}$ are also independent, as there are no common species between them. Thus, the trajectory of each species in $\mathcal{M}$ is the same as that in $\mathcal{M}^{(1)}$ or $\mathcal{M}^{(2)}$. Hence the result that there does not exist an ω-limit point of each trajectory with a positive initial conditions on F_W is obvious.*
2) *X_i and X_j are the same species. In this case, there is a coupling between the dynamics of $\mathcal{M}^{(1)}$ and $\mathcal{M}^{(2)}$. Therefore, we need a new approach to support further research.*

To address the coupling between the subsystems, one approach is to introduce a reduced system.

Definition 6 (Reduced system) *Let $\mathcal{M} = (S, C, R, k, \tau)$ be a delayed mass-action system with dynamics $\dot{x}$, and let $\tilde{S} \subset S$ be a subset of the species. The system $\tilde{\mathcal{M}} =$*

$(\tilde{S}, \tilde{C}, \tilde{R}, \tilde{k}(t), \tilde{\tau})$ *is called a reduced system of* $\mathcal{M}$ *if its dynamics can be expressed as* $\dot{\tilde{x}} = \dot{x}|_{\tilde{S}}$*, where* $\dot{x}|_{\tilde{S}}$ *is the vector obtained by restricting the dynamics denoted as* $\dot{x}$ *to the species in* $\tilde{S}$*. Thus each reaction of* $\tilde{\mathcal{M}}$ *has the form* $\tilde{z}_{\cdot i} \xrightarrow{\tilde{k}_i(t),\ \tilde{\tau}_i} \tilde{z}'_{\cdot i}$ *where*

$$\tilde{z}_{\cdot i} = z_{\cdot i}|_{\tilde{S}},\ \tilde{z}'_{\cdot i} = z'_{\cdot i}|_{\tilde{S}},\ \tilde{k}_i(t) = k_i \prod_{X_j \notin \tilde{S}} x_j^{z_{ji}},\ \tilde{\tau}_i = \tau_i.$$

Remark 2 *Reduced systems just consider the dynamics of the species* $X_j \in \tilde{S}$ *and ignore* $\dot{x}_{j'}$ *where* $X_{j'} \notin \tilde{S}$ *through deleting* $\dot{x}_{j'}$ *from* $\dot{x}$ *and putting the* $x_{j'}(t)$ *in* $\dot{x}_j$ *into the reaction rate parameters* k_i*. Thus the dynamics of the reduced system is actually the projection of* $\dot{x}(t)$ *on* $\mathbb{R}^{\tilde{S}}$*.*

According to the above definition and setting $\tilde{S} = W$, the delayed system $\mathcal{M}$ of the second case in Example 1 can be reduced as

$$\begin{aligned} \tilde{\mathcal{M}}: \quad & 2X_1 \xrightarrow{\tau_1,\ \tilde{k}_1(t)} 3X_1 \\ & \quad\ \nwarrow \qquad \downarrow \tau_2,\ \tilde{k}_2(t) \\ & \tau_3,\ \tilde{k}_3(t) \qquad X_1 \\ & X_2 \underset{\tau_5,\ \tilde{k}_5(t)}{\overset{\tau_4,\ \tilde{k}_4(t)}{\rightleftharpoons}} 2X_2 \end{aligned} \tag{11}$$

where $\tilde{k}_1(t) = k_1$, $\tilde{k}_2(t) = k_2 x_i(t)$, $\tilde{k}_3(t) = k_3 x_i^2(t)$, $\tilde{k}_4(t) = k_4 x_i(t)$, $\tilde{k}_5(t) = k_5$. Through reducing, not only W but the system $\tilde{\mathcal{M}}$ can be divided into two independent parts.

Lemma 2 *Let* $\mathcal{M} = \{S, C, R, k, \tau\}$ *be a DeCBMAS system and* W *be a semilocking set of* $\mathcal{M}$ *that can be divided into independent subsets* $W^{(p)}, p = 1, \cdots, m$*. Suppose that each* $F_{W^{(p)}}$ *is a facet of* $\mathcal{M}$*. Then an* ω*-limit point cannot exist on the boundary of* F_W*.*

Proof. As $W^{(p)}$ are independent, $\mathcal{M}$ can be divided into several subsystems $\mathcal{M}^{(p)}$ according to $W^{(p)}$. And reducing the system $\mathcal{M}$ based on the semilocking set W, each subsystem $\tilde{\mathcal{M}}^{(p)}$ of the reduced system $\tilde{\mathcal{M}}$ are also independent (no common species in $W^{(p)}$). Thus the trajectory of each species in W of the original system $\mathcal{M}$ is the same as that of the reduced subsystem $\tilde{\mathcal{M}}^{(p)}$. So we just need to consider whether the origin of $\tilde{\mathcal{M}}^{(p)}$ can be an ω-limit point of some trajectory.

