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Research article

A Perron-Frobenius strong threshold theorem for (A, B, P, φ) balanced bilinear models

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Abstract: We establish a Perron–Frobenius threshold theorem for positive chemical ODEs, and apply it to a family of bilinear epidemic models with rank-one next-generation matrices (NGMs). The main results are: (i) the Jacobian on every siphon face of a chemical ODE is block-triangular, with a Metzler transversal block (Theorems 2–3); (ii) a Perron–Frobenius strong threshold theorem (Theorem 6) characterizing existence, and under an irreducibility hypothesis uniqueness, of the endemic equilibrium via the spectral condition $\rho(\widetilde{K}(S)) = 1$, with no rank-one assumption; (iii) an algebraic-independence result splitting the rank-one bilinear models of Fall, Iggidr, Sallet, and Bonzi into two distinct classes (Theorems 4–5), unifying and extending these authors' results together with those of Shuai and Van den Driessche; (iv) explicit closed-form Lyapunov functions and equilibrium formulas for this rank-one class, built from the left and right Perron eigenvectors of the NGM (§5), with their modification under linear feedback from infectious to susceptible compartments (§6); and (v) a Kirchhoff matrix-tree formula expressing the same Perron eigenvectors as graph-theoretic diagonal cofactors, valid at arbitrary rank (§7).

Keywords: positive ODE; disease-free and endemic equilibrium; Metzler matrices; next-generation matrix; regular splitting; Perron–Frobenius eigenvectors

Abbreviations

ME: mathematical epidemiology; CRN: chemical reaction network; ODE: ordinary differential equation; NGM: next-generation matrix; DFE: disease-free equilibrium; EE: endemic equilibrium; GAS: globally asymptotically stable; LAS: locally asymptotically stable; CEP: competitive exclusion principle; WAIFW: who acquires infection from whom.

1. Introduction

Bilinear models of mathematical epidemiology (ME) with rank-one next-generation matrices (NGM) form a major part of the ME literature [1–3], contemporary with [4]: the rank-one property of the NGM supports an abstract theory for this class. Its most emblematic instance, established for a specific example in [1], is an explicit Lyapunov function guaranteeing that the unique strictly positive (EE) is globally asymptotically stable (GAS); Earn and McCluskey [5] confirmed this for a larger class, and [6] for a still more general one.

This paper also unifies concepts and terminology across ME, ecology, and chemical reaction network (CRN). The R_0 stability threshold formula of ME, noted already in [2], is the **regular splitting** formula [7] of numerical analysis, applied to the NGM theorem's stability condition

$$R_0 < 1$$

for the disease free equilibrium (DFE); a review focused solely on measles [8] found over 10000 citations employing R_0, yet **regular splitting** remains comparatively little used outside ME, where stability is instead decided by comparing Jacobian spectral abscissas to 0. Works like [1–3] show that **regular splitting** has a clear advantage for rank-one models, where it yields more transparent explicit formulas; whether this advantage persists outside this class is addressed below.

Multi-strain models [9] raise the question of how the (DFE) differs from boundary equilibria at which some strains are already present. Strains correspond to siphons (a Petri-net/CRN concept) [10]: [11] shows the two theories coincide whenever the boundary face under consideration is forward invariant, equivalently siphon-generated. The R_0-analog reflecting instability of a siphon face is called, following [6], an R-invasion number or strain reproduction number.

The discovery of the siphon connection lead us an elegant reformulation of the celebrated next generation matrix (NGM) method as a Jacobian triangularity on siphon faces result, presented below in Section 3. While not surprising, we believe theorem 2 will be of interest to researchers of all the positive ODE subfields.

Next, we review and advance the laws of the DFE to EE stability relay of [1–3, 5]. Note that we completed the original papers with various facts not stated explicitly in our sources, like the fact that there are two classes of (A, B, P, φ) balanced bilinear models, and while five of the "laws" hold for both of them, sometimes with small variations, the determinant law and the Lyapunov function at the endemic point hold only when there is just one susceptible class, in which the two classes of (A, B, P, φ) balanced bilinear models coincide.

Note also that we use occasionally the language of chemical reaction network theory. While the theoretical results here do not rely directly on CRNT results, our example notebooks which use our

Mathematica package Epid-CRN, at `https://github.com/florinav/EpidCRNmodels` use CRNT.

Why CRNT? CRNT and ME contribute complementary halves of the theory built here. From CRNT come the structural, rate-independent notions: siphons, the forward-invariant faces they generate, and the fact that the transversal Jacobian on such a face is Metzler. From ME come the quantitative, rate-dependent tools built on top of that structure: regular splittings, next-generation matrices, and Perron–Frobenius threshold criteria. Neither half is new in isolation; the contribution is combining them into a single chain, so that a chemical ODE's siphon structure determines, without further modeling input, which Perron–Frobenius machinery applies to it.

Summarizing, the principal original contributions of this paper are:

- the generalized Lotka–Volterra representation for disjoint k-siphon models (Theorem 1);
- the triangular Jacobian theorem on siphon faces (Theorem 2);
- the Metzler property of transversal Jacobians on siphon faces (Theorem 3);
- the Perron–Frobenius threshold theorem for endemic equilibria beyond rank one (Theorem 6);
- the reinterpretation of seven classical rank-one formulas through the left and right Perron eigenvectors of the NGM (Section 5, extended with feedback in Section 6);
- the Kirchhoff-theoretic, graph-combinatorial construction of those same Perron eigenvectors (Section 7).

1.1. Contributions and contents

Section 2 offers some definitions which illustrate how CRN and ME intertwine.

The discovery of the siphon connection lead us an elegant proof of the celebrated NGM method, presented in Section 3, where we show that the siphon property used in chemical reaction networks theory forces the Jacobian at any boundary equilibrium residing on a siphon face to have a triangular block form. Hence, the stability problem factorizes in two stability problems, tangential (usually satisfied) and transversal, and the instability of the transversal one leads to possible invasions (which may equivalently be quantified by Jacobian or NGM spectral abscissas). This leads to identifying the transversal Jacobian to a siphon face as the central object for deciding stability of boundary equilibria. We also show in theorem 3

In Section 4, we revisit the general class of (A, B, P, φ) balanced bilinear models, which include the SAIRS, SEAIR, and SIR-PH models in [12, 13], where S, A, I, R, E refer to susceptible, asymptomatic, infectious, recovered, and exposed individuals, respectively, and PH denotes the Phase-type distribution. One notable reason for studying these models is that here there exists a natural choice for the matrices from the regular splitting decomposition of [7], [14–16], specified by the model parameters. These models have a unique interior fixed point, which is also the case for quadratic generalized Lotka-Volterra models. This is a fascinating aspect, which was investigated in papers such as [1–3], which consider models with a specific algebraic structure, [17, 18], which propose a graph-theoretic Lyapunov function construction, [19], which proposes a Poincaré-Hopf type approach based on identifying an invariant compact manifold, and [20], which makes use of the theory of positive systems.

Despite all these efforts, it seems fair to say that a full understanding of the boundary between unique and non-unique interior fixed points is still elusive.

In Section 5 we identify, for the class of rank-one balanced bilinear models without I to S linear feedback, seven laws of the DFE – EE relay (beyond rank one, very little is known currently).

In Section 6, we describe the effect of a feedback $C\boldsymbol{x}$ on the seven laws.

Section 7 recall and applies the computation of Perron eigenvectors via Kirchhoff's matrix-tree theorem, which extends the rank-one approach of the previous sections.

Section 8 provides some conclusions and open questions.

1.2. Logical structure of the paper

The paper follows a single chain of implications, each link supplied by one section or theorem below; this explains why the sections are ordered as they are.

- A *chemical ODE* (Definition 2) is the starting point: it is the minimal structural hypothesis under which every result below is proved.
- Chemical ODEs identify *siphons* (Definition 3) as the relevant boundary sets: a siphon is exactly a set of species that a chemical ODE cannot resupply from outside itself once emptied.
- Siphons generate *forward-invariant faces*: the boundary face where a siphon's species all vanish is invariant under the flow, precisely because the ODE is chemical.
- Forward invariance of the face forces the Jacobian there into *triangular block form* (Theorem 2): the tangential and transversal dynamics decouple at first order.
- The transversal block of that triangular Jacobian is not an arbitrary matrix but a *Metzler matrix* (Theorem 3), because chemical reactions can only add to a vanished species through reactions that consume some other species.
- Being Metzler, the transversal block always admits a *regular splitting* (Corollary 1) into a non-negative production part and an M-matrix removal part.
- A regular splitting turns Jacobian stability into a spectral-radius inequality for the associated *next-generation matrix*.
- Next-generation matrices are nonnegative, so *Perron–Frobenius theory* applies: their spectral radius is a simple eigenvalue with positive left and right eigenvectors, which supply invasion directions and Lyapunov weights (Theorem 6 and Sections 5–7).
- Finally, when the next-generation matrix has *rank one* – the balanced bilinear (A, B, P, φ) balanced bilinear model class of Section 4 – these Perron eigenvectors, and everything built from them, become *explicit closed-form formulas* (Section 5); Section 7 shows that an explicit, graph-combinatorial formula survives even without this rank restriction.

Scope of the paper:

The structural results established in this paper are completely independent of rank-one assumptions. In particular, the generalized Lotka–Volterra factorization (Theorem 1), the triangular Jacobian theorem (Theorem 2), the Metzler property of transversal Jacobians (Theorem 3), and the Perron–Frobenius threshold theorem (Theorem 6) apply to arbitrary chemical ODEs satisfying the stated hypotheses.

Rank-one assumptions enter only when one seeks explicit closed formulas. They allow one to compute analytically the endemic equilibrium, the Perron eigenvectors, the Perron–Volterra Lyapunov functions, and the determinant identities developed in §5–§7.

Extending these explicit constructions beyond rank one is one of the principal open directions identified in Section 8.

2. Why combine CRN and ME methods?

The first characteristic of most models in mathematical epidemiology, ecology, and immuno-virology is that they are positive ODEs (or stochastic models whose mean field is a positive ODE). This means that important phenomena occur when trajectories reach the boundary of the positive orthant, and that the notion of invariant boundary faces is crucial. While boundary faces have been studied in classical ODE theory, the systematic exploitation of simplifications arising for positive ODEs was initiated by CRN works; see notably [21, 22], who showed that all positive polynomial models admit (non-unique) mass-action representations.

Beyond the polynomial case, but assuming a stoichiometric representation, crucial results relating boundary ω-limit points to invariant boundary faces and to the Petri-net concept of siphons were obtained in [23]. A recent proof of the folklore result that the Jacobian has a triangular block form on siphon faces was given in [24, 25], and [26] noted that transversal Jacobians on siphons have the Metzler/cooperativity property. This property further ensures the existence of left and right Perron eigenvectors which, in all cases we have studied, provide Lyapunov functions and escape directions from siphon faces respectively.

Our framework is encapsulated by the following definitions.

Definition 1 (Positive / non-negative ODE [`Pos`]). *An ODE is called* positive *[27] or* non-negative *[28] if the non-negative orthant*

$$\mathbb{R}^n_{\geq 0} := \{x \in \mathbb{R}^n : x_i \geq 0,\ i = 1, \ldots, n\}$$

is forward invariant under the flow.

Definition 2 (Stoichiometric and chemical representation [`Sto`]). *A stoichiometric representation of f is a pair (Γ, r) such that*

$$f(x) = \Gamma r(x), \qquad r(x) \geq 0,$$

where $\Gamma \in \mathbb{R}^{n \times n_R}$ is constant and $r : \mathbb{R}^n_{\geq 0} \to \mathbb{R}^{n_R}_{\geq 0}$ is locally Lipschitz.

An ODE is called chemical if

$$\Gamma_{i\rho} < 0 \implies r_\rho(x) = x_i \tilde{r}_\rho(x), \qquad \tilde{r}_\rho(x) \geq 0,$$

and, moreover, r_ρ depends only on variables in $\mathrm{supp}(r_\rho) \subseteq \Gamma_i^-$ *whenever $\Gamma_{i\rho} < 0$. Furthermore, we assume that each rate $r_\rho(x)$ is monotone non-decreasing with respect to each variable x_k for $k \in$* $\mathrm{supp}(r_\rho)$.

Siphons. Angeli, de Leenheer and Sontag [23], Anderson [29] and Shiu and Sturmfels [30, Prop. 2.1] proved that a boundary face F_σ associated to a nonempty set σ of variables being 0 is forward-invariant for a chemical ODE iff σ is a siphon in the sense of the combinatorial Definition 3:

Definition 3 (Siphon, minimal siphon, total siphon/DFE, critical siphon [`Sip`]).

- *A **siphon set** $\sigma \subseteq \mathcal{S}$ is a nonempty subset of species such that whenever a species in σ appears in a product complex in the RHS of a reaction, at least one species in σ must appear also in the LHS of the reaction (the reactant complex).*
- *A siphon is **minimal** when it contains no other siphon.*
- *The union of all minimal siphons will be called the **total siphon/DFE** and denoted σ_0.*
- *A siphon σ in a CRN with stoichiometric matrix Γ is **critical** if it contains no support of a positive conservation relation, i.e., if there exists no nonzero vector $c \geq 0$ with $c\Gamma = 0$ and $\operatorname{supp} c \subset \sigma$.*

Remark 1 (CRNT suggests definitions for important ME concepts). *The total siphon/DFE set σ_0 is a fundamental object of study in ME, but a rigorous definition for it is available only via CRNT. Similarly, CRNT suggests definitions for multi-strain and ME models–see below.*

We have now the building bricks to define ME and multi-strain systems.

Definition 4 (ME models, k–siphon models, k–strain simple models [`ME`]). *Consider a chemical ODE with at least one critical minimal siphon, and a unique DFE, and let $J_0^{\perp}$ denote the diagonal Jacobian block in the triangularization of the Jacobian corresponding to the DFE siphon, which exists and is Metzler by [24–26].*

*An **epidemic model** is a pair formed from a chemical ODE and a regular splitting (RS) $J_0^{\perp} = F_0 - V_0$ of the transversal Jacobian $J_0^{\perp}$ in the sense of [7, 15] (with $F_0 \geq 0$ and V_0 a non-singular M-matrix, hence $V_0^{-1} \geq 0$). Note that since $J_0^{\perp}$ is Metzler [24], a trivial* **regular splitting** *always exists if all the diagonal elements of $J_0^{\perp}$ have strictly negative parts.*

A k–siphon model is an ME model with precisely k minimal siphons.

A k–strain simple model is a chemical ODE with precisely k disjoint minimal siphons $\sigma_1, \ldots, \sigma_k$.

Theorem 1 (Generalized Lotka–Volterra form of k–strain simple models [`GLVrep`]). *A k–strain simple model with variables*

$$(s, z^1, \ldots, z^k) \in \mathbb{R}^m_{\geq 0} \times \prod_{j=1}^{k} \mathbb{R}^{d_j}_{\geq 0},$$

where each block z^j represents the variables/infected class associated with the strain/siphon σ_j, and $s = (s_1, \ldots, s_m)$ represents the susceptible or uninfected classes, may always be written in generalized Lotka–Volterra form, with the minimal-siphon equations factored, and "regularly split", as follows:

$$\dot{s} = f_s(s, z^1, \ldots, z^k), \qquad \dot{z}^j = (F_j - V_j)(s, z^1, \ldots, z^k) z^j, \qquad j = 1, \ldots, k. \tag{2.1}$$

Here, for each j, letting $\boldsymbol{y}_j$ denote the variables which remain free on the face $z^j = 0$, and putting $F_j(\boldsymbol{y}_j) = F_j(s, z^1, \ldots, z^k)\big|_{z^j=0}$, $V_j(\boldsymbol{y}_j) = V_j(s, z^1, \ldots, z^k)\big|_{z^j=0}$, we may chose F_j, V_j so that

$$J^{\perp}_{\sigma_j}(\boldsymbol{y}_j) = F_j(\boldsymbol{y}_j) - V_j(\boldsymbol{y}_j)$$

is a regular splitting (i.e. $F_j(\boldsymbol{y}_j) \geq 0, V_j(\boldsymbol{y}_j)^{-1} \geq 0$).

Proof. Since σ_j is a siphon, the face $z^j = 0$ is forward invariant; hence the z^j-component g_j of the vector field satisfies $g_j(s, z^1, \dots, 0, \dots, z^k) = 0$. By smoothness,

$$g_j(s, z^1, \dots, z^k) = A_j(s, z^1, \dots, z^k)\, z^j, \qquad A_j = \int_0^1 D_{z^j} g_j(s, z^1, \dots, tz^j, \dots, z^k)\, dt,$$

which yields =refMS with A_j in place of $F_j - V_j$. Setting $t = 0$ in the integrand shows $A_j(\boldsymbol{y}_j, 0) = D_{z^j} g_j(s, z^1, \dots, 0, \dots, z^k) = J^{\perp}_{\sigma_j}(\boldsymbol{y}_j)$, so A_j restricted to the face $z^j = 0$ is exactly the transversal Jacobian.

