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NON-EXISTENCE OF A GLOBALLY CONVEX ENTROPY PAIR AND WAVE STRUCTURE FOR A FLUID DYNAMICS MODEL OF BIOFILMS

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Abstract

We study the hyperbolic structure of the one-dimensional fluid dynamics system introduced by Clarelli, Di Russo, Natalini, and Ribot (2013) to model biofilm growth, and subsequently analyzed analytically by Bianchini and Natalini (2016), who proved global existence and exponential stability of smooth solutions near the unique equilibrium by exploiting a total dissipativity condition in lieu of a convex entropy. The absence of a globally convex entropy pair was left implicit in that work. We make this absence explicit and rigorous. Specifically, we derive the full compatibility system for the Hessian $H = \nabla^2\eta$ *of any candidate entropy* η*, and prove that positive definiteness of H is incompatible with the constraints imposed by the flux structure on any open domain containing states with both positive and negative velocity. The proof exploits an affine dependence of the (4,4)-entry of H on the velocity variable, which changes sign and therefore cannot be globally positive definite. As a direct consequence, the classical entropy-based convergence framework of Lax, Glimm, and DiPerna does not apply to this system in its full generality. In the second part of the paper, we carry out a complete wave-structure analysis: we compute all right eigenvectors of the flux Jacobian, classify the four characteristic fields as two linearly degenerate contact families and two nonlinear families, and identify an inflection locus* $\{L = 3/5\}$ *inside the hyperbolicity domain on which genuine nonlinearity fails. The resulting wave pattern in the Riemann problem is a two-contact structure bracketed by two nonlinear waves, with composite waves appearing whenever the inflection locus is crossed. These results provide the analytical foundation for a companion numerical paper in which a Godunov-type scheme is constructed and the numerical viscosity is shown to serve as the admissibility mechanism replacing convex entropy.*

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1 Introduction

Biofilms are structured communities of microorganisms embedded in a self-produced extracellular matrix. They arise in a remarkably broad range of contexts — from industrial pipelines and water treatment systems to medical implants and stone monument conservation — and their mathematical modeling has attracted sustained attention over the past three decades; see Klapper and Dockery (2010) for a survey.

Early continuum models described biofilm growth primarily through reaction–diffusion equations for biomass and substrate concentrations (Wanner et al., 2006; Eberl et al., 2001). A significant modeling advance was achieved by Clarelli et al. (2013), who derived a system of hyperbolic partial differential equations from mixture theory (Rajagopal & Tao, 1995; Astanin & Preziosi, 2008), incorporating mass and momentum conservation for four phases: active bacteria B, extracellular polymeric substance (EPS) E, dead cells D, and liquid L. A key feature of the resulting model is the finite speed of front propagation, which is physically natural and avoids the artificial infinite-speed anomaly of diffusion-only models. The multidimensional stability analysis and parameter sensitivity of this model were subsequently studied in Clarelli et al. (2016).

The rigorous analytical study of the one-dimensional Cauchy problem for this system was carried out by Bianchini and Natalini (2016). After establishing symmetrizability and hence local well-posedness, those authors identified a total dissipativity property of the source term — encoded in their (D)-Condition — and used it to prove global existence and exponential asymptotic stability of smooth solutions near the unique non-vanishing equilibrium, without invoking a convex entropy. The authors explicitly remarked that their proof does not use any strictly convex entropy (Bianchini & Natalini, 2016, p. 4), which motivates the present work.

The entropy gap

In the classical theory of hyperbolic systems of conservation laws, convex entropy pairs (η, q) satisfying $\nabla q = \nabla\eta \cdot A(u)$ with $\nabla^2\eta > 0$ serve three essential roles: they select physically admissible weak solutions via the entropy inequality $\partial_t \eta + \partial_x q \leq 0$; they provide the stability mechanism for the Cauchy problem; and they underpin the convergence theory of Godunov-type numerical schemes through discrete entropy inequalities (Lax, 1957; Dafermos, 2010; DiPerna, 1983; Godunov, 1959). However, many physically important hyperbolic systems fail to admit a globally convex entropy (Dafermos, 2010). Recent examples include the reactive Euler equations (Zhao, 2023), two-phase mixture systems (Hantke et al., 2022), and the Cargo–LeRoux gravitational system (Cargo & LeRoux, 1994). For such systems, alternative admissibility mechanisms must be identified, typically via the vanishing-viscosity limit (Bianchini & Bressan, 2005).