$F_{W^{(p)}}$ is a facet of $\mathcal{M}$, then $\dim \mathscr{S}|_{W^{(p)}} = 1$. Thus each reduced subsystem $\tilde{\mathcal{M}}^{(p)}$ is a 1d complex balanced network with generalized mass-action kinetics. And $v^{(p)}$ denotes the basis of the stoichiometric subspace of $\tilde{\mathcal{M}}^{(p)}$.

(1) If $v_j^{(p)} = 0$ for some species X_j, the concentration of this species is a constant, namely, $x_j(t) = x_j(0) > 0$ forever. So in this case, the origin can not be an ω-limit point obviously.

(2) If $v_{j_1}^{(p)} \cdot v_{j_2}^{(p)} < 0$ for some species X_{j_1}, X_{j_2}, for each positive initial conditions $\psi(s)$ of $\tilde{\mathcal{M}}^{(p)}$, each element in vector

$$\psi(0) + \sum_{i=1}^{r} \left(\int_{-\tau_i}^{0} k_i(s)\psi(s)^{z_i} ds \right) y_i - \mathbb{0}_{\tilde{n}^{(p)}}$$

is positive, then it can not be expressed by $v^{(p)}$. Thus in this case, the origin is not a point in the stoichiometric compatibility class of any positive initial conditions. Then the corresponding $F_{W^{(p)}}$ of the original system $\mathcal{M}$ is empty.

(3) If each $v_j^{(p)} > 0$, for each linkage class L_l of $\tilde{\mathcal{M}}$, we can find one complex $\bar{z}^l \in L_l$ such that $\bar{z}_j^l - \tilde{z}_j < 0$ for all $X_j \in \tilde{\mathcal{S}}$ and all complex $\tilde{z} \in L_l$ [19]. We assume that the origin is an ω-limit point of some trajectory $x^{\psi}(t)$ of $\mathcal{M}^{(p)}$ with positive initial conditions $\psi(s), s \in [-\tau,\ 0]$. Then for each $\epsilon > 0$ and $t_0 > 0$, there exists some $t > t_0$ such that $x(t)$ is in the ϵ-neighbourhood of the origin. Further combining the fact that

$$\lim_{x \to 0} \frac{x^{z^l}}{x^z} = +\infty, \tag{12}$$

we can obtain that for each constant $k > 0$, there exists a small enough $\epsilon > 0$, such that $x^{\tilde{z}^l} > k x^z$ for each x in the ϵ-neighbourhood of zero. Thus once the trajectory $x^{\psi}(t)$ enters into the ϵ-neighbourhood of zero, the dynamics of each species $X_j \in \mathcal{S}$ can be expressed

$$\begin{aligned} \dot{x}_j &= \sum_{i=1}^{r} k_i(t-\tau_i) x^{\tilde{z}}(t-\tau_i)\tilde{z}'_j - \sum_{i=1}^{r} k_i(t) x^{\tilde{z}}(t)\tilde{z}_j \\ &= \sum_{L_l} \sum_{i=1}^{\tilde{r}_l} [k_i(t-\tau_i) x^{\tilde{z}}(t-\tau_i)\tilde{z}'_j - k_i(t) x^{\tilde{z}}(t)\tilde{z}_j] \end{aligned} \tag{13}$$

From (12), there exists an ϵ_1 such that the sign of $\dot{x}_j$ is determined by

$$\begin{aligned} &\sum_{L_l} \sum_{\tilde{z}_{\cdot i} = \bar{z}^l} [k_i(t-\tau_i) x^{\bar{z}^l}(t-\tau_i)\tilde{z}'_{ij} - k_i(t) x^{\bar{z}^l}(t)\bar{z}_j^l] \\ &= \sum_{L_l} \sum_{\tilde{z}_{\cdot i} = \bar{z}^l} k_i(t) x^{\bar{z}^l}(t)\tilde{z}'_{ij} \left(\frac{k_i(t-\tau_i) x^{\bar{z}^l}(t-\tau_i)}{k_i(t) x^{\bar{z}^l}(t)} - \frac{\bar{z}_j^l}{\tilde{z}'_{ij}} \right) \end{aligned}$$