Since $J^{\perp}_{\sigma_j}(\boldsymbol{y}_j)$ is Metzler by [24], it admits some regular splitting $J^{\perp}_{\sigma_j}(\boldsymbol{y}_j) = F^0_j(\boldsymbol{y}_j) - V^0_j(\boldsymbol{y}_j)$ (the trivial diagonal one always works). It remains to extend F^0_j, V^0_j off the face so that $A_j = F_j - V_j$ holds identically and the extensions restrict to F^0_j, V^0_j on $z^j = 0$. Define

$$F_j(s, z^1, \dots, z^k) = F^0_j(\boldsymbol{y}_j)$$

(i.e. F_j is simply F^0_j, frozen at its face value and read off the z^j-independent variables $\boldsymbol{y}_j$; in particular $F_j \geq 0$ everywhere, since $F^0_j \geq 0$), and

$$V_j = F_j - A_j.$$

Then $A_j = F_j - V_j$ holds everywhere by construction, and on the face, $F_j|_{z^j=0} = F^0_j$ while $V_j|_{z^j=0} = F^0_j - A_j(\boldsymbol{y}_j, 0) = F^0_j - (F^0_j - V^0_j) = V^0_j$, so this simultaneous choice recovers exactly the originally chosen regular splitting on the face, as claimed. This completes the construction: F_j, V_j have been exhibited explicitly, for every j, from the data of the chemical ODE and the chosen face splitting $F^0_j - V^0_j$ alone. □

Remark 2 (k-strain simple models generalize Lotka-Volterra models)**.** *The generalization arises from two directions. First, not all equations are required to have multiplicative structure. Secondly, the scalar multiplications in Lotka-Volterra (corresponding to scalar siphons) are replaced by matrix multiplications in =rMS.*

Definition 5 (R–invasion functions and rank-one k–strain models [R])**.** *For a simple k-strain model, for each strain j and regular splitting, define next generation matrices $K_j(\boldsymbol{y}_j) = (F_j V_j^{-1})(\boldsymbol{y}_j)$ and invasion functions*

$$R_j(\boldsymbol{y}_j) := \rho(K_j(\boldsymbol{y}_j)),$$

$R_j(\boldsymbol{y}_j)$ will be called **R-invasion functions** *(associated with the block j).*

A ***simple k-strain model is rank-one*** *if every Jacobian transversal block $J^{\perp}_{\sigma}$ admits a regular splitting $J^{\perp}_{\sigma} = F_\sigma - V_\sigma$, such that the "new infections" matrix F_σ has rank one. In this case, the R-invasion functions and the Perron data admit explicit rank-one formulas.*

Remark 3 (Previous appearances of the R-invasion functions)**.** *Interestingly, invasion functions appear in a different context in the work of Magal, Webb, and Wu (2019) [31], who develop threshold-based methods for nonlinear epidemic models in a spatial reaction–diffusion setting.*

Definition 6 (reproduction numbers and invasibility numbers [`rep`])**.**

1. *The evaluations*

$$R_i = R_i(E_0), i = 1, ..., k, \tag{2.2}$$

where E_0 is the DFE, and $R_i(\boldsymbol{y}_i)$ are the invasion functions, will be called **basic reproduction numbers** *(of strain i).*

2. *In the case when each minimal siphon has a unique resident fixed point E_j, $j = 1, ..., k$,*

$$\widetilde{R_i^j} := R_i(E_j) \tag{2.3}$$

will be called the **invasibility number of invading block** ***i*** **on resident block** *j.*

A central motivation of our paper is the observation that the explicit results of [1–3,5,18] and others share a common structure: they are rank-one models and exploit the computation of left and right Perron eigenvectors of rank-one NGMs.

Remark 4 (The roles of the Perron eigenvectors of transversal Jacobians on siphon faces)**.** *Once Metzler transversal Jacobians on siphon faces have been identified as the basic objects governing invasion, it is natural to study the roles of their Perron eigenvectors.*

The right Perron vector determines the invasion direction. In the rank-one models considered in this paper and in rank one works like for example [1–3, 5, 26], it also yields the coordinates of the boundary equilibria.

The left Perron vector plays a dual role. It determines both the canonical normalized vector

$$\widetilde{\pi}_k^\top = \frac{\pi_k^\top V_k^{-1}}{\mathcal{R}_k},$$

used in the linear invader part of the Perron–Volterra Lyapunov function, and the associated resident entropy weights

$$\widetilde{w}_{k,j} = \widetilde{\pi}_{k,j} w_{k,j},$$

normalized so $\sum_j \widetilde{w}_{k,j} = 1$.

2.1. The (RHS,var), and the (RN,rts,var) mass-action representation of positive ODEs

Note that the notations RN, rts, and var refer to the reaction network, reaction rates (parameters), and variables, respectively.

For parameterizing ME or CRN ODE models, there are three natural choices:

1. The parametrization used traditionally for all ODE models is $X' = RHS(X)$. A model is thus a pair (RHS, var=X), where RHS denotes the set of formulas for the derivatives, and var are the variables whose rates of change we study.

2. Chemical reaction networks theory starts by breaking the RHS as

$$X' = RHS(X) = G.\mathbf{R}(X). \tag{2.4}$$

   A model is now defined as a triple $(G, \mathbf{R}(X), X)$. The RHS has thus been broken into two parts:

   (a) G is the “stoichiometric matrix” (SM), whose columns represent directions in which several species/compartments change simultaneously; it is also called the structure of the model.

   (b) $\mathbf{R}(X)$ is the vector of rates of change associated to each direction (assumed all to be non-negative), also known as kinetics. They are separated from G, since they are less certain; this fact, well accepted in CRNT, is equally true in ME.

Example 1 (stoichiometric matrix of SIRS [sto])**.** *For example, the simplest Susceptible-Infectious-Recovered-Susceptible (SIRS) ODE without inflows and outflows (=demography) is defined by the triple* $(G, \mathbf{R}, X)$*:*

$$X' = \begin{pmatrix} s' \\ i' \\ r' \end{pmatrix} = \begin{pmatrix} -1 & 0 & 1 & -1 \\ 1 & -1 & 0 & 0 \\ 0 & 1 & -1 & 1 \end{pmatrix} \begin{pmatrix} \beta si \\ \gamma_i i \\ \gamma_r r \\ \gamma_s s \end{pmatrix} := \Gamma \mathbf{R}(X). \tag{2.5}$$

Note this representation is also a natural first step towards defining an associated CTMC model on the integers.

We formalize the above as Definition 2 (§2), which fixes once and for all the meaning of a chemical stoichiometric representation used throughout the paper.

Definition 7 (Identification of consumption and production supports [Ide])**.** *Let* f *be chemical in the sense of Definition 2. For each i, the sets*

$$\Gamma_i^- := \{ j : f_i^-(x) \text{ depends nontrivially on } x_j \} = \bigcup_{\rho:\, \Gamma_{i\rho}<0} \operatorname{supp}(r_\rho),$$
$$\Gamma_i^+ := \{ j : f_i^+(x) \text{ depends nontrivially on } x_j \} = \bigcup_{\rho:\, \Gamma_{i\rho}>0} \operatorname{supp}(r_\rho)$$

are called consumption and production supports.

Assumption 1 (stoichiometric representability)**.** *All systems considered in this paper are assumed to admit a chemical stoichiometric representation (CSR) as above.*

3. We introduce the third sources-products parametrization, the one most used in CRNT, by an example. For SIRS, it is:

$$\left(\begin{array}{c|c} \text{RN} & \text{rts} \\ \hline \text{i + s} \to \text{2i} & \beta\, is \\ \text{i} \to \text{r} & \gamma_i\, i \\ \text{r} \to \text{s} & \gamma_r\, r \\ \text{s} \to \text{r} & \gamma_s\, s \end{array} \right) \tag{2.6}$$

Here each column of G is replaced by a “reaction” (or “interaction”. For example, the second column in (2.5), representing a transfer from the row of i towards that of r, is replaced by $i- > r$.

The $s + i \to 2i$ in the first row is the CRNT mass-action representation (not reviewed here). Note that this provides a quite natural phenomenological representation of infections at the individual level: the meeting of a susceptible and an infectious results in two infectious.

Remark 5. *Note that the (RN,rts) representation of an ODE is not unique. These representations (any of them) have however the advantage of being the only ones which take into account the positivity of an ODE (for polynomial ODEs, positivity is equivalent to the existence of a mass-action representation).*

2.2. Some interactions between CRN and epidemiology

CRNT has focused considerably on graph structures associated with reactions networks, and on simplifications available when these graphs are (weakly) reversible. On the other hand, the most encountered infection reaction in epidemiology, "s" + "i" $\rightarrow$ 2"i" is irreversible, which explains why classic CRN and ME have not interacted much in the past (but SI, SIS, SIRS models appear sometimes in the CRN literature for the purpose of illustrating various results about autocatalytic models – see for example [32, 33]).

However, the key fact that Epidemiologic Strains, Minimal Self-Replicable Siphons, and Autocatalytic Cores are conceptually related seems to have passed unnoticed until [10].

We believe that more information transfer between CRN and ME could be useful to both, as well as to the other positive system subfields. Let us illustrate this by a few examples:

1. The **positivity criterion** of [21] seems unfortunately unknown outside CRNT, and has been reproved in particular cases an uncountable number of times.

2. Especially relevant is the notion of **siphons**. These are in one-to-one correspondence with forward invariant boundary faces, cf. Angeli et al. [23], in fact this yields their simplest definition; siphons, minimal siphons, the total/DFE siphon, and critical siphons are formalized in Definition 3 (§2). We complete that definition here with one further notion needed below:

   Definition 8 (DFE closure/infection [`DFE`]). *The set of all species which are automatically zero whenever every species in the DFE is zero is called the* DFE-closure siphon*, and any eventual fixed point on the corresponding face is called the DFE.*

   Siphons are also related to the existence and stability of fixed points on the boundary of the positive orthant. Indeed, Angeli et al. [23] proved that if a boundary point is an *ω-limit* point, then the species set Σ in which every species has zero concentration must be a siphon.

   Proposition 1. *[23, Prop 1], [29, Thm 2.5], [34, Lem 2.1], [35, Prop. 3.1] If an ω-limit w of a strictly positive initial point belongs to a face*

   $$w \in L_\Sigma := \{X \in \mathbb{R}^n_{\geq 0} : x_i = 0, i \in \Sigma\},$$

   then Σ is a siphon.

   Remark 6. *While the total/DFE siphon is clearly a siphon (since its corresponding face is the intersection of all minimal siphons, hence a siphon), the DFE-closure needs not be a priori a siphon. However, it is so in all epidemic models, because in epidemic models a DFE must exist, and be an ω-limit of strictly positive initial points when $R_0 < 1$, where R_0 is the basic reproduction number defined as the spectral radius of the next generation matrix(this siphon is also critical, since it is unstable when $R_0 > 1$, and hence criticality holds by a further result of [23]).*

   Our Mathematica package starts any analysis by inputting the model as a set of reactions, then determines the minimal siphons (using the Julia algorithm provided by Vincent Du [36]) as a first, easier step towards computing boundary fixed points residing on each siphon-face [25].

3. NGM theorem for forward-invariant faces, and the Metzler property of the transversal Jacobian

Siphon lattice and invariant faces.

- $\mathcal{L}$ denotes the lattice generated by the minimal siphons.
- For $\Sigma \in \mathcal{L}$,
$$\mathcal{F}_\Sigma = \{x_i = 0 : \; i \in \Sigma\}$$
is the associated forward-invariant face.
- $E_\Sigma \in \mathrm{relint}(\mathcal{F}_\Sigma)$ denotes the equilibrium on $\mathcal{F}_\Sigma$ under consideration.
- At E_Σ, one has
$$x_i^* = 0 \text{ for } i \in \Sigma, \qquad x_i^* > 0 \text{ for } i \notin \Sigma.$$

Every stability problem on a siphon face factorizes into a tangential problem and a transversal problem. The tangential block depends only on the reduced dynamics on the face itself, whereas the transversal block measures invasion away from it. Theorem 2 below formalizes this factorization, at the level of the Jacobian and its spectrum; Theorem 3 afterwards explains why Perron–Frobenius theory naturally enters this picture: the transversal block is not just any matrix, but a Metzler one.

Theorem 2 (triangular block form of the Jacobian on forward-invariant faces [`tri`]). *The purpose of this theorem is to explain why the Jacobian on a siphon face separates naturally into tangential and transversal dynamics, and does so from the siphon property alone, with no further structural assumption. The block-triangular reduction itself is a classical consequence of invariance of a coordinate face; the novelty is identifying that face intrinsically, via the siphon property of Definition 2, rather than assuming it as extra structure (generalizing [14–16], [11]).*

Let $x = (z, y) \in \mathbb{R}^m_{\geq 0} \times \mathbb{R}^n_{\geq 0}$ *and let*
$$\dot{z} = f_z(z, y), \qquad \dot{y} = f_y(z, y)$$
be a chemical vector field. Assume that the coordinate face
$$F_z = \{z = 0\}$$
is forward invariant, equivalently, that the set of variables z *is a siphon. Then:*

1. *The mixed Jacobian block*
$$J_{zy}(y) = D_y f_z(0, y)$$
vanishes identically on F_z*. Hence, at every point* $(0, y^*) \in F_z$,
$$J(0, y^*) = \begin{pmatrix} J_z & 0 \\ J_{yz} & J_y \end{pmatrix}, \qquad J_z = D_z f_z(0, y^*), \qquad J_y = D_y f_y(0, y^*).$$

2. *The spectrum of the full Jacobian is*

$$\sigma(J(0, y^*)) = \sigma(J_z) \cup \sigma(J_y).$$

Consequently, the fixed point $(0, y^*)$ *is linearly asymptotically stable if and only if both* J_z *and* J_y *are Hurwitz. If either block has an eigenvalue with positive real part, then* $(0, y^*)$ *is unstable.*

Theorem 2 reduces stability of $(0, y^*)$ to the Hurwitz property of the single transversal block J_z (assuming, as is typical, that the tangential block J_y is already Hurwitz on the face). Theorem 3 below identifies exactly what kind of matrix J_z is, and Corollary 1 afterwards turns this into the familiar NGM spectral-radius criterion.

Proof. Because the variables z form a siphon, every reaction producing a z-species has at least one z-species among its reactants. By Definition 2, every rate consuming such a z-species has that variable as a factor. Therefore, after setting $z = 0$, every reaction contributing to a z-equation vanishes, and hence

$$f_z(0, y) = 0.$$

Differentiating this identity with respect to the free face variable y gives

$$D_y f_z(0, y) = 0.$$

This proves the block lower-triangular form in part (i).

The characteristic polynomial of a block triangular matrix factors:

$$\det(\lambda I - J(0, y^*)) = \det(\lambda I - J_z) \det(\lambda I - J_y).$$

Hence

$$\sigma(J(0, y^*)) = \sigma(J_z) \cup \sigma(J_y),$$

which proves part (ii) by the linearization theorem. Thus the chemical hypothesis alone – without any further structural assumption on the reaction rates – forces the transversal and tangential dynamics to decouple, both in the Jacobian and in its spectrum. □

The forward-invariance hypothesis is not a technical convenience: without it, $D_y f_z(0, y)$ need not vanish, the off-diagonal block in the proof survives, and the block-triangular form – and with it every subsequent theorem in this section – fails.

Theorem 3 (Metzler property of the transversal Jacobian block on a siphon face [`Met`])**.** *The purpose of this theorem is to explain why Perron–Frobenius theory applies on every siphon face: the transversal Jacobian is not just any matrix but a Metzler one. Cooperativity (a Metzler Jacobian) is usually a classical hypothesis in the theory of monotone dynamical systems; the novelty here is that it is not assumed but derived, from the chemical stoichiometric structure of Definition 2 alone.*

Let

$$(z, y) \in \mathbb{R}^m_{\geq 0} \times \mathbb{R}^n_{\geq 0}$$

be the variables of a chemical ODE

$$\dot{x} = \Gamma r(x), \qquad x = (z, y),$$

in the sense of Definition 2. Assume that the set of z–variables is a siphon, so that the coordinate face

$$F_z = \{z = 0\}$$

is forward invariant.

Then, at every point $(0, y) \in F_z$*, the transversal Jacobian*

$$J_z^{\perp}(y) = D_z f_z(0, y)$$

is Metzler:

$$\frac{\partial f_{z_i}}{\partial z_j}(0, y) \geq 0, \qquad i \neq j.$$

Equivalently, the linearized dynamics transversal to the siphon face,

$$\dot{\xi} = J_z^{\perp}(y)\xi,$$

is cooperative.

Proof. Write the ith transversal component as

$$f_{z_i}(z, y) = \sum_{\rho=1}^{n_R} \Gamma_{i\rho} r_\rho(z, y).$$

For $i \neq j$,

$$\frac{\partial f_{z_i}}{\partial z_j}(0, y) = \sum_{\rho=1}^{n_R} \Gamma_{i\rho} \frac{\partial r_\rho}{\partial z_j}(0, y).$$

Consider first a reaction ρ for which

$$\Gamma_{i\rho} < 0.$$

By the chemical property in Definition 2,

$$r_\rho(z, y) = z_i \widetilde{r}_\rho(z, y), \qquad \widetilde{r}_\rho(z, y) \geq 0.$$

Since $i \neq j$,

$$\frac{\partial r_\rho}{\partial z_j} = z_i \frac{\partial \widetilde{r}_\rho}{\partial z_j},$$

and therefore

$$\frac{\partial r_\rho}{\partial z_j}(0, y) = 0.$$

Thus every reaction which consumes z_i makes no contribution to an off-diagonal entry of the transversal Jacobian on the siphon face.