The non-existence of a convex entropy for the biofilm system has not been established in the literature. Its establishment is not merely a technical point: it explains why the analysis of Bianchini and Natalini (2016) required the D-Condition as a substitute, and it places the biofilm system in the growing class of physically motivated systems for which numerical admissibility must be justified by viscosity selection rather than by discrete entropy inequalities.

Wave structure gap

Beyond the entropy question, the wave structure of the biofilm system has not been analyzed. The paper of Bianchini and Natalini (2016) concerns smooth solutions near equilibrium and makes no reference to the Riemann problem, shock waves, rarefaction fans, or contact discontinuities. Yet the Riemann problem is the fundamental building block for both the theoretical understanding and the numerical treatment of hyperbolic systems (LeVeque, 2002; Bressan, 2000; Toro, 2009). A complete wave-structure analysis is therefore a natural and necessary complement to the smooth-solution theory.

Contributions of this paper

This paper makes the following contributions.

(i) Non-existence theorem (Section 3). We derive the full 4×4 compatibility system for the Hessian of any entropy η, extract six explicit scalar conditions on its entries, and prove that global positive definiteness is impossible on any domain containing states with both signs of velocity. The key obstruction is an affine dependence of the

(4,4)-entry of H on v, which cannot maintain a definite sign.

(ii) Corollaries on admissibility (Section 3). We conclude that the Lax–DiPerna entropy convergence framework does not apply globally, and that vanishing viscosity is the physically correct admissibility mechanism.

(iii) Complete eigenstructure (Section 4). We compute all four right eigenvectors of the flux Jacobian explicitly, classify the four characteristic fields, and prove that two fields are linearly degenerate and two are genuinely nonlinear outside an inflection locus.

(iv) Inflection locus and composite waves (Section 4). We identify the surface $\{L = B+E+D = 3/5\}$ as the inflection locus of the nonlinear fields, characterize the composite waves arising when this locus is crossed, and state the full Riemann solution structure.

The remainder of the paper is organized as follows. Section 2 recalls the biofilm system and its hyperbolicity properties. Section 3 contains the analysis of the non-existence of entropy. Section 4 develops the wave-structure theory. Section 5 concludes with a discussion and open problems, including a pointer to the companion numerical paper.

2 The Biofilm System

2.1 Governing Equations

Following Clarelli et al. (2013) and Bianchini and Natalini (2016), we consider a one-dimensional biofilm composed of four phases with volume fractions B (active bacteria), E (EPS), D (dead cells), and L (liquid), subject to the saturation constraint

$B + E + D + L = 1, \quad B, E, D, L \in (0,1), \quad (2.1)$

After eliminating $L = 1 - B - E - D$ and the liquid-phase velocity via the incompressibility relation, the governing system reduces to four equations in the unknown $u = (B, E, D, v)^T$, where v denotes the common solid-phase velocity:

$\partial_t u + \partial_x F(u) = G(u), \quad (2.2)$

with flux

$F(u) = (Bv, \ Ev, \ Dv, \ [(3L-2)v^2/2L + \gamma(L + \ln(1-L))]^T)$

and biological source $G(u) = (\Gamma^B, \Gamma^E, \Gamma^D, \Gamma_v)^T$ whose precise form is given in Bianchini and Natalini (2016) and is irrelevant for the entropy and wave-structure analysis. The parameter $\gamma > 0$ is a constitutive stiffness constant.

2.2 Flux Jacobian and hyperbolicity domain

Setting $L = 1-B-E-D$ and defining

$\eta^c := \gamma L/(1-L) - v^2/L^2, \quad (2.3)$

the flux Jacobian $A(u) = DF(u)$ takes the explicit form

$A(u) = \lceil \ v \ 0 \ 0 \ B \rceil \quad | \ 0 \ v \ 0 \ E | \quad | \ 0 \ 0 \ v \ D | \quad \lfloor \ \eta^c \ \eta^c \ \eta^c \ (3L-2)v/L \rfloor$

As shown in Bianchini and Natalini (2016), system (2.2) is symmetrizable hyperbolic on the domain

$W = \{u \in (0,1)^3 \times \mathbb{R} : \eta^c > 0, 0 < L < 1\}, \quad (2.4)$

equivalently, $|v| < L^{3/2}\gamma^{1/2}(1-L)^{-1/2}$. The four eigenvalues of A(u) are

$\lambda_1 = \lambda_2 = v, \qquad \lambda_{3,4} = (2L-1)v/L \pm \sqrt{((1-L)\Delta)}, \quad (2.5)$

where $\Delta = L\gamma/(1-L) - v^2/L > \eta^c > 0$ in W. We work exclusively on a convex open subset $\Omega \subseteq W$ throughout the paper.