As $\tilde{z}'_{ij} > \bar{z}_j^l > 0$, $\frac{\bar{z}_j^l}{\tilde{z}'_{ij}} < 1$. Further from the fact that each ω-limit point $\phi \in \bar{\mathscr{C}_+}$ of the trajectory $x^{\psi}(t)$ presented in the Definition 2 can only be a constant equilibrium for DeCBMAS, then there exists $x_j(t), x_j(t-\tau)$ converging to the same value for each species X_j. Thus the following equation holds

$$\lim_{\tilde{x} \to 0} \frac{k_i(t-\tau_i) x^{\bar{z}^l}(t-\tau_i)}{k_i(t) x^{\bar{z}^l}(t)} = 1.$$

There exists an $\epsilon_2 > 0$ such that

$$\frac{k_i(t-\tau_i) x^{\bar{z}^l}(t-\tau_i)}{k_i(t) x^{\bar{z}^l}(t)} - \frac{\bar{z}_j^l}{\tilde{z}'_{ij}} > 0, \text{ for each } L_l.$$

So once the trajectory $x^{\psi}(t)$ enters into the ϵ-neighbourhood of zero where $\epsilon = \min\{\epsilon_1, \epsilon_2\}$, there exists $x_j(t) > 0$ for some X_j. This is obviously in contradiction with the fact that the origin is an ω-limit point of the trajectory $x^{\psi}(t)$.

We can conclude that F_W can not contain an ω-limit point of any trajectory with positive initial conditions. ■

Thus the results of the persistence of DeCBMAS can be generalized by using Lemma 2.

Theorem 3 *Consider a DeCBMAS $\mathcal{M} = (S, C, R, k, \tau)$ of dynamics of the form (5) and let $W \subset S$ be a semilocking set that can be divided into several independent subsets $W^{(p)}$, such that for each p, the set $F_{W^{(p)}}$ defined by Definition 3 is either empty or a facet of the stoichiometric compatibility class. Then the DeCBMAS $\mathcal{M}$ is persistent.*

Proof. The result can be concluded directly by using Lemma 2. ■

Thus going back to Example 1, the system $\mathcal{M}$ is persistent regardless of whether X_i and X_j are the same species or not.

B. Semilocking sets composed of subsets sharing common species

In this subsection, we consider the semilocking set W which can be divided into several $W^{(p)}$. According to $W^{(p)}$, the system $\mathcal{M}$ can be seen as a combination of sub-systems $\mathcal{M}^{(p)} = \{S^{(p)}, C^{(p)}, R^{(p)}, k^{(p)}, \tau^{(p)}\}$, where $p = 1, \cdots, m$. Each boundary $F_{W^{(p)}}$ is a facet of the stoichiometric compatibility class of the system $\mathcal{M}^{(p)}$. However, different from Subsection III-A, $W^{(p)}, p = 1, \cdots, m$ can have common species here. Additionally, there should not exist any interaction between two species in W that are not in the same $W^{(p)}$, namely, they cannot participate in the same reaction.

Example 2 *$\mathcal{M}$ is a delayed system in the following form which is slightly different from the system in Example 1.*

$$\mathcal{M}:\quad 2X_1 \xrightarrow{\tau_1,\ k_1} 3X_1 + X_i,\quad 2X_1 \xleftarrow{\tau_3,\ k_3} X_1 + 2X_i \xrightarrow{\tau_2,\ k_2} 3X_1 + X_i$$
$$X_1 + X_2 \underset{\tau_5,\ k_5}{\overset{\tau_4,\ k_4}{\rightleftharpoons}} 2X_2,\qquad X_i \underset{\tau_7,\ k_7}{\overset{\tau_6,\ k_6}{\rightleftharpoons}} X_3$$

$$\mathcal{M}^{(1)}:\quad 2X_1 \xrightarrow{\tau_1,\ k_1} 3X_1 + X_i,\quad 2X_1 \xleftarrow{\tau_3,\ k_3} X_1 + 2X_i \xrightarrow{\tau_2,\ k_2} 3X_1 + X_i$$
$$\mathcal{M}^{(2)}:\quad X_1 + X_2 \underset{\tau_5,\ k_5}{\overset{\tau_4,\ k_4}{\rightleftharpoons}} 2X_2,\qquad X_i \underset{\tau_7,\ k_7}{\overset{\tau_6,\ k_6}{\rightleftharpoons}} X_3$$