Now consider a reaction ρ for which

$$\Gamma_{i\rho} > 0.$$

If r_ρ does not depend on z_j, then

$$\frac{\partial r_\rho}{\partial z_j}(0, y) = 0.$$

If it does depend on z_j, the monotonicity assumption in Definition 2 gives

$$\frac{\partial r_\rho}{\partial z_j}(0, y) \geq 0.$$

Hence, in either case,

$$\Gamma_{i\rho} \frac{\partial r_\rho}{\partial z_j}(0, y) \geq 0.$$

Reactions satisfying $\Gamma_{i\rho} = 0$ contribute nothing. Consequently,

$$\frac{\partial f_{z_i}}{\partial z_j}(0, y) \geq 0 \qquad \text{for every } i \neq j.$$

Therefore $J_z^{\perp}(y)$ is Metzler. The variational equation generated by a Metzler matrix is cooperative, which proves the equivalent statement. Thus the chemical assumptions of Definition 2 alone imply that every transversal Jacobian on a siphon face is cooperative, with no further hypothesis on the reaction rates. □

The chemical hypothesis cannot be relaxed to a general stoichiometric representation (Definition 2): without the sign and support conditions on r_ρ, the cross term $\partial r_\rho / \partial z_j$ used above need not vanish or stay nonnegative, off-diagonal entries of $J_z^{\perp}$ can become negative, and Metzler-ness – hence the applicability of Perron–Frobenius theory in the remainder of the paper – can fail.

Remark 7 (Why regular splittings appear naturally)**.** *Regular splittings are not assumed here as a modeling convenience, or because they are the tool epidemiologists happen to prefer: they appear automatically, because J_z is Metzler (Theorem 3). Indeed, a Metzler matrix always admits at least the trivial regular splitting $J_z = (J_z + cI) - cI$ for c large enough that $J_z + cI \geq 0$; in epidemic models a much sparser, epidemiologically meaningful splitting into new-infection and removal rates is typically available instead. Either way, once such a splitting is fixed, Theorem 2's Hurwitz condition on J_z becomes the familiar NGM spectral-radius criterion:*

Corollary 1. (Regular splitting and the NGM threshold). *In the setting of Theorem 2, suppose that*

$$J_z = F - V,$$

where (F, V) is a regular splitting, so that

$$F \geq 0, \qquad V^{-1} \geq 0,$$

with V a nonsingular M-matrix. Then

$$s(J_z) < 0 \quad \Longleftrightarrow \quad \rho(FV^{-1}) < 1,$$

$$s(J_z) = 0 \quad \Longleftrightarrow \quad \rho(FV^{-1}) = 1,$$

and

$$s(J_z) > 0 \quad \Longleftrightarrow \quad \rho(FV^{-1}) > 1.$$

Thus, if J_y is Hurwitz, the fixed point $(0, y^*)$ of Theorem 2 is linearly asymptotically stable when $\rho(FV^{-1}) < 1$, and it is unstable when $\rho(FV^{-1}) > 1$.

Proof. Since V is a nonsingular M-matrix and $F \geq 0$, the standard regular-splitting theorem gives

$$V - F \text{ is a nonsingular } M\text{-matrix} \iff \rho(FV^{-1}) < 1.$$

Since

$$J_z = F - V,$$

this is equivalent to $s(J_z) < 0$. The corresponding threshold and supercritical statements follow from the same M-matrix spectral comparison theorem [7]. Combining this with Theorem 2(ii) proves the stability claim. □

4. Balanced bilinear models

The works of [1–3], followed by [18], building on the celebrated [15], suggested that several connections between the stability of the DFE and that of the EE might exist. In retrospect, this connection is not surprising, since the DFE and EE are often members of a "stability relay team" — one takes over the stability from the other –see [25] for further remarks in this direction. This connection translates into a list of seven laws concerning both the EE and the DFE for rank-one balanced bilinear models presented below, which use the same common building bricks.

Let us mention that some of these laws are continually being reproved in particular examples in the ME literature, without making reference to the common structure of (A, B, P, φ) balanced bilinear models [1–3], which shows the interest in the unification we propose.

The models we study here are of the form:

Definition 9 (balanced bilinear model [`bal`])**.** *A positive ODE system is called a* balanced bilinear model *if, after a permutation of coordinates, it can be written as*

$$\begin{cases} S' = \varphi(S) - \mathrm{Diag}(S)\, BI + CI, \ \varphi(S) = \Lambda + A_S S \\ I' = P\ \mathrm{Diag}(S)\, BI + AI, \end{cases} \tag{4.1}$$

where

$$S \in \mathbb{R}^m_+, \qquad I \in \mathbb{R}^n_+,$$

and:

1. *$I \in \mathbb{R}^n_+$ are n DFE closure/infection compartments.*
2. *$S \in \mathbb{R}^m_+$ are m non-infection/susceptible compartments (the complement of I).*
3. *$C \in \mathbb{R}^{m\times n}_+$ yields feedback from I to S.*
4. *$\varphi(S)$ is the dynamics in the S compartments, in the absence of the I compartments. Below we always assume $\varphi(S) = \Lambda + A_S S, \Lambda \in \mathbb{R}^m_+, A_S \in \mathbb{R}^{m,m}$.*
5. *$A_S \in \mathbb{R}^{m\times m}, A \in \mathbb{R}^{n,n}$ are stable Metzler matrices modeling the intra-flows between S and I compartments, respectively. The second is precisely the matrix appearing in the NGM formula $K = F(-A)^{-1}$.*

6. *$B \in \mathbb{R}_+^{m\times n} > 0$ is the WAIFW (Who Acquires Infection From Whom) matrix, and $B(i, j)$ denotes the contact and infectivity rate of I_j within the group S_i. This matrix, which exists only for models which are bilinear in S, I, is related to the square matrix F from the NGM formula.*

7. *$P \in \mathbb{R}_+^{n\times m}$ is a column-stochastic matrix that distributes the vector $\mathrm{Diag}(S)\,BI$ among the I compartments of the infection. The fact that $1.P = 1$ implies that the bilinear terms cancel out in the sum of all equations, suggesting the name "balanced bilinear" for this class.*

Hypothesis 1. • *Any susceptible compartment is accessible from a susceptible compartment with inflow/recruitment.*

- *Any infected-infectious compartment is accessible from at least one entry-point for infection.*

Definition 10 (linear forces of infection and bilinear rates of infection [`lin`])**.** *Below, a function*

$$F(S) := P\ \mathrm{Diag}(S)\,B = \sum_{i=1}^{m} S_i\, p_i\, \vec{b}_i \quad \in \mathbb{R}_+^{n\times n}, \quad S \in \mathbb{R}_+^m, \tag{4.2}$$

where P, B satisfy the conditions of definition 9, and p_i, $\vec{b}_i$ are the i-th column of P and i-th row of B, respectively, will be called a linear force of infection, and

$$F(S)\,I = P\ \mathrm{Diag}(S)\,BI = P\,\mathrm{Diag}(BI)S \quad \in \mathbb{R}_+^n$$

will be called a bilinear rate of infection.

Remark 8 (some alternative representations for bilinear rates of infection $F(S)$)**.** *A bilinear rate of infection may be written as*

$$F(S)\,I = P\ \mathrm{Diag}(S)\,BI = P\,(S \odot BI) = P\,\mathrm{Diag}(BI)S, \tag{4.3}$$

where $\odot$ denotes the componentwise (Hadamard) product, and the identities follow from the standard vector identity $\mathrm{Diag}(a)\,b = a \odot b = \mathrm{Diag}(b)\,a$.

The **"Diag switch"** *equality between the second and forth will be used below.*

The following two formulas hold independently of the dimension of S and of rank one assumptions:

1. If A_S is Metzler stable (ensuring the element-wise positivity of $(-A_S)^{-1}$)), then the DFE is unique, given by:
$$S_0 = (-A_S)^{-1}\Lambda \in \mathbb{R}_+^m.$$

2. the basic reproduction number is
$$R_0 = \rho\,(K(S_0)) = \rho\left(F(S_0)\,(-A)^{-1}\right),$$
where S_0 is the disease-free equilibrium.

4.1. Rank one models of P-type and B-type

Remark 9. *Several of the explicit formulas in Section 5 hold only when either* $P = \boldsymbol{\alpha}_n (1, 1, ..., 1)$ *or* $B = \boldsymbol{\alpha}_m \vec{\boldsymbol{\beta}}$ *are of rank one. Since the coefficients* S_i *vary independently in* $\mathbb{R}_+^m$*, it follows that* $\mathrm{rank}(F(S)) = 1$ *for all interior* S *if and only if either* $\mathrm{rank}(P) = 1$ *or* $\mathrm{rank}(B) = 1$. *We have thus two (non-disjoint) cases:*

- Case (P): $P = \boldsymbol{\alpha}_n \vec{\mathbf{1}}, \quad \boldsymbol{\alpha}_n \in \mathbb{R}_+^n, \ \vec{\mathbf{1}}\boldsymbol{\alpha}_n = 1; \quad F(S)I = \boldsymbol{\alpha}_n (\vec{S} B I).$
- Case (B): $B = \boldsymbol{\alpha}_m \vec{\boldsymbol{\beta}}, \quad \boldsymbol{\alpha}_m \in \mathbb{R}_+^m, \vec{\mathbf{1}}\boldsymbol{\alpha}_m = 1, \vec{\boldsymbol{\beta}} \in \mathbb{R}_+^{1\times n}; \quad F(S)I = P\,\mathrm{Diag}(S)\boldsymbol{\alpha}_m \cdot (\vec{\boldsymbol{\beta}} I).$

In both cases the (A, B, P, φ) *balanced bilinear model* (4.1) *without feedback from* I *to* S *reads*

$$\begin{cases} S' = \varphi(S) - \mathrm{Diag}[S]\,BI + CI, \\ I' = [F(S) + A]\,I := [K(S) - Id_n]\,(-A)I, \qquad K(S) := F(S)(-A)^{-1}, \end{cases} \tag{4.4}$$

where $K(S)$ *is the NGM.*

In Case (P) once infected, individuals enter the infectious compartments according to the stochastic vector $\boldsymbol{\alpha}$, regardless of their susceptible class of origin. In Case (B), the infectivity row $\vec{\boldsymbol{\beta}}$ is common to all susceptible classes, which differ only through $\boldsymbol{\alpha}_m$.

Remark 10 (Rank-one factorizations of K and $\widetilde{K}$)**.** *Recall* $F(S) = P\ \mathrm{Diag}(S)\,B$, *and*

$$\widetilde{K}(S_0) = (-A)^{-1}F(S_0), \qquad K(S_0) = F(S_0)(-A)^{-1} = (-A)\,\widetilde{K}(S_0)\,(-A)^{-1},$$

so $K(S_0)$ *and* $\widetilde{K}(S_0)$ *are similar.*

Case (P). $P = \boldsymbol{\alpha}_n \vec{\mathbf{1}}, \qquad \vec{\mathbf{1}}\boldsymbol{\alpha}_n = 1$, *implying* $F(S_0) = \boldsymbol{\alpha}_n S_0 B$, *and therefore*

$$K(S_0) = \boldsymbol{\alpha}_n \vec{\pi}_K, \qquad \vec{\pi}_K := S_0 B(-A)^{-1}.$$

Hence one may choose Perron eigenvectors of $K(S_0)$ *as*

$$\textit{right: } \mathbf{w}_K = \boldsymbol{\alpha}_n, \qquad \textit{left: } \vec{\pi}_K = S_0 B(-A)^{-1}.$$

For $\widetilde{K}(S_0)$ *one has*

$$\widetilde{K}(S_0) = \mathbf{w}_{\widetilde{K}} \vec{\pi}_{\widetilde{K}}, \qquad \textit{right: } \ \mathbf{w}_{\widetilde{K}} := (-A)^{-1}\boldsymbol{\alpha}_n, \qquad \textit{left: } \ \vec{\pi}_{\widetilde{K}} := S_0 B.$$

Case (B). $B = \boldsymbol{\alpha}_m \vec{\boldsymbol{\beta}}, \qquad \vec{\mathbf{1}}\boldsymbol{\alpha}_m = 1, \qquad \vec{\boldsymbol{\beta}} \in \mathbb{R}_+^{1\times n}$, *implying* $F(S_0) = \mathbf{w}_F \vec{\boldsymbol{\beta}}, \qquad \mathbf{w}_F := P\ \mathrm{Diag}(S_0)\,\boldsymbol{\alpha}_m$, *and therefore*

$$K(S_0) = \mathbf{w}_K \vec{\pi}_K, \qquad \mathbf{w}_K := P\ \mathrm{Diag}(S_0)\,\boldsymbol{\alpha}_m, \qquad \vec{\pi}_K := \vec{\boldsymbol{\beta}}(-A)^{-1}.$$

Summarizing, one may choose Perron eigenvectors as follows:

Case	Assumption	$K(S_0)$		$\widetilde{K}(S_0) = \mathbf{w}_{\widetilde{K}} \vec{\pi}_{\widetilde{K}}$	
		right $\mathbf{w}_K$	left $\vec{\pi}_K$	right $\mathbf{w}_{\widetilde{K}}$	left $\vec{\pi}_{\widetilde{K}}$
(P)	$P = \boldsymbol{\alpha}_n \vec{\mathbf{1}}$	$\boldsymbol{\alpha}_n$	$S_0 B(-A)^{-1}$	$(-A)^{-1}\boldsymbol{\alpha}_n$	$S_0 B$
(B)	$B = \boldsymbol{\alpha}_m \vec{\boldsymbol{\beta}}$	$P\ \mathrm{Diag}(S_0)\,\boldsymbol{\alpha}_m$	$\vec{\boldsymbol{\beta}}(-A)^{-1}$	$(-A)^{-1}P\ \mathrm{Diag}(S_0)\,\boldsymbol{\alpha}_m$	$\vec{\boldsymbol{\beta}}$

In both cases,

$$R_0 = \rho(K(S_0)) = \rho(\widetilde{K}(S_0)) = \vec{\pi}_K \, \mathbf{w}_K = \vec{\pi}_{\widetilde{K}} \, \mathbf{w}_{\widetilde{K}}.$$

Moreover, the right and left Perron eigenvectors of $K(S_0)$ *and* $\widetilde{K}(S_0)$ *are related by*

$$\mathbf{w}_K = (-A)\, \mathbf{w}_{\widetilde{K}}, \qquad \vec{\pi}_{\widetilde{K}} = \vec{\pi}_K \, (-A).$$

4.2. Independence of the two rank–one assumptions

Recall that the infection dynamics in (4.4) may be written

$$I' = F(S)I + AI, \qquad F(S) := P \ \mathrm{Diag}(S)\, B,$$

with simplifying cases

$$\text{(P)} \quad P = \boldsymbol{\alpha}_n(\vec{\mathbf{1}}), \qquad \text{(B)} \quad B = \boldsymbol{\alpha}_m \vec{\boldsymbol{\beta}}.$$

We show now that the two assumptions are algebraically independent.

Lemma 1 (Rigidity of the factorization)**.** *Let* $F(S) = P\,\mathrm{Diag}(S)B$*. Assume that every row of* B *and of* $\widetilde{B}$ *is nonzero. If two column-stochastic pairs* (P, B) *and* $(\widetilde{P}, \widetilde{B})$ *generate the same infection operator for all* S*:*

$$P\,\mathrm{Diag}(S)B = \widetilde{P}\,\mathrm{Diag}(S)\widetilde{B} \qquad \forall\, S \in \mathbb{R}^m,$$

then necessarily

$$P = \widetilde{P}, \qquad B = \widetilde{B}.$$

Proof. Write

$$P\,\mathrm{Diag}(S)B = \sum_{i=1}^{m} S_i \, p_i \, \vec{b}_i,$$

where p_i is the ith column of P and $\vec{b}_i$ the ith row of B. The same expansion holds for $(\widetilde{P}, \widetilde{B})$:

$$\sum_{i=1}^{m} S_i \, p_i \, \vec{b}_i = \sum_{i=1}^{m} S_i \, \tilde{p}_i \tilde{\vec{b}}_i \qquad \forall\, S. \tag{4.5}$$

Since the coefficients S_i are independent, we obtain

$$p_i \, \vec{b}_i = \tilde{p}_i \tilde{\vec{b}}_i \qquad \text{for each } i.$$

Since P and $\widetilde{P}$ are column-stochastic, each column satisfies $\vec{\mathbf{1}} p_i = 1$ and $\vec{\mathbf{1}} \tilde{p}_i = 1$. Because $\vec{b}_i \neq 0$ and $\tilde{\vec{b}}_i \neq 0$, the outer products above have rank one, hence

$$p_i = \lambda_i \tilde{p}_i$$

for some scalar $\lambda_i > 0$. Applying both unit-sum conditions gives $\lambda_i = 1$, hence $p_i = \tilde{p}_i$. It then follows from $p_i(\vec{b}_i - \tilde{\vec{b}}_i) = 0$ and $p_i \neq 0$ that $\vec{b}_i = \tilde{\vec{b}}_i$. Hence $P = \widetilde{P}$ and $B = \widetilde{B}$. □

This lemma shows that the infection dynamics uniquely determines the column-stochastic pair (P, B), so one cannot transform a model satisfying one of the two assumptions into the other without changing the dynamics.

