Structure-preserving Interpolatory Model Reduction for Port-Hamiltonian Differential-Algebraic Systems

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Dedicated to Thanos Antoulas on the occasion of his 70th birthday

Abstract We examine interpolatory model reduction methods that are well-suited for treating large scale port-Hamiltonian differential-algebraic systems in a way that is able to preserve and take advantage of the underlying structural features of the system. We introduce approaches that incorporate regularization together with prudent selection of interpolation data. We focus on linear time-invariant systems and present a systematic treatment of a variety of model classes that include combinations of index-1 and index-2 systems, describing in particular how constraints may be represented in the transfer function and then preserved with interpolatory methods. We propose an algorithm to generate effective interpolation data and illustrate its effectiveness on a numerical example.

1 Introduction

Port-Hamiltonian (pH) systems are network-based models that arise within a modeling framework in which a physical system model is decomposed into submodels that are interconnected principally through the exchange of energy. Submodels may themselves be decomposed into submodels and at some level of branching they typically reflect one of a variety of core modeling paradigms that describe phenomenological aspects of the dynamics having different physical character, such as e.g. electrical, thermodynamic, or mechanical. The pH framework is able to knit together submodels featuring dramatically different physics through disciplined focus on energy flux as a principal mode of system interconnection; pH structure is inherited via power conserving interconnection, and a variety of physical properties

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and functional constraints (e.g., passivity and energy and momentum conservation) are encoded directly into the structure of the model equations [5, 25, 31]. Interconnection of submodels often creates further constraints on system behavior and evolution, originating as conservation laws (e.g., Kirchoff's laws or mass balance), or as position and velocity limitations in mechanical systems. As a result system models are often naturally posed as combinations of dynamical system equations and algebraic constraint equations, see e.g., [21]. *Port-Hamiltonian descriptor systems* and *port-Hamiltonian differential-algebraic equations* (pHDAE) are alternate terms for this model class.

When a pHDAE system is linearized around a stationary solution, one obtains a linear time-invariant pHDAE with specially structured coefficient matrices, see [5]. Although the approach we develop here can be extended easily to more general settings, we narrow our focus to a particular formulation as one of the simpler among alternative formulations laid out in [5, 24].

Definition 1 A linear time-invariant DAE system of the form

$$\begin{aligned} \mathbf{E}\dot{\mathbf{x}} &= (\mathbf{J}-\mathbf{R})\,\mathbf{x} + (\mathbf{B}-\mathbf{P})\,\mathbf{u}, \quad \mathbf{x}(t_0) = 0, \\ \mathbf{y} &= (\mathbf{B}+\mathbf{P})^T\,\mathbf{x} + (\mathbf{S}+\mathbf{N})\,\mathbf{u}, \end{aligned} \tag{1}$$

with $\mathbf{E}, \mathbf{J}, \mathbf{R} \in \mathbb{R}^{n\times n}$, $\mathbf{B}, \mathbf{P} \in \mathbb{R}^{n\times m}$, $\mathbf{S} = \mathbf{S}^T$, $\mathbf{N} = -\mathbf{N}^T \in \mathbb{R}^{m\times m}$, on a compact interval $\mathbb{I} \subset \mathbb{R}$ is a pHDAE system if the following properties are satisfied:

1. The differential-algebraic operator

   $$\mathbf{E}\frac{d}{dt} - \mathbf{J} : C^1(\mathbb{I}, \mathbb{R}^n) \to C^0(\mathbb{I}, \mathbb{R}^n)$$

   is *skew-adjoint*, i.e., we have that $\mathbf{J}^T = -\mathbf{J}$ and $\mathbf{E} = \mathbf{E}^T$,
2. $\mathbf{E}$ is positive semidefinite, i.e., $\mathbf{E} \geq 0$, and
3. the *passivity* matrix

   $$\mathbf{W} = \begin{bmatrix} \mathbf{R} & \mathbf{P} \\ \mathbf{P}^T & \mathbf{S} \end{bmatrix} \in \mathbb{R}^{(n+m)\times(n+m)}$$

   is symmetric positive semi-definite, i.e., $\mathbf{W} = \mathbf{W}^T \geq 0$.

Does not require anything about EQ=Q'E, so it is of high index

The associated quadratic *Hamiltonian function* $\mathcal{H} : \mathbb{R}^n \to \mathbb{R}$ of the system is $\mathcal{H}(\mathbf{x}) = \frac{1}{2}\mathbf{x}^T\mathbf{E}\mathbf{x}$.

In Definition 1, the Hessian matrix of $\mathcal{H}(\mathbf{x})$ is the *energy matrix*, $\mathbf{E}$. $\mathbf{R}$ is the *dissipation matrix*; $\mathbf{J}$ is the *structure matrix* describing the energy flux among internal energy storage elements; and $\mathbf{B} \pm \mathbf{P}$ are *port matrices* describing how energy enters and leaves the system. $\mathbf{S}$ and $\mathbf{N}$ are matrices associated with a *direct feed-through* from input $\mathbf{u}$ to output $\mathbf{y}$. If the system has a (classical) solution $\mathbf{x} \in C^1(\mathbb{I}, \mathbb{R}^n)$ in $\mathbb{I}$ when presented with a given input function $\mathbf{u}$, then the dissipation inequality

$$\frac{d}{dt}\mathcal{H}(\mathbf{x}) = \mathbf{u}^T\mathbf{y} - \begin{bmatrix} \mathbf{x} \\ \mathbf{u} \end{bmatrix}^T \mathbf{W} \begin{bmatrix} \mathbf{x} \\ \mathbf{u} \end{bmatrix}$$

must hold, i.e., the system is both *passive* and *Lyapunov stable*, as $\mathcal{H}$ defines a *Lyapunov function*, see [5].