The system $\mathcal{M}$ is a 4-dimensional weakly reversible network with zero deficiency, making it a DeCBMAS. The subset $W = \{X_1, X_2\}$ is a semilocking set with a boundary L_W that can be represented as follows:

$$L_W = \{\psi \in \bar{\mathscr{C}}^+ | \psi(s) = (0, 0, \psi_3(s), \psi_i(s))^\top, s \in [-\tau_{\max}, 0], \psi_3(s) > 0, \psi_i(s) > 0\}$$

Both vectors $(0, 0, 1, 0)$ and $(0, 0, 0, 1)$ are in the stoichiometric subspace $\mathscr{S}$. Although W is not a facet of $\mathcal{M}$, it can be decomposed into two subsets $W_1 = \{X_1\}$ and $W_2 = \{X_1, X_2\}$, where F_{W_1} and F_{W_2} are both facets of $\mathcal{M}^{(1)}$ and $\mathcal{M}^{(2)}$, respectively. Note that W cannot be divided into the form in Example 1 because X_1 and X_2 participate in the same reaction. Therefore further analysis is needed to address this case.

By reducing the system $\mathcal{M}$ to $\tilde{\mathcal{M}}$ based on the semilocking set W, as defined in Definition 6, we can address the coupling caused by the species X_i. However, the reduced subsystems $\mathcal{M}^{(1)}$ and $\mathcal{M}^{(2)}$ are not independent due to the common species X_1.

Fortunately, we can use the following result to handle this situation.

Lemma 4 *Consider a DeCBMAS $\mathcal{M}$ and W is a semilocking set of $\mathcal{M}$ that can be partitioned into subsets $W^{(p)}, p = 1, \cdots, m$. $\mathcal{M}$ can be divided into subsystems $\mathcal{M}^{(p)} = \{S^{(p)}, C^{(p)}, R^{(p)}, k^{(p)}, \tau^{(p)}\}$ accordingly. The corresponding boundary F_W cannot contain an ω-limit point of any trajectory with a positive initial conditions if the following conditions hold:*

- *Each $F_{W^{(p)}}$ is a facet of the subsystem $\mathcal{M}^{(p)}$.*
- *$S^{(p)} \cap (W - W^{(p)}) = \emptyset$.*

Proof. We start by reducing the system $\mathcal{M}$ based on W according to Definition 6 to derive the reduced system $\tilde{\mathcal{M}}$. The reduced system can be partitioned into m 1d subsystems $\tilde{\mathcal{M}}^{(p)} = \{\tilde{S}^{(p)}, \tilde{C}^{(p)}, \tilde{R}^{(p)}, \tilde{k}(t)^{(p)}, \tilde{\tau}^{(p)}\}, p = 1, \cdots, m$.

Assume F_W contains an ω-limit point of some trajectory with positive initial conditions of $\mathcal{M}$, then the origin will be the ω-limit point of the reduced system $\tilde{\mathcal{M}}$. If $\tilde{S}^{(p_1)} \cap \tilde{S}^{(p_2)} = \emptyset$ for any p_1 and p_2, i.e., if $\mathcal{M}^{(p_1)}$ and $\mathcal{M}^{(p_2)}$ are independent, the situation reduces to Lemma 2. If there exists a common species X_j between the sets $W^{(p)}$, the reduced system $\tilde{\mathcal{M}}$ is composed of 1d generalized mass-action systems that are not independent. The dynamics of species X_j can be written as:

$$\dot{x}_j(t) = \sum_{p=1}^{m} \dot{x}_j^{(p)}(t)$$

where $\dot{x}_j^{(p)}(t)$ denotes the dynamics of X_j in generalized mass-action subsystem $\mathcal{M}^{(p)}$ and $\dot{x}_j^{(p)}(t) = 0$ if $X_j \notin W^{(p)}$.
(1) X_j only exists in one $\tilde{\mathcal{M}}^{(p)}$. As $\tilde{\mathcal{M}}^{(p)}$ is 1d, similar with Lemma 2, we can find a $\bar{z}^l$ in each linkage class L_l in $\mathcal{M}^{(p)}$ such that $\bar{z}_j^l - \tilde{z}_j^{(p)} < 0$ for each $X_j \in W^{(p)}$ and $\tilde{z}^{(p)} \in L_l$. Thus we can directly conclude that $\dot{x}_j(t) > 0$ when $x(t)$ comes into the ϵ-neighbourhood of zero for some $\epsilon > 0$ from the proof of Lemma 2.
(2) X_j is the common species which exists in more than one subsystems $\tilde{\mathcal{M}}^{(p)}$. Although there exists coupling between the dynamics $\dot{x}_j^{(p)}(t)$, it does not affect the value of the complex in each subsystem $\tilde{\mathcal{M}}$. Then as each subsystem is 1d, the minimal complex $\bar{z}^l$ for each linkage class and each $\mathcal{M}^{(p)}$ exists. Thus for each p, there exists a $\epsilon^p > 0$ such that $\dot{x}_j^{(p)}(t) > 0$ when $x(t)$ comes into the ϵ^p-neighbourhood of zero. Then $\dot{x}_j(t) > 0$ when the trajectory $x(t)$ comes into the ϵ-neighbourhood of zero where $\epsilon = \min\{\epsilon^p\}$.