Theorem 4 (Existence of Case (P) without Case (B) [`Exi`]). *There exist systems of the form* (4.1) *with* $P = \boldsymbol{\alpha}_n(\vec{\mathbf{1}})$ *but B not of rank one.*

Proof. Consider $m = n = 2$ and

$$\boldsymbol{\alpha}_n = \begin{pmatrix} 1/3 \\ 2/3 \end{pmatrix}, \qquad P = \boldsymbol{\alpha}_n(1,1) = \begin{pmatrix} 1/3 & 1/3 \\ 2/3 & 2/3 \end{pmatrix}.$$

Let

$$B = \begin{pmatrix} 1 & 2 \\ 3 & 4 \end{pmatrix}.$$

Then

$$\det B = -2 \neq 0,$$

so $\mathrm{rank}(B) = 2$. Hence the model satisfies Case (P) but not Case (B).

By Lemma 1, no alternative rank-one matrix $\widetilde{B}$ can reproduce the same infection operator $F(S) = P\,\mathrm{Diag}(S)B$. □

Theorem 5 (Existence of Case (B) without Case (P) [`Exi`]). *There exist systems of the form* (4.1) *with B rank one but with no representation satisfying* $P = \boldsymbol{\alpha}_n(\vec{\mathbf{1}})$.

Proof. Again take $m = n = 2$ and define

$$\boldsymbol{\alpha}_m = \begin{pmatrix} 1/3 \\ 2/3 \end{pmatrix}, \qquad \vec{\boldsymbol{\beta}} = \begin{pmatrix} 3 & 9 \end{pmatrix}, \qquad B = \boldsymbol{\alpha}_m \vec{\boldsymbol{\beta}} = \begin{pmatrix} 1 & 3 \\ 2 & 6 \end{pmatrix}.$$

Thus B has rank one.

Now take

$$P = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}.$$

This matrix is column-stochastic but its columns are not proportional, so it cannot be written in the form $\boldsymbol{\alpha}_n(\vec{\mathbf{1}})$.

Suppose that the same infection operator could be written using $\widetilde{P} = \boldsymbol{\alpha}_n(\vec{\mathbf{1}})$. Then since B is common to both representations;

$$P\,\mathrm{Diag}(S)B = \widetilde{P}\,\mathrm{Diag}(S)B \qquad \forall\, S.$$

By Lemma 1 this would imply $P = \widetilde{P}$, which is impossible because the columns of P are not proportional.

Hence Case (B) does not imply Case (P). □

Conclusion: The two simplifying assumptions

$$P = \boldsymbol{\alpha}_n(\vec{\mathbf{1}}), \qquad B = \boldsymbol{\alpha}_m \vec{\boldsymbol{\beta}}$$

are independent structural properties of the bilinear epidemic model. Neither can be deduced from the other without changing the infection dynamics.

4.3. Perron-Frobenius strong threshold theorem for (A, B, P, φ) balanced bilinear model models without feedback

The following result, motivated by (A, B, P, φ) balanced bilinear models introduced in Section 4, is independent of the dimension of S and does not rely on rank-one assumptions. Previous constructions of endemic equilibria in this spirit were formulated only for particular cases; see for example [1,3,18], where explicit rank-one representations are used.

We show that such constructions may be replaced by a two-step procedure based on Perron–Frobenius theory. First, one determines S by solving the scalar equation

$$\rho(\widetilde{K}(S)) = 1,$$

where $\widetilde{K}(S)$ is the next-generation operator associated with the infected subsystem. Second, one recovers the infected equilibrium direction from a positive left Perron eigenvector of $\widetilde{K}(S)$, and determines its amplitude through the susceptible subsystem.

This yields a constructive characterization of endemic equilibria under the sole assumption that the infected Jacobian block admits a regular splitting and is irreducible. While the argument extends to all epidemiological models satisfying these conditions, we formulate it here for (A, B, P, φ) balanced bilinear models in order to relate it to subsequent results in the rank-one setting.

Theorem 6 (Perron-Frobenius strong threshold theorem for ABP models without feedback [`Per`])**.** *The purpose of this theorem is to characterize endemic equilibria of (A, B, P, φ) balanced bilinear models without any rank-one assumption on $\widetilde{G}$. It separates the nonlinear equilibrium computation into a spectral problem for S (finding the level at which $\rho(\widetilde{K}(S)) = 1$) and a linear Perron eigenvector problem for I (finding the invasion direction once that level is fixed). Unlike previous threshold theorems, which start from an already-constructed next-generation matrix, the threshold condition here is read directly off the transversal Jacobian on a siphon face – the next-generation matrix $\widetilde{K}$ is a derived object, not the starting point.*

Fix $S \in \mathbb{R}^m_{\geq 0}$, and consider the linear equilibrium equation

$$0 = AI + P\ \mathrm{Diag}(S)\, BI, \tag{4.6}$$

where A is Metzler–Hurwitz and $P, B \geq 0$. Introduce:

$$\widetilde{K}(S) := \widetilde{G}\ \mathrm{Diag}(S), \qquad \widetilde{G} := B(-A)^{-1}P,$$

and assume that $\widetilde{G}$ is irreducible. Epidemiologically, $\widetilde{G}$ is irreducible precisely when every infectious compartment can influence every other one through some chain of infection and internal transfer: disconnected disease stages, or disconnected host classes with no shared transmission or transfer route, are exactly what produce a reducible $\widetilde{G}$. Theorem 6(ii) guarantees a unique *Perron ray only in this irreducible case; when $\widetilde{G}$ is reducible, existence in part (i) still holds block by block on each irreducible component, but the ray in part (ii) need not be unique. Then:*

(i) For the fixed S, Equation (4.6) admits a nonzero solution $I>0$ if and only if

$$\rho(\widetilde{K}(S)) = 1.$$

In particular, $I = 0$ is always a solution of (4.6). Moreover, it is the unique nonnegative solution if and only if $\rho(\widetilde{K}(S)) < 1$.

(ii) *If* $\rho(\widetilde{K}(S)) = 1$ *and* $S \gg 0$*, then all nonzero nonnegative solutions of* (4.6) *form a one-dimensional positive ray:*

$$I = k\,(-A)^{-1}P\ \mathrm{Diag}(S)\,v(S), \qquad k > 0,$$

where $v(S) \gg 0$ *is a Perron eigenvector of* $\widetilde{K}(S)$*, unique up to multiplication by a positive scalar.*

(iii) *Let* $S_0 \gg 0$ *be the disease-free value, and set*

$$R_0 := \rho(\widetilde{K}(S_0)).$$

If $R_0 < 1$*, then for every* $0 \le S \le S_0$*,*

$$\rho(\widetilde{K}(S)) \le R_0 < 1.$$

Hence, for every $0 \le S \le S_0$*, equation* (4.6) *admits only the trivial nonnegative solution* $I = 0$*.*

(iv) *If* $R_0 = 1$*, then* S_0 *itself lies on the threshold hypersurface*

$$\rho(\widetilde{K}(S)) = 1.$$

(v) *If* $R_0 > 1$*, then there exists a unique equilibrium point on the ray* tS_0*,* $t \ge 0$*, with*

$$\bar{S} := \frac{1}{R_0}S_0,$$

and moreover

$$\rho(\widetilde{K}(\bar{S})) = 1.$$

(vi) *More generally, if* $S^* \gg 0$ *satisfies*

$$\rho(\widetilde{K}(S^*)) = 1,$$

then the I-equation determines a unique positive ray

$$I = k\,I_*(S^*), \qquad k > 0,$$

where

$$I_*(S^*) := (-A)^{-1}P\ \mathrm{Diag}(S^*)\,v(S^*).$$

Remark 11 ($\widetilde{K}$ is cyclic permutation of the next-generation matrix)**.** *At* $S = S_0$*, the operator* $\widetilde{K}(S_0)$ *is the cyclically permuted form of the usual next-generation matrix*

$$K(S_0) = P\ \mathrm{Diag}(S_0)\,B(-A)^{-1}.$$

Indeed,

$$\widetilde{K}(S_0) = B(-A)^{-1}P\ \mathrm{Diag}(S_0),$$

and the matrices $K(S_0)$ *and* $\widetilde{K}(S_0)$ *have the same nonzero spectrum. Hence*

$$R_0 = \rho(K(S_0)) = \rho(\widetilde{K}(S_0)).$$

This is why Theorem 6 applies also with the standard next generation matrix replacing $\widetilde{K}$*.*

4.4. What survives beyond rank one?

Theorem 6 is stated and proved without any rank-one assumption on $\widetilde{G}$; the table below records which of the paper's remaining results require it.

Result	**Arbitrary rank?**
Threshold ($\rho(\widetilde{K}) = 1$ characterization)	Yes (Theorem 6)
Endemic existence	Yes (Theorem 6(i))
Endemic uniqueness (Perron ray)	Only if $\widetilde{G}$ irreducible
Explicit closed-form endemic equilibrium	Rank one only (§5)
DFE Lyapunov function	Diagonal A_S only (Theorem 8); non-diagonal case open, cf. [6]
Determinant identity	Rank one, $m = 1$ only (Theorem 10)
Explicit Perron eigenvectors	Closed-form: rank one only; graph-combinatorial: any rank (§7)

In short, existence and instability/stability of the DFE are structural facts, valid at any rank; it is uniqueness, closed-form equilibria, and closed-form Lyapunov weights that are rank-one (or diagonal-A_S, or Kirchhoff-computable) phenomena.

Remark 12 (Meaning of the threshold ray)**.** *Fixing an $S^* \gg 0$ such that*

$$\begin{cases} 0 = AI + P\,\mathrm{Diag}(S^*)\,BI \\ \rho(\widetilde{K}(S^*)) = 1 \end{cases}$$

like in the last subpoint does not determine a unique equilibrium vector I, but only a one-dimensional positive ray

$$I = k\,I_*(S^*), \qquad k > 0,$$

where $I_*(S^*)$ is fixed up to normalization.

In particular:

- *the profile of the infected state (i.e. the ratios between components of I) is uniquely determined by the Perron eigenvector of $\widetilde{K}(S^*)$;*
- *the magnitude of I is not determined at the linear level, and remains free up to a positive scalar factor.*

Thus, at threshold, the system selects a unique infection pattern but not its amplitude. The latter is fixed only when coupling with the nonlinear S-equation.

Proof. Since A is Hurwitz, it is invertible, and since A is Metzler, one has

$$(-A)^{-1} \geq 0.$$

Thus (4.6) is equivalent to

$$I = (-A)^{-1}P\,\mathrm{Diag}(S)\,BI. \tag{4.7}$$

Applying B gives

$$u = \widetilde{K}(S)\,u, \qquad u := BI \geq 0. \tag{4.8}$$

To prove (i), suppose first that (4.6) admits a nonzero solution $I \geq 0$. Then $u = BI \neq 0$, and (4.8) shows that 1 is an eigenvalue of the nonnegative matrix $\widetilde{K}(S)$ with a nonzero nonnegative eigenvector. Hence

$$\rho(\widetilde{K}(S)) = 1.$$

Conversely, assume that $\rho(\widetilde{K}(S)) = 1$ and let $v(S) \geq 0$, $v(S) \neq 0$, satisfy

$$\widetilde{K}(S)\, v(S) = v(S).$$

Define

$$I^* := (-A)^{-1} P \ \mathrm{Diag}(S)\, v(S) \geq 0.$$

Then

$$BI^* = \widetilde{K}(S)\, v(S) = v(S),$$

and therefore (4.7) holds for I^*. Thus I^* is a nonzero nonnegative solution of (4.6). This proves (i).

For (ii), assume that $\rho(\widetilde{K}(S)) = 1$ and $S \gg 0$. Since

$$\widetilde{K}(S) = \widetilde{G}\ \mathrm{Diag}(S),$$

and $\mathrm{Diag}(S)$ is positive diagonal, $\widetilde{K}(S)$ has the same zero pattern as $\widetilde{G}$, hence is irreducible. By Perron–Frobenius, the eigenspace of $\widetilde{K}(S)$ for the eigenvalue $1 = \rho(\widetilde{K}(S))$ is one-dimensional and generated by a vector $v(S) \gg 0$, unique up to multiplication by a positive scalar.

Let $I \geq 0$, $I \neq 0$, solve (4.6), and set $u = BI$. Then $u \neq 0$ and (4.8) gives

$$u = \widetilde{K}(S)\, u.$$

Hence $u = k\, v(S)$ for some $k > 0$. Substituting into (4.7) yields

$$I = k\, (-A)^{-1} P \ \mathrm{Diag}(S)\, v(S).$$

Conversely, every vector of this form satisfies (4.7). This proves (ii).

For (iii), if $0 \leq S \leq S_0$, then

$$\mathrm{Diag}(S) \leq \mathrm{Diag}(S_0),$$

hence

$$\widetilde{K}(S) = \widetilde{G}\ \mathrm{Diag}(S) \leq \widetilde{G}\ \mathrm{Diag}(S_0) = \widetilde{K}(S_0)$$

entrywise, because $\widetilde{G} \geq 0$. By monotonicity of the spectral radius on nonnegative matrices,

$$\rho(\widetilde{K}(S)) \leq \rho(\widetilde{K}(S_0)) = R_0 < 1.$$

The last statement follows from (i).

Part (iv) is immediate from the definition of R_0.

For (v), if $t \geq 0$, then

$$\widetilde{K}(tS_0) = \widetilde{G}\ \mathrm{Diag}(tS_0) = t\,\widetilde{G}\ \mathrm{Diag}(S_0) = t\,\widetilde{K}(S_0),$$

so

$$\rho(\widetilde{K}(tS_0)) = t\, R_0.$$

Hence $\rho(\widetilde{K}(tS_0)) = 1$ if and only if $t = 1/R_0$, and therefore the threshold hypersurface is met on the ray tS_0 at the unique point $\bar{S} = S_0/R_0$.

Finally, (vi) is an immediate application of (ii) with $S = S^*$. Thus existence and – once $\widetilde{G}$ is irreducible – uniqueness of the endemic ray, are both consequences of the single spectral condition $\rho(\widetilde{K}(S)) = 1$, with no rank-one or other structural assumption beyond irreducibility. □

Remark 13 (DFE corollary for the coupled model)**.** *For the coupled balanced bilinear system*

$$\begin{cases} S' = \Lambda + A_S S - \mathrm{Diag}(S)\, BI + CI, \\ I' = AI + P\ \mathrm{Diag}(S)\, BI, \end{cases} \qquad S_0 = -A_S^{-1}\Lambda,$$

with A_S Metzler–Hurwitz, Theorem 6(iii) provides the existence/uniqueness part of the disease-free analysis: if $R_0 < 1$, then for every $0 \le S \le S_0$ the I-equation admits only the trivial nonnegative solution $I = 0$. Thus $(S_0, 0)$ is the unique disease-free equilibrium. The additional stability statement for the full coupled system is then obtained by linearization of the (S, I)-system at $(S_0, 0)$.

Remark 14 (Spectral mechanism and CEP reduction)**.** *Theorem 6 isolates the essential structure of the equilibrium problem*

$$\rho(\widetilde{K}(S)) < 1 \iff I = 0, \qquad \rho(\widetilde{K}(S)) = 1 \iff \exists\, I \neq 0.$$

Hence every nontrivial equilibrium must lie on the hypersurface

$$\rho(\widetilde{K}(S)) = 1.$$

On this hypersurface, the I-equation determines a unique positive ray

$$I = k\, I_*(S), \qquad k > 0.$$

Thus the equilibrium problem separates into two steps:

$$\textit{(i) solve } \rho(\widetilde{K}(S)) = 1, \qquad \textit{(ii) determine the scalar } k \textit{ from the } S\textit{-equation.}$$

In particular, if the spectral equation admits a unique solution $S^* \gg 0$, then the only remaining unknown is the scalar amplitude k. This is the precise form of the CEP mechanism beyond rank one.

Remark 15 (Loop interpretation)**.** *The operator*

$$\widetilde{K}(S) = B(-A)^{-1} P\ \mathrm{Diag}(S)$$

represents one full circulation through the positive feedback loop

$$I \xrightarrow{B} \mathbb{R}^m \xrightarrow{\mathrm{Diag}(S)} \mathbb{R}^m \xrightarrow{P} \mathbb{R}^n \xrightarrow{(-A)^{-1}} \mathbb{R}^n.$$

If $z = BI$, then the equilibrium condition becomes

$$z = \widetilde{K}(S)\, z.$$

Thus $\rho(\widetilde{K}(S)) = 1$ expresses exact balance between dissipation through A and amplification through the feedback loop. This is the structural origin of the threshold.

The general theory developed so far ends with the transversal Jacobian and its Perron eigenvectors: existence and stability of the endemic equilibrium are governed by the spectral radius and Perron directions of $\widetilde{K}$, valid for an arbitrary regular splitting, with no further structural assumption on B, P, or A. Rank-one models become exceptional precisely because, in this class, all of the Perron quantities involved – the endemic equilibrium itself, the Perron eigenvectors, and the resulting Lyapunov coefficients – become completely explicit, rather than merely existing abstractly. This is why Section 5 below switches register, from qualitative Perron–Frobenius statements to closed-form formulas.