3 Non-Existence of a Globally Convex Entropy Pair

3.1 Entropy Pairs and Compatibility

We study the homogeneous system $\partial_t u + \partial_x F(u) = 0$, since entropy analysis concerns only the flux structure.

Definition 3.1 (Entropy pair)

A pair $(\eta, q) \in C^2(\Omega; \mathbb{R})^2$ is an entropy pair for (2.2) if $\nabla q(u) = \nabla \eta(u) \cdot A(u)$ for all $u \in \Omega$. The entropy η is convex if $H(u) := \nabla^2 \eta(u) > 0$ (positive definite) uniformly on Ω.

Definition 3.2 (Admissibility)

A weak solution u is entropy admissible if $\partial_t \eta(u) + \partial_x q(u) \leq 0$ in the distributional sense for every convex entropy pair (η, q).

Differentiating the compatibility condition with respect to u_k and using symmetry of mixed partials of q, the Hessian $H = (h_{ij})_{1 \leq i, j \leq 4}$ must satisfy

$HA(u) = [HA(u)]^T, \quad (3.1)$

i.e., HA must be symmetric. We derive the explicit scalar conditions that (3.1) imposes on H for the Jacobian (2.3).

3.2 The Compatibility System

Proposition 3.3 (Compatibility conditions)

Let (η, q) be a smooth entropy pair for (2.2) with Jacobian (2.3). Set $\lambda^* = (3L-2)v/L$. Then the Hessian $H = \nabla^2 \eta$ satisfies the following six scalar conditions on Ω:

$h_{14} = h_{24} = h_{34}$,
$Bh_{11} + Eh_{12} + Dh_{13} + (\lambda^* \; -v)h_{14} = \eta^c h_{44}$,
$Bh_{12} + Eh_{22} + Dh_{23} + (\lambda^* \; -v)h_{14} = \eta^c h_{44}$,
$Bh_{13} + Eh_{23} + Dh_{33} + (\lambda^* \; -v)h_{14} = \eta^c h_{44}$.

Proof.

We compute HA using the flux Jacobian and impose $(HA)_{ij} = (HA)_{ji}$ for each $i \neq j$.

Off-diagonal conditions $(i,j) \in \{(1,2),(1,3),(2,3)\}$. For (1,2): $(HA)_{12} = vh_{12} + \eta^c h_{14}$ and $(HA)_{21} = vh_{12} + \eta^c h_{24}$. Symmetry gives $\eta^c(h_{14}-h_{24})=0$; since $\eta^c>0$ on Ω, this yields $h_{14}=h_{24}$. The pairs (1,3) and (2,3) give $h_{14}=h_{34}$ and $h_{24}=h_{34}$ by identical arguments.

Conditions $(i,j)=(k,4)$ for k=1,2,3. For (1,4): $(HA)_{14} = Bh_{11}+Eh_{12}+Dh_{13}+\lambda^* \, h_{14}$, $(HA)_{41} = vh_{14}+\eta^c h_{44}$. Noting $\lambda^* \, -v = -2(1-L)v/L$, symmetry gives the stated condition. Conditions for k=2,3 follow by the same calculation. ☐

Remark 3.4

Subtracting the second condition from the third yields $B(h_{11}-h_{12})+E(h_{12}-h_{22})+D(h_{13}-h_{23})=0$, and subtracting the fourth from the third gives $B(h_{12}-h_{13})+E(h_{22}-h_{23})+D(h_{23}-h_{33})=0$. Since B,E, D>0 are independent in the physical domain, these are genuine polynomial constraints that force relationships among the diagonal and off-diagonal entries of H, severely restricting its structure.

3.3 The main non-existence theorem

Theorem 3.5 (Non-existence of a globally convex entropy pair)

The biofilm system does not admit a globally convex entropy pair (η, q) with $\nabla^2\eta \; > \; 0$ uniformly on any open set $\Omega' \; \subseteq W$ that contains states with both $v > 0$ and $v < 0$.

Proof.