However, this contradicts the assumption that the origin is one ω-limit point of some trajectory with a positive initial conditions of the reduced system $\mathcal{M}$. Thus we can conclude the result. ■

Then by using above lemma, we can generalize the persistence of DeCBMASs.

Theorem 5 *$\mathcal{M}$ is a DeCBMAS consisting of several sub-DeCBMAS $\mathcal{M}^{(p)} = \{S^{(p)}, C^{(p)}, R^{(p)}, k^{(p)}, \tau^{(p)}\}$. If each*

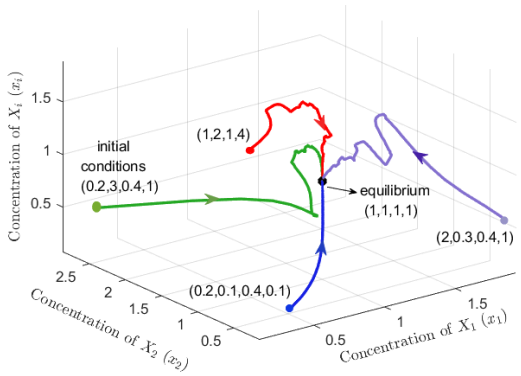


Fig. 1. The evolution of the concentrations of X_1, X_2, X_i of the system $\mathcal{M}$ in Example 2 with four different initial conditions (red line: initial condition:$(1,2,1,4)$, $\tau = (1,1,1,1,1,2,5)$; green line:initial condition:$(0.2,3,0.4,1)$, $\tau = (1,1,1,1,1,1,1)$; blue line:initial condition $(0.2,0.1,0.4,1)$, $\tau = (1,1,1,1,1,1,1)$; purple line:initial condition:$(2,0.3,0.4,1)$, $\tau = (1,1,1,1,1,1,1)$) and $k_i = 1, i = 1,\cdots,7$.

semilocking set W of $\mathcal{M}$ can be decomposed into several $W^{(p)}$ such that each $F_{W^{(p)}}$ is a facet of $\mathcal{M}^{(p)}$ with $S^{(p)} \cap (W - W^{(p)}) = \emptyset$, then $\mathcal{M}$ is a persistent system.

Proof. It is obviously from Lemma 4. ■

Based on the theorem stated above, we can conclude that the DeCBMAS $\mathcal{M}$ in Example 2 is a persistent system, as illustrated in Fig. 1. The figure displays the evolution of the concentrations of the three species for four different initial conditions and delays. As we can see from the plot, all the trajectories converge to the unique equilibrium.

IV. CONCLUSIONS AND FUTURE WORKS

The main focus of this paper is to generalize the persistence for DeCBMASs. Specifically, we aim to investigate whether there exist ω-limit points of some trajectory starting from a positive initial conditions on a complex boundary that is not a facet or a vertex of the stoichiometric compatibility class. To achieve this goal, we focus on analyzing special complex boundaries F_W, where W can be partitioned into several subsets $W^{(p)}$ such that each $W^{(p)}$ is a facet of a subsystem $\mathcal{M}^{(p)}$. By using this decomposition method and the properties of facets, we can determine whether the ω-limit points exist on these complex boundaries or not, thereby expanding the scope of DeCBMASs with persistence property.

In the future, we will give further consideration to the complex boundary F_W. We can divide W into subsets $W^{(p)}$, and each subset $W^{(p)}$ will correspond to a facet or vertex of F_W. Additionally, we will consider cases where two species in the semilocking set W but not in the same subset $W^{(p)}$ participate in the same reaction. This decomposition approach significantly simplifies the analysis of complex boundaries by breaking its corresponding semilocking set down into smaller, more manageable parts.

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