5. Seven explicit formulas for rank one (A, B, P, φ) balanced bilinear models without linear feedback matrix C

5.1. The computation of the DFE and EE for rank one (A, B, P, φ) balanced bilinear models without linear feedback matrix C

Theorem 7 (Explicit consequences of the Perron-Frobenius strong threshold theorem for rank-one [Exp])**.** *For any rank-one (A, B, P, φ) balanced bilinear model* (4.4) *satisfying Hypothesis 1, there exists a unique endemic equilibrium $(\bar{I}, \bar{S})$ with strictly positive coordinates if and only if $R_0 > 1$. Moreover, the following four laws hold:*

1. ***First Law: Basic Reproduction Number [2, (3.2)], [3, (6)]*** *R_0 may be written as:*

$$R_0 = S_0 \mathcal{R}, \tag{5.1}$$

where $\mathcal{R} \in \mathbb{R}^m_+$ is the replacement vector of Definition 11 below.

Definition 11 (Replacement vector [Rep])**.** *The* **replacement vector** *$\mathcal{R} \in \mathbb{R}^m_{\geq 0}$ is given by*

$$\mathcal{R} := \begin{cases} B(-A)^{-1}\boldsymbol{\alpha} & \textit{Case (P)}, \\ \mathrm{Diag}(\boldsymbol{\alpha}_m)\,[\vec{\boldsymbol{\beta}}(-A)^{-1}P]^\top & \textit{Case (B)}, \end{cases} \tag{5.2}$$

equivalently in Case (B): $\mathcal{R}_i = (\boldsymbol{\alpha}_m)_i \vec{\boldsymbol{\beta}}(-A)^{-1} p_i$, $i = 1, \ldots, m$, where p_i is the i-th column of P.

Remark 16. *$\mathcal{R}$ is the vector whose ith component is the expected number of infections generated by a single susceptible individual in class i.*

2. ***Second Law: $\bar{I}$ is proportional to right eigenvector and "dwell times" [2, (3.5)]***

$$\bar{I} = k\,(-A)^{-1}\boldsymbol{\alpha}_{\mathrm{eff}}, \qquad \boldsymbol{\alpha}_{\mathrm{eff}} := \begin{cases} \boldsymbol{\alpha}_n & \textit{Case (P)}, \\ P\,\mathrm{Diag}(\bar{S})\boldsymbol{\alpha}_m & \textit{Case (B)}. \end{cases} \tag{5.3}$$

In Case (P), $D_w := (-A)^{-1}\boldsymbol{\alpha}_n$ is a fixed vector (independent of the equilibrium), so the direction of $\bar{I}$ is constant, determined by these parameters alone.

Definition 12 (dwell times)**.** *For any Metzler-Hurwitz matrix A, or, equivalently, for any finite-space irreducible CTMC with absorbing states and transitions between the transient states encapsulated in a matrix A, dwell times are the (positive) elements of $(-A)^{-1}$.*

(This name, used in the theory of Markov processes, and which has also been useful in mathematical epidemiology– see for example [37, 38], is explained by the well-known fact that these are precisely the means (averages) of times before absorption, conditioned on both a starting point and a last point before absorption).

$D_w = (-A)^{-1}\boldsymbol{\alpha}_n$ *may be interpreted as "expected infection times until recovery", starting in the first state with law* $\boldsymbol{\alpha}_n$*.*

3. ***Third Law: Endemic $\bar{S}$ as function of the normalization constant***

$$\bar{S} = \left(\mathrm{Diag}[B\bar{I}] - A_S\right)^{-1}\Lambda = \left(k\,\mathrm{Diag}[\boldsymbol{a}] - A_S\right)^{-1}\Lambda, \qquad \boldsymbol{a} := \begin{cases} \mathcal{R} & \textit{Case (P)}, \\ \boldsymbol{\alpha}_m & \textit{Case (B)} \end{cases} \tag{5.4}$$

holds, whenever the intervening matrix is invertible.

4. ***Fourth Law: $\bar{S}$ normalization [2, (3.6)], [3, (4)]*** *Define now, whenever the intervening matrix is invertible,*

$$H(k) := \mathcal{R}\left(k\,\mathrm{Diag}[\boldsymbol{a}] - A_S\right)^{-1}\Lambda. \tag{5.5}$$

Then

$$\rho(K(\bar{S}(k))) = H(k), \tag{5.6}$$

and the normalization constant $k = \bar{S}B\bar{I}$ *is the unique positive solution of*

$$H(k) = 1; \tag{5.7}$$

equivalently,

$$\bar{S}(k)\mathcal{R} = 1.$$

When $A_S = -\mathrm{Diag}(\mu_S)$ *for example,* $H(k) = \sum_j \frac{\mathcal{R}_j \Lambda_j}{k\,a_j + \mu_j}$*, and for* $n = m = 1$*:*

$$\bar{S} = \frac{1}{\mathcal{R}}, \qquad k = \mu_S \bar{S}(R_0 - 1) = \Lambda - \frac{\mu_S}{\mathcal{R}}. \tag{5.8}$$

Remark 17. *When* $m > 1$*,* k *is in general not rational, making an explicit determination of* $(\bar{I}, \bar{S})$ *difficult.*

Proof. **Step 1.** The argument follows [2, (3.4–3.7)]; we give it uniformly for both cases. Let $F(\bar{S}) = \boldsymbol{u}_e\,\vec{\boldsymbol{w}}_e$ be the rank-one factorisation at the EE, where

Case (P): $\boldsymbol{u}_e = \boldsymbol{\alpha}$, $\vec{\boldsymbol{w}}_e = \bar{S}B$; Case (B): $\boldsymbol{u}_e = P\,\mathrm{Diag}(\bar{S})\boldsymbol{\alpha}_m$, $\vec{\boldsymbol{w}}_e = \vec{\boldsymbol{\beta}}$.

Step 2. At the EE, $I' = 0$ gives

$$(F(\bar{S}) + A)\bar{I} = 0,$$

hence

$$\boldsymbol{u}_e(\vec{\boldsymbol{w}}_e\bar{I}) = -A\bar{I}.$$

Therefore

$$\bar{I} = k(-A)^{-1}\boldsymbol{u}_e, \qquad k := \vec{\boldsymbol{w}}_e\bar{I} > 0, \tag{5.9}$$

which is (5.3).
Step 3. The equation $S' = 0$ gives

$$\bar{S} = (\mathrm{Diag}[B\bar{I}] - A_S)^{-1}\Lambda.$$

Using

$$B\bar{I} = k\,B(-A)^{-1}\boldsymbol{\alpha} = k\mathcal{R} \qquad \text{in Case (P)},$$

and

$$B\bar{I} = \boldsymbol{\alpha}_m\vec{\boldsymbol{\beta}}\bar{I} = k\boldsymbol{\alpha}_m \qquad \text{in Case (B)},$$

yields

$$\bar{S}(k) = (k\,\mathrm{Diag}[\boldsymbol{a}] - A_S)^{-1}\,\Lambda,$$

which is (5.4).
Step 4. Multiplying (5.9) by $\vec{\boldsymbol{w}}_e$ gives

$$k = k\,\vec{\boldsymbol{w}}_e(-A)^{-1}\boldsymbol{u}_e.$$

Since $k > 0$, division by k yields

$$\vec{\boldsymbol{w}}_e(-A)^{-1}\boldsymbol{u}_e = 1.$$

In both cases this is exactly

$$\bar{S}\,\mathcal{R} = 1.$$

Substituting $\bar{S} = \bar{S}(k)$ gives

$$H(k) = \mathcal{R}\,(k\,\mathrm{Diag}[\boldsymbol{a}] - A_S)^{-1}\,\Lambda = 1.$$

Step 5. Since $K(\bar{S})$ has rank one, its unique nonzero eigenvalue equals its trace. In both cases this gives

$$\rho(K(\bar{S})) = \bar{S}\,\mathcal{R}.$$

Therefore, for $\bar{S} = \bar{S}(k)$,

$$\rho(K(\bar{S}(k))) = \vec{\mathcal{R}}\,(k\,\mathrm{Diag}[\boldsymbol{a}] - A_S)^{-1}\,\Lambda = H(k),$$

which is (5.6). Hence the Perron condition

$$\rho(K(\bar{S}(k))) = 1$$

is equivalent to the normalization law

$$H(k) = 1,$$

or equivalently $\bar{S}(k)\mathcal{R} = 1$.
Step 6. Uniqueness of the positive solution follows since H is strictly decreasing,

$$\lim_{k\to\infty} H(k) = 0, \qquad H(0) = R_0 > 1.$$

□

Fifth Law: An explicit Lyapunov function establishing global asymptotic stability of the DFE for rank-one balanced bilinear model (Case P) when $R_0 < 1$.

The following result is for Case (P) ($P = \boldsymbol{\alpha}_n \vec{\mathbf{1}}$).

Theorem 8 (Stability of DFE for (P) rank-one balanced bilinear models [Sta])**.** *For an I-S ODE*

$$\begin{cases} S' = \varphi(S) - \mathrm{Diag}[S]\, BI, \\ I' = [\boldsymbol{\alpha}_n S\, B + A]\, I, \end{cases}$$

let R_0 be defined by the natural regular splitting of the Jacobian matrix of the invasion vector field with respect to the invasion variables into $\boldsymbol{\alpha}_n S\, B$ and A. The following holds:

- *If $R_0 > 1$, then the disease-free equilibrium is unstable.*
- *If $R_0 \leq 1$, and $A_S = -\mathrm{Diag}(\mu_S)$ is a strictly negative diagonal matrix, then*

$$V_{DF}(I, S) = R_0 \left(\vec{\mathbf{1}} S - S_0 \ln(S)\right) + S_0 B(-A)^{-1} I \tag{5.10}$$

is a Lyapunov function, whose minimum is attained uniquely at the DFE, which is therefore globally asymptotically stable.

Remark 18 (Lyapunov weights are related to the left NGM eigenvector)**.** *The function* (5.10) *is of the form*

$$\mu H(S) + L(I), \qquad \mu = R_0,$$

with tangential Goh–Volterra–Horn–Jackson term

$$H(S) = \vec{\mathbf{1}} S - S_0 \ln(S)$$

and with transversal Perron term

$$L(I) = S_0 B(-A)^{-1}, I,$$

whose weights are a left Perron eigenvector of $K(S_0) = F(S_0)(-A)^{-1}$ in both cases (P) and (B).

Proof of Theorem 8. At the DFE one has

$$S_0 = (-A_S)^{-1}\Lambda, \qquad A_S = -\mathrm{Diag}(\mu_S),$$

hence

$$\Lambda = \mathrm{Diag}(\mu_S) S_0, \qquad \varphi(S) = \Lambda + A_S S = -\mathrm{Diag}(\mu_S)(S - S_0).$$

Set

$$H(S) := \vec{\mathbf{1}} S - S_0 \ln(S), \qquad L(I) := S_0 \Pi I, \qquad \Pi := B(-A)^{-1}.$$

Then

$$V_{DF}(I, S) = R_0\, H(S) + L(I).$$

We compute the two derivatives separately.

First,

$$\dot{W} = \vec{\mathbf{1}}\, S' - S_0 \frac{S'}{S} = \vec{\mathbf{1}}(\varphi(S) - \mathrm{Diag}(S) BI) - S_0 \frac{\varphi(S) - \mathrm{Diag}(S) BI}{S}.$$

Since

$$\vec{\mathbf{1}}\,\mathrm{Diag}(S)BI = S\,BI, \qquad S_0\frac{\mathrm{Diag}(S)BI}{S} = S_0\,BI,$$

this gives

$$\dot{W} = \vec{\mathbf{1}}\varphi(S) - S_0\frac{\varphi(S)}{S} - S\,BI + S_0\,BI.$$

Next,

$$\dot{Q} = S_0\Pi I' = S_0\Pi(\alpha_n S\,B + A)I = S_0\Pi\alpha_n\,S\,BI + S_0\Pi AI.$$

Using

$$R_0 = S_0\Pi\alpha_n, \qquad \Pi A = B(-A)^{-1}A = -B,$$

we obtain

$$\dot{Q} = R_0\,S\,BI - S_0\,BI.$$

Therefore

$$\dot{V}_{DF} = R_0\dot{W} + \dot{Q} = R_0\Big(\vec{\mathbf{1}}\varphi(S) - S_0\frac{\varphi(S)}{S}\Big) + (R_0 - 1)S_0\,BI.$$

Since

$$\vec{\mathbf{1}}\varphi(S) - S_0\frac{\varphi(S)}{S} = (S - S_0)\frac{\varphi(S)}{S},$$

and

$$\varphi(S) = -\,\mathrm{Diag}(\mu_S)(S - S_0),$$

it follows that

$$\dot{V}_{DF} = -R_0\sum_j \frac{\mu_{S,j}(S_j - S_{0,j})^2}{S_j} + (R_0 - 1)S_0\,BI. \tag{5.11}$$

If $R_0 < 1$, both terms in (5.11) are nonpositive, with equality only if

$$S = S_0, \qquad I = 0.$$

Hence V_{DF} is a strict Lyapunov function and the DFE is globally asymptotically stable.

If $R_0 = 1$, then

$$\dot{V}_{DF} = -\sum_j \frac{\mu_{S,j}(S_j - S_{0,j})^2}{S_j} \leq 0.$$

On the set $\{\dot{V}_{DF} = 0\}$ one has $S = S_0$, and then

$$0 = S' = -\,\mathrm{Diag}(S_0)BI,$$

so $BI = 0$. Therefore

$$I' = AI.$$

Since A is Hurwitz, the only invariant point is $I = 0$. By LaSalle's invariance principle, the DFE is globally asymptotically stable when $R_0 = 1$.

If $R_0 > 1$, the unstable infected block has spectral bound $\lambda_{\max}(J_{DFE}) > 0$, where $\lambda_{\max}(J_{DFE})$ is the largest real part of eigenvalues of Jacobian of infected equations with respect to infected variables, evaluated at the DFE, so the DFE is unstable. □

Remark 19 (Role of the diagonal hypothesis on A_S)**.** *Diagonality of A_S is used at exactly one step of the proof, and is essential to it. Writing $\varphi(S) = A_S(S - S_0)$ for a general (not necessarily diagonal) stable Metzler A_S, the tangential term becomes*

$$\vec{\mathbf{1}}\varphi(S) - S_0\frac{\varphi(S)}{S} = \sum_j (S_j - S_{0,j})\frac{\varphi_j(S)}{S_j} = \sum_{j,k}(A_S)_{jk}\frac{(S_j - S_{0,j})(S_k - S_{0,k})}{S_j}.$$

When $A_S = -\mathrm{Diag}(\mu_S)$, this collapses to the manifestly nonpositive sum of squares $-\sum_j \mu_{S,j}(S_j - S_{0,j})^2/S_j$ used in (5.11)*. For a general Metzler A_S, it is instead an indefinite quadratic form in $S - S_0$, weighted by $1/S_j$, whose sign is not controlled merely by A_S being Metzler and Hurwitz. Extending* (5.10) *to non-diagonal A_S therefore requires replacing the unweighted entropy $H(S) = \mathbf{1}^\top S - S_0 \ln(S)$ by a weighted one, $\sum_j c_j(S_j - S_{0,j}\ln S_j)$, with weights c chosen (e.g. as a left Perron or graph-cofactor vector of $-A_S$, in the spirit of Section 7) so that the resulting quadratic form becomes negative semidefinite. This construction is not carried out here; see the open problems of Section 8.*

Sixth Law: A Lyapunov function establishing the global stability of the endemic equilibrium for rank–one balanced bilinear models with one–susceptible class.

The works [1–3] suggested the natural question of the existence of an explicit Lyapunov function which establishes the global stability of the EE of rank-one balanced bilinear models when $R_0 > 1$. They offered a positive answer for the case where A is bidiagonal. More recently, Earn and McCluskey [5] showed that this restriction is unnecessary when $m = 1$, by exploiting Volterra-type entropy identities.