Suppose for contradiction that (η, q) is a smooth entropy pair with $H = \nabla^2\eta > \; 0$ on Ω'. From the compatibility condition for (k=1), solving for h_{44}:

$h_{44} = (Bh_{11} + Eh_{12} + Dh_{13})/\eta^c - [2(1-L)v/(\eta^c L)]\, h_{14}$.

Here η^c, L, $1-L > 0$ on W, and B, E, D > 0. For fixed (B, E, D) — equivalently fixed L — this expression is an affine function of v:

$h_{44} = C_1(B,E,D,h_{ij}) - C_2(B,E,D,h_{14}) \cdot v$,

where $C_2 = 2(1-L)h_{14}/(\eta^c L)$. We claim $C_2 \neq 0$ generically. If $h_{14} = 0$, then by the first compatibility condition we also have $h_{24} = h_{34} = 0$, so the fourth row and column of H are decoupled from the first three. For $C_2 \neq 0$, the function $v \mapsto h_{44}$ is a non-constant affine function. Since Ω' contains both positive and negative velocities, the velocity interval $I_v = (-L^{3/2}\gamma^{1/2}(1-L)^{-\;1/2}, +L^{3/2}\gamma^{1/2}(1-L)^{-\;1/2})$ has positive length, and a non-constant affine function changes sign on I_v. Hence $h_{44} < 0$ for some $v \in I_v$, contradicting $H > \; 0$. If $C_2 = 0$ (i.e., $h_{14} = 0$), then η^c depends on v and $\eta^c \to 0^+$ for large |v| within W, forcing $h_{11} = h_{12} = h_{13} = 0$, again contradicting $H > \; 0$. In both cases we reach a contradiction, completing the proof. ☐

Remark 3.6 (Relation to the equilibrium point)

At the unique equilibrium $\bar{u} = (B\ ,E\ ,D\ ,0)$ identified in Bianchini and Natalini (2016), the velocity component is $v\ \; = 0$, so $C_2 v\ \; = 0$ and the sign-change argument does not apply locally. This is precisely why the symmetrizer $A_0\ (\bar{u})$ constructed in Bianchini and Natalini (2016) provides a local positive-definite structure near $\bar{u}$, without contradicting Theorem 3.5. The theorem asserts a global obstruction, which activates whenever $v \neq 0$.

Remark 3.7 (Comparison with Cargo–LeRoux)

The mechanism of Theorem 3.5 is structurally identical to the entropy non-existence in the Cargo–LeRoux gravitational system (Cargo & LeRoux, 1994): in both cases, the off-diagonal compatibility conditions force a diagonal entry of H to be an affine function of a state variable that ranges over an interval, making uniform positive definiteness impossible. The biofilm system presents a stronger constraint because the multi-component structure forces $h_{14} = h_{24} = h_{34}$, making the overdetermination more severe.

3.4 Consequences for admissibility and numerics

Corollary 3.8 (Failure of entropy-based convergence)

No discrete entropy inequality of the form $\eta(u_i^{n+\;\;1}) \leq \eta(u_i^n) - (\Delta t/\Delta x)(q_{i+\;\frac{1}{2}} - q_{i-\;\frac{1}{2}})$ can be established globally for system (2.2). The classical Lax–DiPerna compensated-compactness framework does not apply to this system on any domain containing states of both velocity signs.

Corollary 3.9 (Vanishing viscosity admissibility)

For the regularised system $\partial_t \;\; u + \partial_x F(u) = \varepsilon\partial_{xx}u$, smooth solutions u! exist for each $\varepsilon > 0$. The physically admissible weak solution of (2.2) is the limit $u = \lim_{! \to 0} u^{!}$ in L^{1Loc}, in the sense of the vanishing viscosity theory of Bianchini and Bressan (2005). Shock waves that are admissible in this sense satisfy the Liu entropy condition (Liu, 1976), which reduces to the Lax condition (Lax, 1957) in regions where genuine nonlinearity holds.

4 Wave Structure and Riemann Problem

4.1 Eigenvectors of the Flux Jacobian

We compute the right eigenvectors of $A(u)$ for all four eigenvalue families.

Eigenvectors for $\lambda_{1,2} = v$ (multiplicity 2)

Solving $(A-vI)r = 0$: the first three rows give $Br_4 = Er_4 = Dr_4 = 0$, hence $r_4 = 0$ (since $B, E, D > 0$). The fourth row then gives $r_1 + r_2 + r_3 = 0$. Two linearly independent solutions are

$$r_1 = (1,-1,0,0)^T, \quad r_2 = (0,1,-1,0)^T. \qquad (4.1)$$

Both have zero v-component: the corresponding waves affect only the biological composition, not the flow speed.

Eigenvectors for $\lambda_{3,4}$

Setting $\sigma = \sqrt{((1-L)\Delta)}$ and $\mu_\pm = -(1-L)v/L \pm \sigma$, so that $\lambda_{3,4} - v = \mu_\pm$, the first three rows give $r_1 = B/\mu_\pm$, $r_2 = E/\mu_\pm$, $r_3 = D/\mu_\pm$ (with $r_4 = 1$). Rescaling:

$$r_3 = (B, E, D, \mu_-)^T, \quad r_4 = (B, E, D, \mu_+)^T. \qquad (4.2)$$

The four vectors $\{r_1, r_2, r_3, r_4\}$ are linearly independent whenever $\mu_+ \neq \mu_-$, i.e., $\sigma > 0$, which holds on all of W.

4.2 Genuine Nonlinearity and Linear Degeneracy

Definition 4.1 (GNL/LD)

The k-th characteristic field is genuinely nonlinear (GNL) if $\nabla\lambda_k \cdot r_k \neq 0$ for all $u \in \Omega$, and linearly degenerate (LD) if $\nabla\lambda_k \cdot r_k \equiv 0$.

Proposition 4.2 (Linear degeneracy of fields 1 and 2)

The characteristic fields associated with λ_1 and λ_2 are linearly degenerate on Ω.

Proof.

Since $\lambda_{1,2} = v$, we have $\nabla\lambda_{1,2} = (0,0,0,1)^T$. Thus $\nabla\lambda_1 \cdot r_1 = (0,0,0,1)\cdot(1,-1,0,0)^T = 0$ and $\nabla\lambda_2 \cdot r_2 = (0,0,0,1)\cdot(0,1,-1,0)^T = 0$. ☐

Proposition 4.3 (GNL with inflection locus for fields 3 and 4)

Defining $\Sigma := \partial\sigma/\partial L = (\gamma + v^2/L^2)/(2\sigma)$, the characteristic variation of fields 3 and 4 evaluates to an expression that vanishes precisely on the locus $\{L = 3/5\}$. Specifically, at $v = 0$:

$$\nabla\lambda_{3,4} \cdot r_{3,4}\big|_{v=0} = \pm\sqrt{(\gamma/L)} \cdot (5L-3)/2. \qquad (4.3)$$

This vanishes precisely on the locus $\{L = 3/5\}$.

Remark 4.4 (Physical interpretation of the inflection locus)

The surface $\{L=3/5\}$, equivalently $\{B+E+D=2/5\}$, separates two regions: for $L>3/5$ (liquid-rich regime), $\nabla\lambda_{3,4}\cdot r_{3,4}$ is positive/negative for fields 4/3; for $L<3/5$ (solid-rich regime), the signs reverse. Across this surface, the wave type transitions between convex and concave characteristics, producing composite (compound) waves — a rarefaction joined continuously to a shock — in the Riemann solution. This is analogous to the non-convex scalar conservation law, where the Liu entropy condition (Liu, 1976) governs admissibility across the inflection point.

4.3 Elementary Waves

Contact discontinuities (fields 1 and 2)

Linear degeneracy implies that fields 1 and 2 produce only contact discontinuities propagating at speed $s = v$. Across such a wave:

$[v] = 0, \quad [L] = 0,$ while $[B/E]$ or $[B/D]$ may be arbitrary.

The velocity and liquid fraction are continuous; the biological composition (ratios of B:E:D) can jump freely.

Rankine–Hugoniot conditions

A shock connecting left state u^L to right state u^R at speed s must satisfy $s[u] = [F(u)]$, giving

$s[B] = [Bv], \quad s[E] = [Ev], \quad s[D] = [Dv],$

$s[v] = [(3L-2)v^2/(2L) + \gamma(L + \ln(1-L))].$

For a nonlinear shock with $[v] \neq 0$, the speed is $s = [(3L-2)v^2/(2L) + \gamma(L+\ln(1-L))]/[v]$. Admissibility of the shock is governed by the Liu entropy condition (Corollary 3.9), which reduces to the Lax condition outside the inflection locus $\{L=3/5\}$.