Theorem 9 (GAS of the EE for rank-one balanced bilinear models with one susceptible class [`GAS`])**.** *Consider*

$$\begin{cases} S' = \Lambda - \mu_S S - S\,\vec{\boldsymbol{\beta}} I, \\ I' = (S\,\boldsymbol{\alpha}\vec{\boldsymbol{\beta}} + A)I, \end{cases} \qquad S \in \mathbb{R}_+,\ I \in \mathbb{R}_+^n, \tag{5.12}$$

where $\boldsymbol{\alpha} \in \mathbb{R}_+^n$ satisfies $\vec{1}\,\boldsymbol{\alpha} = 1$, $\vec{\boldsymbol{\beta}} \in \mathbb{R}_+^{1\times n}$ is not identically zero, and A is Metzler and Hurwitz. If $R_0 > 1$, the endemic equilibrium $(\bar{S}, \bar{I}) \in \mathbb{R}_{>0} \times \mathbb{R}^n_{>0}$ is globally asymptotically stable on $\mathbb{R}_+^{n+1} \setminus \{I = 0\}$. A Lyapunov function is (5.14) *with weights $\vec{a} = \bar{S}\,\vec{\boldsymbol{\beta}}(-A)^{-1} \geq 0$.*

Proof. The endemic equilibrium is unique and satisfies

$$\Lambda = \mu_S \bar{S} + \bar{S}\,\vec{\boldsymbol{\beta}}\bar{I}, \qquad A\bar{I} = -\boldsymbol{\alpha}\,\bar{S}\,\vec{\boldsymbol{\beta}}\bar{I}. \tag{5.13}$$

Let $G(\theta) = \theta - 1 - \ln\theta$ and define

$$V(S, I) = \bar{S}\,G\Big(\frac{S}{\bar{S}}\Big) + \sum_{k=1}^{n} a_k\,\bar{I}_k\,G\Big(\frac{I_k}{\bar{I}_k}\Big). \tag{5.14}$$

Set $s = S/\bar{S}$ and $y_k = I_k/\bar{I}_k$. Then

$$\dot{V} = (1 - \tfrac{1}{s})S' + \sum_{k=1}^{n} a_k(1 - \tfrac{1}{y_k})I_k'. \tag{5.15}$$

Step 1: the S-term. Using (5.13) and the identity $(A-B)\sum_i T_i$ with zero-sum equilibrium weights, one obtains

$$(1-\tfrac{1}{s})S' = -\Lambda\, G(1/s) - \mu_S \bar{S}\, G(s) + \sum_{j=1}^{n} \bar{S}\beta_j \bar{I}_j [G(y_j) - G(y_j s)]. \tag{5.16}$$

Step 2: the I-terms. Using (5.13),

$$(1-\tfrac{1}{y_k})I_k' = \sum_j \alpha_k \bar{S}\beta_j \bar{I}_j (1-\tfrac{1}{y_k})(y_j s - y_k) + \sum_j A_{kj}\bar{I}_j (1-\tfrac{1}{y_k})(y_j - y_k). \tag{5.17}$$

Applying the entropy identity $(A_1 - A_2)(B_1 - B_2)$ to each term yields

$$(1-\tfrac{1}{y_k})I_k' = \sum_j \alpha_k \bar{S}\beta_j \bar{I}_j [G(y_j s) - G(y_k) - G(y_j s/y_k)] + \sum_j A_{kj}\bar{I}_j [G(y_j) - G(y_k) - G(y_j/y_k)]. \tag{5.18}$$

Step 3: cancellation. Summing (5.16) and $\sum_k a_k$ times (5.18), cancellation of all $G(y_\ell)$ terms requires

$$\vec{a}A = -\bar{S}\vec{\boldsymbol{\beta}}, \tag{5.19}$$

which has the unique solution

$$\vec{a} = \bar{S}\,\vec{\boldsymbol{\beta}}(-A)^{-1} \geq 0. \tag{5.20}$$

The $G(y_\ell s)$ terms cancel since $\vec{a}\boldsymbol{\alpha} = \bar{S}\,\vec{\boldsymbol{\beta}}(-A)^{-1}\boldsymbol{\alpha} = \bar{S}\,\mathcal{R} = 1$.

Thus

$$\dot{V} = -\Lambda\, G(1/s) - \mu_S \bar{S}\, G(s) - \sum_{i,j} c_{ij}\, G\Big(\frac{y_j}{y_i}\Big) - \sum_{i,j} d_{ij}\, G\Big(\frac{y_j s}{y_i}\Big), \tag{5.21}$$

with $c_{ij}, d_{ij} \geq 0$. Hence $\dot{V} \leq 0$ on $\mathbb{R}^{n+1}_{>0}$.

Moreover, $\dot{V} = 0$ implies $s = 1$ and $y_j = y_i$ for all i, j, hence $I = \bar{I}$. By LaSalle's invariance principle, $(\bar{S}, \bar{I})$ is globally asymptotically stable on $\mathbb{R}^{n+1}_{+} \setminus \{I = 0\}$. □

Remark 20 (Relay relation between DFE and EE Lyapunov weights)**.** *With $m = 1$, the endemic equilibrium satisfies $\bar{S} = 1/\mathcal{R}$ (Fourth Law, (5.8)), which is C-independent. Denoting $\vec{a}_0 := S_0 B(-A)^{-1}$ the DFE Lyapunov weight (Remark 10), the EE Lyapunov weight $\vec{a}$ satisfies the* relay relation

$$\vec{a} = \bar{S}\; B(-A)^{-1}.$$

Thus the EE and DFE Lyapunov weights are proportional, related by the C-independent scalar $S_0/\bar{S} = S_0\mathcal{R} = R_0$, and are in fact equal if their Volterra parts are assumed to have the same dependence in S (but with different $S_0, \bar{S}$).

Seventh Law: A determinant law for rank–one balanced bilinear models with one–susceptible class.

The determinant identity proved in [12] for the Susceptible-Asymptomatic-Infectious-Recovered (SAIR) model

$$\det(J_{EE}) = -\det(J_{DFE}),$$

extends to the whole class of rank–one balanced bilinear models with one susceptible class (in this case (P) and (B) coincide):

$$\begin{cases} S' = \Lambda - \mu_S S - S\,\vec{\boldsymbol{\beta}} I, \\ I' = \boldsymbol{\alpha} S\,\vec{\boldsymbol{\beta}} I + AI, \end{cases} \qquad \boldsymbol{\alpha} \in \mathbb{R}^n_+,\ \vec{\mathbf{1}}\boldsymbol{\alpha} = 1, \tag{5.22}$$

with A Metzler–Hurwitz.

Theorem 10 (Determinant law [Det]). *Consider* (5.22)*, and assume* $R_0 > 1$*, where*

$$R_0 = \frac{\Lambda}{\mu_S}\vec{\boldsymbol{\beta}}(-A)^{-1}\boldsymbol{\alpha}.$$

Let J_{DFE} and J_{EE} denote the Jacobians at the disease–free and endemic equilibria. Then

$$\det(J_{EE}) = -\det(J_{DFE}). \tag{5.23}$$

More explicitly,

$$\det(J_{DFE}) = -\mu_S \det(A)\,(1 - R_0), \qquad \det(J_{EE}) = \mu_S \det(A)\,(1 - R_0). \tag{5.24}$$

Proof. At the DFE, $S_0 = \Lambda/\mu_S$ and $I = 0$, hence

$$J_{DFE} = \begin{pmatrix} -\mu_S & -S_0\vec{\boldsymbol{\beta}} \\ 0 & A + S_0\boldsymbol{\alpha}\vec{\boldsymbol{\beta}} \end{pmatrix},$$

so

$$\det(J_{DFE}) = -\mu_S\ \det(A + S_0\boldsymbol{\alpha}\vec{\boldsymbol{\beta}}).$$

By the matrix determinant lemma,

$$\det(A + S_0\boldsymbol{\alpha}\vec{\boldsymbol{\beta}}) = \det(A)(1 + S_0\vec{\boldsymbol{\beta}}A^{-1}\boldsymbol{\alpha}).$$

Since

$$R_0 = S_0\vec{\boldsymbol{\beta}}(-A)^{-1}\boldsymbol{\alpha} = -S_0\vec{\boldsymbol{\beta}}A^{-1}\boldsymbol{\alpha},$$

it follows that

$$\det(A + S_0\boldsymbol{\alpha}\vec{\boldsymbol{\beta}}) = \det(A)(1 - R_0),$$

which yields the first identity in (5.24).

At the endemic equilibrium $(\bar{S}, \bar{I})$, define $q^* := \vec{\boldsymbol{\beta}}\bar{I}$. Then

$$J_{EE} = \begin{pmatrix} -\mu_S - q^* & -\bar{S}\vec{\boldsymbol{\beta}} \\ q^*\boldsymbol{\alpha} & A + \bar{S}\boldsymbol{\alpha}\vec{\boldsymbol{\beta}} \end{pmatrix}.$$

Perform the row operation $R_{i+1} \mapsto R_{i+1} + \boldsymbol{\alpha}_i R_1, i = 1, ..., n$ to obtain

$$\widetilde{J}_{EE} = \begin{pmatrix} -\mu_S - q^* & -\bar{S}\vec{\boldsymbol{\beta}} \\ -\mu_S\boldsymbol{\alpha} & A \end{pmatrix}.$$

Hence, by Schur's formula

$$\det(J_{EE}) = \det(A)\Big(-\mu_S - q^* - (-\bar{S}\vec{\boldsymbol{\beta}})A^{-1}(-\mu_S \boldsymbol{\alpha})\Big).$$

Using the endemic identity

$$A\bar{I} = -\boldsymbol{\alpha}\,\bar{S}\,\vec{\boldsymbol{\beta}}\bar{I},$$

we obtain

$$\det(J_{EE}) = \det(A)(-\mu_S - q^* + \mu_S) = -q^* \det(A).$$

From $0 = \Lambda - \mu_S\bar{S} - \bar{S}q^*$ and $\bar{S} = S_0/R_0$, it follows that $q^* = \mu_S(R_0 - 1)$, hence

$$\det(J_{EE}) = \mu_S(1 - R_0)\det(A),$$

which proves (5.23). □

Remark 21 (Index interpretation)**.** *Assume that all equilibria are hyperbolic. The local index of an equilibrium is* sign(det J).

At the DFE,

$$\det(J_{DFE}) = -\mu_S \det(A)(1 - R_0),$$

and since A is Hurwitz, $\det(A) = (-1)^n|\det(A)|$. *Thus the index of the DFE changes sign at $R_0 = 1$.*

At the EE,

$$\det(J_{EE}) = -\det(J_{DFE}),$$

so the two equilibria have opposite index.

This is consistent with degree theory: on any positively invariant compact region of $\mathbb{R}_+^{n+1}$ containing both equilibria and no others, the sum of indices is zero. Hence the appearance of the endemic equilibrium at $R_0 = 1$ is accompanied by a sign change of the Jacobian determinant, and the two equilibria necessarily have opposite stability types.

Remark 22 (Limitations)**.** *The identity* $\det(J_{EE}) = -\det(J_{DFE})$ *relies on:*

1. *the rank–one infection structure $\boldsymbol{\alpha}\,S\,\vec{\boldsymbol{\beta}}I$;*
2. *the single susceptible equation, which allows elimination of the rank–one perturbation at the EE.*

For multi–susceptible systems, this mechanism fails and no general determinant sign law is expected.

6. Effect of feedback CI in S' on the seven laws, case (P)

Theorem 11 (Effect of feedback CI in S' on the seven laws, case (P) [`Eff`])**.** *Consider the* (A, B, P, φ) *balanced bilinear model* (4.1) *with recovery feedback $C \in \mathbb{R}_+^{m\times n}$, $m \geq 1$. Since CI vanishes at the DFE and leaves the infection subsystem invariant, the DFE S_0, $\mathcal{R} = B(-A)^{-1}\boldsymbol{\alpha}$, $R_0 = S_0\mathcal{R}$, the normalization $\boldsymbol{y}_e\mathcal{R} = 1$, and $D_w = (-A)^{-1}\boldsymbol{\alpha}$ are C-independent and unchanged. The direction of $\bar{I}$* (5.3)*, $\bar{I} \propto D_w$, is also preserved.*

The modifications are:

1. ***For any*** $m > 1$ ***(Case P).*** *The modified Law 3:*

$$\bar{S} = (k\ \mathrm{Diag}[\mathcal{R}] - A_S)^{-1}(\Lambda + C\bar{I}), \qquad \bar{I} = kD_w. \tag{6.1}$$

The normalization condition $\vec{y}\mathcal{R} = 1$ *yields*

$$H_C(k) := \vec{\mathbf{1}}\mathcal{R}(k\ \mathrm{Diag}[\mathcal{R}] - A_S)^{-1}(\Lambda + kCD_w) = 1. \tag{6.2}$$

If $R_0 > 1$*, at least one positive solution of* (6.2) *exists.*

If, moreover,

$$\|CD_w\|_\infty < \frac{\min_i \mu_{S,i}}{\max_i \mathcal{R}_i}, \tag{6.3}$$

then (6.2) *admits a unique positive solution.*

2. ***For*** $m = 1$***,*** *the system* (4.1) *becomes*

$$\begin{cases} S' = \Lambda - \mu_S S - S\,\vec{\boldsymbol{\beta}} I + CI, \\ I' = \left[S\,\boldsymbol{\alpha}\vec{\boldsymbol{\beta}} + A\right] I, \end{cases} \qquad C \in \mathbb{R}_+^{1\times n}. \tag{6.4}$$

Laws 0–5 and 7 are unchanged. Only Law 6 is affected: the derivative of the EE Lyapunov function acquires the additional term

$$\Big(1 - \frac{\bar{S}}{S}\Big)\sum_j C_j I_j,$$

so global asymptotic stability of the EE is no longer automatic.

Conjectures and observations

1. **[Loss of monotonicity]:** Let $D = \mathrm{Diag}[\mathcal{R}]$ and $M(k) = (kD - A_y)^{-1}$. Then

$$H_C(k) = \vec{\mathbf{1}}\mathcal{R}\,M(k)\Lambda + k\,\vec{\mathbf{1}}\mathcal{R}\,M(k)CD_w.$$

The first term is strictly decreasing, while the second is nonnegative but not monotone in general. Hence H_C need not be monotone, in contrast with the case $C = 0$.

2. **[Multiplicity of endemic equilibria]:** When (6.3) fails, H_C may admit several positive roots, corresponding to several endemic equilibria. Thus uniqueness of the EE is no longer structural.

3. **[Backward bifurcation mechanism]:** Backward bifurcation may occur: (6.2) may admit a positive solution even when $R_0 < 1$. A sufficient mechanism is the existence of $k_1, k_2 > 0$ such that

$$H_C(k_1) > 1, \qquad H_C(k_2) < 1,$$

which implies, by continuity, at least one solution of (6.2).

4. **[Index and determinant interpretation in the one–susceptible case]:** In the one–susceptible case $m = 1$, each positive root of (6.2) yields an endemic equilibrium. Thus loss of monotonicity of H_C is the scalar signature of multiplicity of endemic equilibria.

   When the corresponding equilibria are hyperbolic, changes in the number of positive roots are accompanied by changes of local index, and hence by sign changes of the Jacobian determinant. In particular, saddle–node creation or annihilation of endemic equilibria corresponds to a zero of the Jacobian determinant along the endemic branch. This connects the feedback mechanism studied here with the determinant and index considerations of the previous subsection.

5. **[Scalar reduction, index, and saddle–node mechanism]:** In the one–susceptible case $m = 1$, the endemic equilibria are in one-to-one correspondence with the positive roots of the scalar equation (6.2). Thus the feedback problem reduces to the study of the real function $H_C(k) - 1$.

   Assume that the corresponding equilibria are hyperbolic. Then each simple root k^* of (6.2) defines an equilibrium whose local index is given by

   $$\operatorname{ind}(E(k^*)) = \operatorname{sign}(\det J(k^*)).$$

   Loss of monotonicity of H_C allows the creation or annihilation of pairs of roots. At such critical parameter values, there exists k^* such that

   $$H_C(k^*) = 1, \qquad H_C'(k^*) = 0,$$

   which characterises a saddle–node bifurcation of endemic equilibria.

   At this point, the Jacobian determinant vanishes:

   $$\det J(k^*) = 0,$$

   and the index changes sign. Thus multiplicity of endemic equilibria corresponds precisely to index redistribution along the endemic branch.

   This provides a direct connection between:

   - the scalar equation (6.2),
   - the loss of monotonicity induced by the feedback C,
   - and the determinant sign structure described in the Seventh law introduced above.

   In particular, backward bifurcation corresponds to the appearance of a pair of equilibria of opposite index below threshold.

6.1. A two-group worked example illustrating Theorem 6 and the loss of monotonicity of $H_C(k)$

We consider a Case (P) model with $m = 2$ susceptible classes $S = (S_1, S_2)^\top$ and two infected compartments $I = (E, I)^\top$:

$$\dot{S} = \Lambda + A_S S - \operatorname{Diag}(S) BI + CI, \qquad \dot{I} = (P \operatorname{Diag}(S) B + A)I, \tag{6.5}$$

with

$$A_S = \begin{pmatrix} -1 & 0 \\ 0 & -1.6 \end{pmatrix}, \qquad \Lambda = \begin{pmatrix} 0.05 \\ 0.85 \end{pmatrix}, \qquad A = \begin{pmatrix} -2 & 0 \\ 2 & -2 \end{pmatrix},$$

$$P = \begin{pmatrix} 1 & 1 \\ 0 & 0 \end{pmatrix}, \qquad B = \begin{pmatrix} 0 & 4 \\ 0 & 3 \end{pmatrix}, \qquad C = \begin{pmatrix} 0 & 1.5 \\ 0 & 0.3 \end{pmatrix}.$$

Equivalently, the system reads

$$\begin{aligned} \dot{S}_1 &= 0.05 - S_1 - 4S_1 I + 1.5I, \\ \dot{S}_2 &= 0.85 - 1.6S_2 - 3S_2 I + 0.3I, \\ \dot{E} &= (4S_1 + 3S_2)I - 2E, \\ \dot{I} &= 2E - 2I. \end{aligned} \tag{6.6}$$

This is a low-dimensional two-group SEI/SEAIR-type example in the sense that the infected block is two-dimensional and $m = 2$.