Composite waves near the inflection locus

When the Riemann data (u^L, u^R) are such that the solution path of field 3 or 4 crosses $\{L=3/5\}$, a composite wave arises: a rarefaction fan attached to a shock, with the junction at the inflection locus. The shock component satisfies the Liu entropy condition, and the rarefaction component is the integral curve of $r_{3,4}$ within the region where the field is GNL.

4.4 Structure of the Riemann solution

Theorem 4.5 (Riemann solution structure)

For initial data $(u^L, u^R) \in \Omega\times\Omega$ sufficiently close, the Riemann problem for (2.2) has a unique self-similar weak solution consisting of the wave pattern

$u^L \longrightarrow(\text{ə}_3)\ u^{m_1} \longrightarrow(\text{cD}_1)\ u^{m_2} \longrightarrow(\text{cD}_2)\ u^{m_3} \longrightarrow(\text{ə}_4)\ u^R$,

where $\text{ə}_{3,4}$ denotes a nonlinear wave (shock, rarefaction, or composite) of the 3rd/4th family, $\text{cD}_{1,2}$ are contact discontinuities, and u^{m_1}, u^{m_2}, u^{m_3} are constant intermediate states satisfying $v^{m_1} = v^{m_2} = v^{m_3} =: v^m$, $L^{m_1} = L^{m_2} = L^{m_3} =: L^m$. The pair (v^m, L^m) is determined by a 2×2 nonlinear system arising from the intersection of the 3-wave curve through u^L and the 4-wave curve through u^R.

Proof Sketch

The ordering $\lambda_3 < v < \lambda_4$ on W (verified at $v=0$: $\lambda_3 = -\sqrt{(L\gamma)} < 0 < \sqrt{(L\gamma)} = \lambda_4$, and preserved for small v by continuity) places the two contacts between the two nonlinear waves. The contact conditions force v and L to remain constant across the contact region, thereby establishing the intermediate-state conditions. The two-wave curves for fields 3 and 4 are smooth by the implicit function theorem away from $\{L=3/5\}$ and can be connected to the contact region by the intermediate conditions. Near $\{L=3/5\}$, composite waves arise as described above.

Remark 4.6 (Wave ordering and physical interpretation)

The 2–2 wave pattern mirrors the Euler equations: two acoustic-type nonlinear waves bracket a contact region. In the biofilm setting, the contacts carry jumps in the biological composition ratios B:E:D, representing the redistribution of species without changing the total solid fraction $1-L$ or the velocity v. The nonlinear waves carry compressive or expansive changes in L and v, representing pressure-driven rearrangement of the mixture.

5 Conclusion and Outlook

We have established two results for the one-dimensional biofilm system of Clarelli et al. (2013):

(i) Non-existence of a globally convex entropy pair. The compatibility system for the Hessian of any entropy η forces the (4,4)-entry of $\nabla^2\eta$ to be an affine function of v, which cannot remain positive on domains containing states of both velocity signs (Theorem 3.5). This places the biofilm system outside the Lax–DiPerna entropy framework and identifies vanishing viscosity as the correct admissibility mechanism (Corollaries 3.8–3.9).

(ii) Complete wave structure. Fields 1 and 2 are linearly degenerate (contact discontinuities carrying biological composition jumps). Fields 3 and 4 are genuinely nonlinear except on the inflection locus $\{L=3/5\}$, where composite waves arise. The Riemann solution has a 2–2 pattern with constant v and L across the contact region (Theorem 4.5).

Open problems

Several directions remain open.

(a) Bounded domain. The global-existence result of Bianchini and Natalini (2016) is restricted to the whole line; the bounded-domain problem with physical boundary conditions is explicitly identified there as future work. The Riemann solver developed here provides a tool for its numerical treatment.

(b) Multi-dimensional wave structure. The present analysis is one-dimensional. Extension to the multi-dimensional model of Clarelli et al. (2016) requires a planar-wave Riemann analysis and is substantially more complex.

(c) Large-data theory. Theorem 4.5 is a local result (small data). Global Riemann solutions for large data, shock formation, and blow-up times are open.

(d) Numerical scheme. A companion paper constructs a Godunov-type scheme based on the Riemann solver of Theorem 4.5, derives the modified equation showing that the numerical viscosity matrix $(\Delta x/2)|A(u)|$ is positive definite (replacing convex entropy as the admissibility mechanism), and presents numerical experiments verifying exponential decay to equilibrium, shock formation for large data, and shock thickness scaling.

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