Let $a = (1, 0)^\top$. Then

$$Dw := (-A)^{-1}a = \begin{pmatrix} 1/2 \\ 1/2 \end{pmatrix}, \qquad R := B(-A)^{-1}a = \begin{pmatrix} 2 \\ 3/2 \end{pmatrix}, \qquad CDw = \begin{pmatrix} 3/4 \\ 3/20 \end{pmatrix}.$$

Hence

$$\|CDw\|_\infty = \frac{3}{4} \;>\; \frac{\min_i \mu_{S,i}}{\max_i R_i} = \frac{1}{2},$$

so condition (6.3) is violated.

By Theorem 11, every endemic equilibrium must satisfy

$$\bar{I} = kDw = k\begin{pmatrix} 1/2 \\ 1/2 \end{pmatrix}, \qquad \bar{S}(k) = \big(k\,\mathrm{Diag}(R) - A_S\big)^{-1}(\Lambda + kCDw).$$

Therefore

$$\bar{S}_1(k) = \frac{0.05 + 0.75k}{1 + 2k}, \qquad \bar{S}_2(k) = \frac{0.85 + 0.15k}{1.6 + 1.5k}. \tag{6.7}$$

The normalization condition $\bar{S}(k)^\top R = 1$ becomes

$$H_C(k) := 2\bar{S}_1(k) + \frac{3}{2}\bar{S}_2(k) = \frac{540k^2 + 1065k + 287}{20\,(30k^2 + 47k + 16)}. \tag{6.8}$$

Moreover,

$$H_C(k) - 1 = \frac{-60k^2 + 125k - 33}{20(2k+1)(15k+16)}. \tag{6.9}$$

Thus the positive roots are

$$k_\pm = \frac{125 \pm \sqrt{7725}}{120} \approx 0.3102,\ 1.7732. \tag{6.10}$$

Also,

$$H_C'(k) = \frac{-6570k^2 + 60k + 3551}{20(2k+1)^2(15k+16)^2}, \tag{6.11}$$

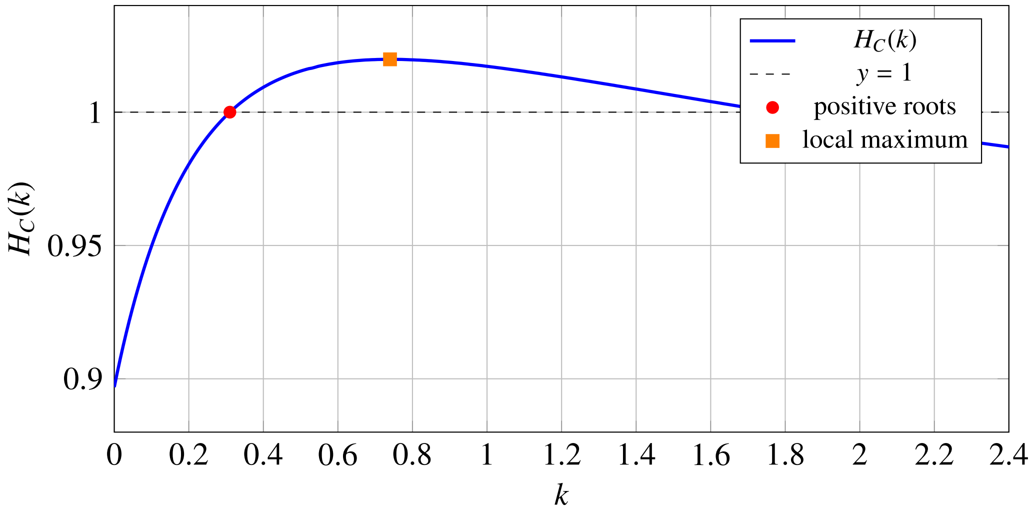

Figure 1. Bifurcation diagram for the scalar normalization equation $H_C(k) = 1$. The function H_C loses monotonicity once (6.3) is violated and intersects the level 1 twice.

which changes sign at

$$k_* \approx 0.7398, \qquad H_C(k_*) \approx 1.01982.$$

Hence $H_C(k)$ is not monotone. In particular, this example exhibits two positive roots of the normalization equation and therefore two endemic equilibria. Since

$$S^0 = (-A_S)^{-1}\Lambda = \begin{pmatrix} 0.05 \\ 0.53125 \end{pmatrix}, \qquad R_0 = (S^0)^\top R = \frac{287}{320} = 0.896875 < 1,$$

this same example also displays a backward-bifurcation configuration.

For the threshold set of Theorem 6, the cyclically permuted next-generation matrix is

$$\widetilde{K}(S) = B(-A)^{-1}P\,\mathrm{Diag}(S) = \begin{pmatrix} 2S_1 & 2S_2 \\ \frac{3}{2}S_1 & \frac{3}{2}S_2 \end{pmatrix}.$$

Since this matrix has rank one,

$$\rho(\widetilde{K}(S)) = 2S_1 + \frac{3}{2}S_2. \tag{6.12}$$

Therefore the threshold hypersurface is the straight line

$$\rho(\widetilde{K}(S)) = 1 \iff 2S_1 + \frac{3}{2}S_2 = 1. \tag{6.13}$$

Interpretation. Theorem 6 identifies the threshold through the spectral equation $\rho(\widetilde{K}(S)) = 1$, while Theorem 11 reduces the endemic equilibrium computation to the scalar equation $H_C(k) = 1$. In this example the threshold set is geometrically simple, but the feedback term CI bends the scalar normalization map enough to destroy monotonicity. This produces two positive roots of H_C, and therefore two endemic equilibria, despite $R_0 < 1$.

7. The computation of Perron eigenvectors for matrices admitting regular splittings in the sense of [7], via Kirchhoff's matrix-tree theorem

Up to this point, the Perron eigenvectors of $\widetilde{K}$ (or of a general regular splitting) have been treated as abstract objects: Theorems 6, 8, and 9 assert their existence and use them as Lyapunov weights, but say nothing about how to compute them when no rank-one formula is available. This section closes that gap: it explains how to compute Perron eigenvectors combinatorially, from weighted spanning trees of the associated graph, rather than by explicit rank-one algebra. In this sense the present section is computational rather than theoretical – it supplies a method, not a new existence or stability statement.

We provide first a Kirchhoff matrix-tree theorem 12 which applies both to computing stationary distributions of Markov processes and to computing Lyapunov weights at the DFE for ME (or CRN) models, under a condition of [18].

We consider Metzler matrices J admitting a regular splitting [7]

$$J = F - V,$$

where $F \geq 0$ and V is a nonsingular M-matrix with $V^{-1} \geq 0$ [7]. When J arises as the transversal Jacobian of a compartmental epidemic model at the DFE (with tangential variables $\boldsymbol{y}$ fixed), it describes the linearised infection dynamics.

If the matrix J is also diagonally dominant (with nonnegative off-diagonal entries and nonpositive row sums), then it defines, after transposition if needed, the generator of a continuous-time Markov process with possible killing. Below threshold ($\lambda_P < 0$), it is a subgenerator, and at threshold ($\lambda_P = 0$) it becomes conservative. This interpretation connects Markov processes with killing (see for example [39]) to epidemic models [14, 15, 18, 40].

For a conservative irreducible generator Q, Kirchhoff's Markov matrix-tree theorem states that the unique (up to scaling) positive left null vector $\vec{\pi} > 0$ satisfying $\vec{\pi}Q = 0$ has components proportional to the **diagonal cofactors** $C_{kk}(-Q)$ [39, 41]. Here

$$C_{kk}(M) = \det M^{(k,k)},$$

where $M^{(k,k)}$ is obtained from M by deleting the k-th row and the k-th column. Also, for a conservative irreducible generator Q, $\mathrm{rank}(Q) = n - 1$, and $\mathrm{adj}(Q) = \{(-1)^{k+j} C_{kj}(Q)\}_{j,k}$ is of rank one, with rows proportional to $\vec{\pi}$ and columns proportional to $\mathbf{1}$.

In our setting, the role of (sub)generator is played by $J = F - V$, while $V - F$ is the associated M-matrix entering the adjugate formula.

Theorem 12 (Kirchhoff–Perron formula for regular splittings [`Kir`])**.** *Let J be an irreducible Metzler matrix with spectral abscissa λ_P. Then λ_P is a simple eigenvalue of J.*

1. (Perron–Frobenius.) *There exist unique (up to scaling) positive left and right Perron eigenvectors:*

$$\vec{\pi} J = \lambda_P \vec{\pi}, \qquad J \boldsymbol{w} = \lambda_P \boldsymbol{w}, \qquad \vec{\pi} > 0, \quad \boldsymbol{w} > 0.$$

2. (Adjugate factorisation at the Perron root.) *The matrix $J - \lambda_P I$ is singular with rank $n - 1$, and its adjugate has rank one and factors as*

$$\mathrm{adj}(J - \lambda_P I) = c\, \boldsymbol{w}\, \vec{\pi}, \qquad c \neq 0.$$

Hence all columns of $\mathrm{adj}(J - \lambda_P I)$ *are proportional to* $\mathbf{w}$*, all rows are proportional to* $\vec{\pi}$*, and*

$$C_{kk}(\lambda_P I - J) \propto \mathbf{w}_k \pi_k.$$

Remark 23. *In the Markov case* ($\lambda_P = 0$)*,* J *is a conservative generator* ($J\mathbf{1} = 0$) *and Kirchhoff's theorem applied to the Laplacian* $-J$ *yields*

$$C_{kk}(-J) = c_0 \pi_k, \qquad c_0 > 0.$$

Theorem 13 (Roles of NGM eigenvectors at a unique DFE [`Rol`])**.** *Assume that the disease-free system*

$$S' = g(S, 0)$$

has a unique equilibrium $S_0 > 0$*, where the transversal Jacobian* $J = J_x(S_0, 0)$ *is irreducible Metzler and admits a regular splitting:*

$$J = F(S_0) - V(S_0).$$

Define

$$K = K(S_0) := F(S_0)V(S_0)^{-1}, \qquad \widetilde{K} := V(S_0)^{-1}F(S_0), \qquad R_0 := \rho(K) = \rho(\widetilde{K}).$$

(K *and* $\widetilde{K}$ *are similar matrices –* $\widetilde{K} = V^{-1}(FV^{-1})V = V^{-1}KV$ *– hence share the same nonzero spectrum, as already noted in Remark 11;* $\widetilde{K}$ *is used below because its Perron eigenvectors act directly on the I-coordinates.) Then:*

1. $\lambda_P(J) = 0$ *iff* $R_0 = 1$.
2. *Let* $\boldsymbol{w}$ *denote the right Perron eigenvector of* $K = F(S_0)V^{-1}$*. Then*

   $$D_w := V^{-1}\boldsymbol{w}$$

   is the right Perron eigenvector of $\widetilde{K} = V^{-1}F(S_0)$*, and*

   $$J(S_0)D_w = (R_0(S_0) - 1)\boldsymbol{w}$$

   holds.

   At threshold $R_0(S_0) = 1$*, the vector* D_w *is a right null vector of* $J(S_0)$*, and if an endemic branch bifurcates from* $(S_0, 0)$ *at threshold, then its infected component is tangent to the ray spanned by* D_w*.*

   In rank-one Case (P), one has

   $$\bar{I} = kD_w, \qquad k > 0,$$

   for the unique endemic equilibrium, so the whole local endemic branch lies on that ray.
3. *Let* $\vec{\pi}$ *be the left Perron eigenvector of* $K = F(S_0)V^{-1}$

   $$\vec{\pi}K = \vec{\pi}F(S_0)V^{-1} = R_0\vec{\pi},$$

   and let

   $$\vec{q} = \vec{\pi}V$$

denote the left Perron eigenvector of $\widetilde{K} = V^{-1}F(S_0)$. *Put*

$$Q(I) = \vec{q}\, I = \vec{\pi} V I.$$

If, moreover,

$$I' = (F(S_0) - V)I - f(S, I), \qquad f(S, I) \geq 0,$$

then

$$Q' = (R_0 - 1)\vec{\pi}\, I - \vec{\pi} V f(S, I),$$

and therefore Q *is a transversal Lyapunov function for the invariant manifold* $\{I = 0\}$ *whenever* $R_0 < 1$.

Proof. Item (1) is the standard equivalence for regular splittings:

$$\lambda_P < 0 \iff \rho(F(S_0)V^{-1}) < 1, \qquad \lambda_P = 0 \iff \rho(F(S_0)V^{-1}) = 1.$$

For item (2), let $\boldsymbol{w} > 0$ satisfy

$$K\boldsymbol{w} = F(S_0)V^{-1}\boldsymbol{w} = R_0\boldsymbol{w},$$

and define

$$D_w := V^{-1}\boldsymbol{w}.$$

Since V is nonsingular, $D_w \neq 0$. Multiplying the eigenvalue relation by V^{-1} on the left gives

$$V^{-1}F(S_0)V^{-1}\boldsymbol{w} = R_0 V^{-1}\boldsymbol{w}, \Leftrightarrow \widetilde{K} D_w = V^{-1}F(S_0)\, D_w = R_0 D_w.$$

Hence D_w is the right Perron eigenvector of $\widetilde{K}$.

At threshold, $R_0 = 1$, and therefore

$$JD_w = (F(S_0) - V)D_w = F(S_0)V^{-1}\boldsymbol{w} - \boldsymbol{w} = (K - I)\boldsymbol{w} = 0.$$

Thus D_w is the right null vector of J.

Assume now that an endemic branch

$$(\bar{S}(\varepsilon), \bar{I}(\varepsilon)), \qquad \varepsilon \geq 0,$$

bifurcates from the DFE $(S_0, 0)$ at $R_0 = 1$, is differentiable at $\varepsilon = 0$, and satisfies

$$(\bar{S}(0), \bar{I}(0)) = (S_0, 0).$$

Write

$$\bar{I}(\varepsilon) = \varepsilon d + o(\varepsilon), \qquad \varepsilon \downarrow 0.$$

Since $(\bar{S}(\varepsilon), \bar{I}(\varepsilon))$ is an equilibrium, the infected equilibrium equation has the form

$$0 = (F(\bar{S}(\varepsilon)) - V)\bar{I}(\varepsilon) + N(\bar{S}(\varepsilon), \bar{I}(\varepsilon)),$$

where $N(S, I) = o(\|I\|)$ as $I \to 0$. Dividing by ε and letting $\varepsilon \downarrow 0$ yields

$$(F(S_0) - V)d = Jd = 0.$$

Hence $d \in \ker J$. Since J is irreducible Metzler and 0 is its simple Perron eigenvalue at threshold, $\ker J$ is one-dimensional. Therefore

$$d = \eta D_w$$

for some scalar $\eta \neq 0$. Thus the infected component of the endemic branch is tangent at $(S_0, 0)$ to the ray spanned by D_w.

In rank-one Case (P), one has

$$F(S) = \boldsymbol{\alpha}\, \vec{w}(y),$$

so at the unique endemic equilibrium on the branch,

$$0 = (F(\bar{S}) + A)\bar{I} = \boldsymbol{\alpha}(\vec{w}(y_e)\bar{I}) + A\bar{I}.$$

Writing

$$k := \vec{w}(\bar{S})\bar{I},$$

we obtain

$$A\bar{I} = -k\boldsymbol{\alpha}, \qquad \text{hence} \qquad \bar{I} = k(-A)^{-1}\boldsymbol{\alpha} = kD_w.$$

Thus, in rank-one Case (P), the whole local endemic branch lies on the ray spanned by D_w.

For item (3), since

$$\vec{\pi}K = \vec{\pi}F(S_0)V^{-1} = R_0\vec{\pi},$$

right-multiplying first by V yields

$$\vec{\pi}F(S_0) = R_0\vec{\pi}V,$$

and then right-multiplying by V^{-1} gives

$$\vec{\pi}V^{-1}F(S_0) = R_0\vec{\pi}.$$

Thus, define

$$\vec{q} := \vec{\pi}V,$$

which is the left Perron eigenvector of $\tilde{K} = V^{-1}F(S_0)$.

Define

$$Q(I) := \vec{q}\, I.$$

Using the decomposition $I' = (F(S_0) - V)I - f(S, I)$, we compute $Q' = \vec{q}\, I' = \vec{q}(F(S_0) - V)I - \vec{q}\, f(S, I)$.

Since $\vec{q}V^{-1}F(S_0) = R_0\vec{q}$, it follows that $\vec{q}(F(S_0) - V) = (R_0 - 1)\vec{q}$.

Therefore, $Q' = (R_0 - 1)\, \vec{q}I - \vec{q}\, f(S, I)$.

Because $\vec{q} > 0$, $I \geq 0$, and $f(S, I) \geq 0$, we obtain

$$Q' \leq 0 \quad \text{whenever } R_0 < 1.$$

Therefore Q is a transversal Lyapunov function for the invariant manifold $\{I = 0\}$. □

Sections 4–6 show how Perron eigenvectors determine thresholds, endemic equilibria, and Lyapunov functions. The present section shows that these same Perron vectors admit explicit graph-theoretic representations, through Kirchhoff's matrix-tree theorem, whenever an explicit rank-one formula is not available. Thus the complete threshold theory of this paper can be read either spectrally (Perron–Frobenius eigenvectors of a regular splitting) or combinatorially (diagonal cofactors of the associated Laplacian) – the two readings agreeing wherever both are defined.

7.1. Notation and preliminaries

Let $\mathbb{R}^n$ denote the space of $n \times 1$ column vectors and $\| \cdot \|_2$ the Euclidean norm. The set of column vectors with positive entries is denoted $\mathbb{R}^n_+$, while the set of column vectors with nonnegative entries is denoted by $\mathbb{R}^n_{\geq 0}$. The set of $n \times m$ matrices with real entries is denoted $\mathbb{R}^{n \times m}$. The family $\{e_1, \ldots, e_n\}$ denotes the canonical basis of the vector space $\mathbb{R}^n$. A^t denotes the transpose of A, and A^{-t} the transpose of the inverse of A. If $z \in \mathbb{R}^n$, we denote by z_i the ith component of z (equivalently $z_i = e_i^t.z$). For a matrix A, we denote by $A(i, j)$ the entry in row i, column j. For matrices A and B, we write $A \leq B$ if $A(i, j) \leq B(i, j)$ for all i and j, $A < B$ if $A \leq B$ and $A \neq B$, and $A \ll B$ if $A(i, j) < B(i, j)$ for all i and j.

Definition 13 (spectral radius [spe]). *A) The spectral radius of a matrix A is defined by*

$$\rho(A) = max\{|\lambda|, \lambda \in Sp(A)\},$$

where $Sp(A)$ denotes the spectrum of A.

B) The largest real part among the eigenvalues of A is denoted by

$$s(A) = \max\{\mathrm{Re}(\lambda) \ : \ \lambda \in Sp(A)\}.$$

C) A matrix A is said to be Hurwitz if $s(A) < 0$.

Definition 14 (Metzler matrix [Met]). *A Metzler matrix A is a matrix such that $i \neq j \Longrightarrow A(i, j) \geq 0$. These matrices are also called quasi-positive matrices.*

$\vec{b}, \vec{\beta}$, ... will be used to denote row vectors. Scalar functions like the logarithm and quotients will be applied to vectors componentwise:

$$\ln y = (\ln y_1, \ln y_2, ...), \frac{1}{y} = \left(\frac{1}{y_1}, \frac{1}{y_2}, \ldots\right), \frac{y^*}{y} = \left(\frac{y_1^*}{y_1}, \frac{y_2^*}{y_2}, \ldots\right).$$

State variables and ambient state space. The full state is denoted by

$$X = (S, I) \in \mathbb{R}^m_+ \times \mathbb{R}^n_+,$$

where

- $I = (I_1, \ldots, I_n) \in \mathbb{R}^n_+$ denotes the infection variables (exposed, infected, bacterial, ... compartments),
- $S = (S_1, \ldots, S_m) \in \mathbb{R}^m_+$ denotes the susceptible-like or resident variables (susceptible, partially immune, ... compartments).

When the state is partitioned relative to a siphon face $\mathcal{F}_\Sigma$, we use

$$x = (z_\Sigma, y_\Sigma) \in \mathbb{R}^N_+,$$

where z_Σ denotes the variables transversal to $\mathcal{F}_\Sigma$ and y_Σ the variables tangent to $\mathcal{F}_\Sigma$.

Regular splitting and face next-generation matrices. For an invader block $\sigma \subseteq \Sigma$,

- $$J_\sigma(E_\Sigma) = F_\sigma(E_\Sigma) - V_\sigma(E_\Sigma)$$

  denotes a regular splitting, with $F_\sigma \geq 0$ and $V_\sigma^{-1} \geq 0$;

- $$K_\sigma(E_\Sigma) = F_\sigma(E_\Sigma)V_\sigma(E_\Sigma)^{-1}$$

  is the face next-generation matrix;

- $$\widetilde{K}_\sigma(E_\Sigma) = V_\sigma(E_\Sigma)^{-1}F_\sigma(E_\Sigma)$$

  is the cyclically permuted next-generation matrix;

- $$R_\sigma(E_\Sigma) = \rho\big(K_\sigma(E_\Sigma)\big)$$

  is the face reproduction number.

The classical basic reproduction number R_0 is the special case corresponding to the DFE face.

Spectral abscissae and Perron invasion directions.

- $$\alpha_\sigma(E_\Sigma) := s\big(J_\sigma(E_\Sigma)\big)$$

  is the spectral abscissa of the released invader block σ at E_Σ.
- $w_\sigma \gg 0$ denotes a right Perron eigenvector of $K_\sigma(E_\Sigma)$.
- $\tilde{w}^\sigma \gg 0$ denotes a right Perron eigenvector of $\widetilde{K}_\sigma(E_\Sigma)$.
- $$D_{w,\sigma} := V_\sigma(E_\Sigma)^{-1}w_\sigma$$

  is the Perron invasion direction.
- $a_\sigma > 0$ denotes the amplitude scalar fixing the equilibrium on the released face.

Face-adapted Lyapunov functions. For $\Sigma \in \mathcal{L}$,

$$V_\Sigma(x) = \sum_{i\notin\Sigma} a_i^\Sigma\, y_i^*\, G\Big(\frac{y_i}{y_i^*}\Big) + \sum_{j\in\Sigma} b_j^\Sigma\, z_j,$$

with coefficients

$$a_i^\Sigma > 0, \qquad b_j^\Sigma > 0.$$

Here:

- a_i^Σ are the Volterra (resident) weights;
- b_j^Σ are the linear (invader) weights.

For rank-one rank-one balanced bilinear model with $m = 1$, one has the relay relation

$$\vec{l} = \bar{S}\,\vec{\pi}.$$

Flux, Laplacian, and Kirchhoff notation.

- $\Phi_{ij}(z) \geq 0$ denotes the directed flux from species i to species j in a decomposition

$$f_i = \sum_k (\Phi_{ki} - \Phi_{ik}).$$

- $$c_{ij} := \partial_{z_i}\Phi_{ij}(z^*) \geq 0$$

  denotes the linearized flux coefficient at equilibrium.
- $\kappa_{\Sigma\Sigma'} \geq 0$ denotes the edge weight in the relay graph associated with the inclusion or release step under consideration.
- L denotes the Laplacian of the relay graph

$$L_{\Sigma\Sigma} = \sum_{\Sigma' \sim \Sigma} \kappa_{\Sigma\Sigma'}, \qquad L_{\Sigma\Sigma'} = -\kappa_{\Sigma\Sigma'} \text{ for } \Sigma' \neq \Sigma.$$

- $$La = B$$

  denotes the Laplacian balance system for the resident weights.
- $C_{\Sigma\Sigma}(L)$ denotes the diagonal cofactor of L. By Kirchhoff's matrix-tree theorem, one has

$$a_\Sigma \propto C_{\Sigma\Sigma}(L)$$

  when $La = 0$.

CRN notation. The stoichiometric matrix is Γ. A reaction ρ is the index of a column in Γ, and

$$\gamma_\rho := O(\rho) - S(\rho) \in \mathbb{Z}^n$$

is the stoichiometric vector of ρ, decomposed as a difference between output and and source non-negative vectors. In the mass action case, ρ may be viewed as a transition between two complexes $y \to y'$.

A reaction may be viewed also as a pair

$$\rho = (\Gamma^-(\rho), \Gamma^+(\rho)),$$

where $\Gamma^-(\rho)$ is the set of incoming species with negative signs and $\Gamma^+(\rho)$ is the set of outcoming species with positive signs.

$r_\rho(z) \geq 0$ is the rate of ρ; under mass action,

$$r_\rho(z) = \kappa_\rho\, z^{S(\rho)}.$$

Remark 24. *The symbol ρ has two distinct meanings: as a reaction index/ hyper-arc in expressions such as r_ρ, γ_ρ, $\sum_\rho$, and as the spectral radius in expressions such as $\rho(K)$. The distinction is always by context.*

Object	Role in dynamics	Transformations
$\tilde{w}$ (right evec of $\widetilde{K}$)	Escape direction	$w := (-A)^{-1}\tilde{w}$
$\tilde{\pi}^T$ (left evec of $\widetilde{K}$)	–	$\pi^T := \tilde{\pi}^T(-A)^{-1}$
w (right evec of K)	–	$\tilde{w} = (-A)\,w$
π^T (left evec of K)	Lyapunov weights	$\tilde{\pi}^T = \pi^T(-A)$

where evec denotes the eigenvector.

8. Conclusion

8.1. Theorem dependency graph

The results of this paper form a single logical backbone, not a collection of unrelated results; each result below is used in the proof, or the interpretation, of the next.

$$\begin{gathered}
\text{Definition 2 (chemical ODE)}\\
\Downarrow\\
\text{Theorem 2 (triangular Jacobian on a siphon face)}\\
\Downarrow\\
\text{Theorem 3 (transversal block is Metzler)}\\
\Downarrow\\
\text{Theorem 6 (Perron–Frobenius threshold, arbitrary rank)}\\
\Downarrow\\
\text{Theorems 7–10 (explicit rank-one formulas, §5)}\\
\Downarrow\\
\text{Theorem 12 (Kirchhoff–Perron formula, §7)}
\end{gathered}$$

8.2. Synthesis

Stripped of model-specific detail, the paper establishes a chain of five ideas.

(i) Chemical ODEs naturally generate Metzler transversal Jacobians on every siphon face (Theorems 2–3) – this is a structural fact about chemical reaction networks, independent of any rate constants.

(ii) Regular splittings convert Jacobian stability into a spectral-radius inequality for the associated next-generation matrix (Corollary 1), replacing an eigenvalue problem for a general matrix with a Perron eigenvalue problem for a nonnegative one.

(iii) Perron–Frobenius theory then supplies invasion directions, Lyapunov weights, and –under an irreducibility hypothesis– a unique endemic ray (Theorem 6).

(iv) Rank-one models (the balanced bilinear (A, B, P, φ) balanced bilinear model class) are precisely the class where every object in (i)–(iii) becomes an explicit closed-form formula, rather than merely existing abstractly (§5–6).

(v) Kirchhoff's matrix-tree theorem provides a graph-theoretic, spanning-tree interpretation of the same Perron eigenvectors, giving an explicit formula even where the rank-one structure of (iv) is absent (§7).

8.3. Comparison with the classical single-DFE theory

Classical ME	**This paper**
DFE	Arbitrary siphon face
Basic reproduction number R_0	R-invasion functions
Infected subsystem	Transversal Jacobian
NGM	Regular splitting
NGM threshold theorem	Perron–Frobenius threshold theorem (Theorem 6)
Endemic equilibrium formula	Perron ray + nonlinear closure (§5)

Read this way, the classical single-DFE theory is the special case of the present framework in which the siphon face under consideration is the DFE face itself.

Several further themes emerge from the results above.

First, rank one plays two rather different roles. On the one hand, it yields explicit formulas for Perron eigenvectors, endemic equilibria, and Goh–Volterra coefficients. On the other hand, the DFE theory itself is not inherently tied to this assumption: the Perron Lyapunov weight persists for higher-rank NGMs, although it is no longer explicit. Thus the assumption is best viewed not as the source of the theory, but as the regime in which the general theory becomes closed-form.

Second, the relation between DFE and EE stability is stronger than is usually emphasized. In the rank-one (A, B, P, φ) balanced bilinear model setting, both rely on the same building blocks: the Perron data of the NGM, the dwell-time vector, and a normalization law. This suggests that DFE and EE Lyapunov theories should not be developed separately, but rather as two parts of a common stability relay. At present this relay is fully understood only in special cases.

Third, the comparison with Shuai–van den Driessche shows a sharp distinction between what remains valid at general rank and what does not. The DFE Lyapunov weight remains Perron-theoretic, but EE Lyapunov weights are generally no longer Perron eigenvectors; they are instead related to Kirchhoff-type cofactors. Thus one should expect a genuine bifurcation in the theory at higher rank: Perron theory controls the DFE, while graph-theoretic constructions control the EE.

These observations lead to the following open problems.

Problem 1 (Perron–Volterra Lyapunov functions beyond diagonal A_S)**.** *Extend the Perron–Volterra Lyapunov construction of Theorem 8 from diagonal A_S, and the irreducible 2×2 case established in the companion paper [6], to arbitrary irreducible M-matrices A_S.*

A first subproblem is to determine whether the DFE Perron term and the EE Goh–Volterra term can be completed into a single general construction, valid beyond rank one. A second is to decide whether the higher-rank EE coefficients should be sought through Perron theory, through Kirchhoff cofactors, or through a genuinely new mechanism. A positive answer would extend Theorem 8 to the full class of irreducible transversal blocks A_S; a negative answer – a genuine obstruction beyond the diagonal and 2×2 cases – would exhibit the first provable limit of Perron-explicit DFE Lyapunov theory.

Problem 2 (Uniqueness of the threshold solution)**.** *Theorem 6(ii) gives a unique Perron ray whenever $\widetilde{G}$ is irreducible. Characterize precisely when the threshold equation $\rho(\widetilde{K}(S)) = 1$ admits a unique* *solution on a given ray when $\widetilde{G}$ is reducible, and more generally whether formulas such as*

$$\begin{cases} R_i = R_i(E_0), R_0 = \max\left[R_1, R_2\right], \\ \mathcal{R}_{\bar{i}}^{j} = R_j(E_i), \\ R_2 < R_{2,c} := \frac{R_2(E_0)}{R_2(E_1)} \Longrightarrow E_1 \text{ is LAS} \end{cases} \tag{8.1}$$

where R_0, R_i denote the reproduction numbers, $\mathcal{R}_{\bar{i}}^{j}$ the invasion numbers of resident strain i by strain j, and $R_i(x)$ the reproduction functions, hold for some general class of epidemic models.

More generally, one may ask whether reproduction functions admit a structural interpretation analogous to that of NGMs, and whether invasion criteria can be derived from Jacobian factorizations without requiring explicit knowledge of the competing endemic equilibria. A positive answer would extend Theorem 6(ii) from the irreducible to the reducible case; a negative answer would exhibit the first genuine multiplicity obstruction to the Perron-ray uniqueness underlying the entire rank-one theory of §5.

Problem 3 (Intrinsic CRNT characterization of balanced bilinear models)**.** *Characterize (A, B, P, φ) balanced bilinear models within CRN theory, and investigate extensions of the bilinear results under rates which are admissible in the sense of [23].*

This includes at least three natural questions: how to recognize (A, B, P, φ) balanced bilinear model structure directly from a reaction network; which parts of the seven-law theory survive under admissible non-bilinear rates; and whether siphons, minimal siphons, or related CRN objects provide the correct structural substitute for the rank-one assumptions. A positive answer would place the balanced bilinear class, and hence Theorems 4–5, inside the general chemical-ODE framework of Theorem 2 without further ad hoc hypotheses; a negative answer would show that balanced bilinearity is a genuinely extra-CRNT assumption.

Problem 4 (Graph conditions for endemic uniqueness)**.** *Determine graph-theoretic conditions on the underlying reaction network – beyond irreducibility of $\widetilde{G}$ and beyond the single-siphon case – that guarantee uniqueness of the endemic equilibrium.*

A natural conjecture is that persistence and endemic uniqueness should hold whenever every minimal siphon supports a repelling boundary face, equivalently whenever the restriction of the infection dynamics to each such face has spectral radius greater than one. A positive answer would extend the persistence and uniqueness theory underlying Theorem 6 from a single minimal siphon to arbitrarily many; a negative answer would exhibit the first example where single-siphon intuition fails, and would identify exactly which multi-siphon configurations require a genuinely new argument.

Problem 5 (Determinant identity beyond rank one)**.** *Theorem 10 establishes the determinant law only for rank-one (A, B, P, φ) balanced bilinear models with a single susceptible class ($m = 1$). Determine whether the determinant law, relay relations between DFE and EE weights, and related inheritance phenomena extend beyond this one-susceptible rank-one setting.*

Even partial extensions would clarify which features are genuinely tied to rank one and which are manifestations of a broader algebraic structure underlying epidemic Jacobians. A positive answer would extend Theorem 10 beyond $m = 1$; a negative answer would show that the determinant identity is a genuinely rank-one, one-susceptible phenomenon, rather than the shadow of a more general law.

Stripped of epidemiological vocabulary, this paper identifies one mathematical pipeline:

chemistry $\to$ siphons $\to$ invariant faces $\to$ Metzler matrices $\to$ Perron–Frobenius $\to$ thresholds $\to$ endemic equilibria $\to$ Lyapunov functions.

Every arrow in this chain is a general fact about positive dynamic systems with a chemical (stoichiometric) representation, not a fact about epidemic models specifically. The pipeline therefore applies, without modification of its structural half (up to and including Theorem 6), to any chemical ODE with the required siphon structure – population dynamics, ecology, and viro-immunology among them; only the last, explicit half of the pipeline (Sections 5–7) uses the balanced bilinear structure specific to the epidemic models studied here.

Use of Generative-AI tools declaration

During the preparation of this manuscript, the authors used Claude for symbolic manipulations, numerical checks, and consistency verification of computations, and ChatGPT to assist in literature searches and in improving the clarity and organization of the presentation. All mathematical results, proofs, interpretations, and conclusions were verified by the authors, who take full responsibility for the content of the manuscript.

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Conflict of interest

The authors declare that they have no competing financial interests or personal relationships that could have influenced the work reported in this paper.

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