In practice, network-based automated modeling tools such as MODELICA, MATLAB/SIMULINK, or or 20-sim[1] each may produce system models that are very often overdetermined as a consequence of redundant modeling, a situation that is often difficult to avoid. Thus, they contain either explicit or hidden algebraic constraints and so, the automated generation of a system model usually must be followed by a reformulation and regularization procedure that makes the system model compatible with standard simulation, control and optimization tools. When the system is pH, this regularization step should additionally respect the pH structure.

Note that pHDAE models may be very large and very complex, e.g., models that arise from semi-discretized (in space) continuum models in hydrodynamics [11, 20, 30], or mechanics [14, 26]. In such cases, model reduction techniques are necessary to enable application of control and optimization methods. Preservation of the pH, the constraint, and the interconnection structure is necessary to maintain model integrity.

Our focus in this work is on the construction of high fidelity reduced models for such pHDAE systems. For linear time-invariant pH systems with strictly positive-definite Hamiltonians (i.e., positive-definite $\mathbf{E}$), structure-preserving model reduction methods are well-developed, including tangential interpolation approaches [16, 17], moment matching [27, 29, 32] as well as effort and flow constraint reduction methods [28]. Interpolatory approaches have been extended to nonlinear pH systems as well, in [2] and [9].

We have special interest in the case of singular $\mathbf{E}$, for which only recently in [11, 19] have approaches been proposed extending model reduction techniques that preserve pH structure to this case. In order to obtain physically meaningful results it is essential to preserve both explicit and hidden constraints; see [18, 20, 26, 30] for the case of general unstructured DAE systems.

We discuss model reduction methods incorporating both regularization and interpolation for linear pHDAE systems having the form (1), taking advantage and respecting the structure. For different model classes we describe how constraints are represented in the transfer function, and how they can be preserved with interpolatory model reduction methods. The key step identifies, as in [5, 25], all the redundancies as well as both explicit and implicit system constraints, partitioning the system equations into redundant, algebraic, and dynamic parts. Only the dynamic part is then reduced in a way that preserves structure.

We proceed in §2 to recall basic properties of general DAE systems which will be important for later developments. In §3, we restrict consideration to pHDAEs and note important simplifications of the general regularization procedure to pHDAEs of the form (1). Structure preserving model reduction of pHDAEs using interpolatory methods is discussed first in general terms in §4, and then in more detail for specific model structures that include semi-explicit index-1 pHDAE systems (§4.1), semi-explicit pHDAE systems with index-2 constraints (§4.2), and finally, semi-explicit

[1] `https://www.modelica.org/`, `http://www.mathworks.com`, `https://www.20sim.com`

pHDAE systems with a combination of index-1 and index-2 constraints (4.3). We propose an algorithm to generate effective interpolation data in §5.1 followed by a numerical example that demonstrate its effectiveness.

2 General Differential-Algebraic Systems

In this section we recall some basic properties of general linear constant coefficient DAE systems

$$\begin{aligned} \mathbf{E}\dot{\mathbf{x}} &= \mathbf{A}\mathbf{x} + \mathbf{B}\mathbf{u}, \ \mathbf{x}(t_0) = 0, \\ \mathbf{y} &= \mathbf{C}\mathbf{x} + \mathbf{D}\mathbf{u}, \end{aligned} \tag{2}$$

where $\mathbf{E}$, $\mathbf{A} \in \mathbb{R}^{n\times n}$, $\mathbf{B} \in \mathbb{R}^{n\times m}$, $\mathbf{C} \in \mathbb{R}^{p\times n}$, $\mathbf{D} \in \mathbb{R}^{p\times m}$; for details, see, e.g., [7].

The matrix pencil $\lambda\mathbf{E} - \mathbf{A}$ is said to be *regular* if $\det(\lambda\mathbf{E} - \mathbf{A}) \neq 0$ for some $\lambda \in \mathbb{C}$. For regular pencils, the *finite eigenvalues* are the values $\lambda \in \mathbb{C}$ for which $\det(\lambda\mathbf{E} - \mathbf{A}) = 0$. If the *reversed pencil* $\lambda\mathbf{A} - \mathbf{E}$ has the eigenvalue 0 then this is the *infinite eigenvalue* of $\lambda\mathbf{E} - \mathbf{A}$.

With zero initial conditions $\mathbf{x}(t_0) = 0$ as in (2) and a regular pencil $\lambda\mathbf{E} - \mathbf{A}$, we obtain, in the frequency domain, the rational *transfer function*

$$\mathbf{H}(s) = \mathbf{C}(s\mathbf{E} - \mathbf{A})^{-1}\mathbf{B} + \mathbf{D}, \tag{3}$$

which maps Laplace transforms of the input functions $\mathbf{u}$ to the Laplace transforms of the corresponding output functions $\mathbf{y}$. If the transfer function is written as

$$\mathbf{H}(s) = \mathbf{G}(s) + \mathbf{P}(s),$$

where $\mathbf{G}(s)$ is a proper rational matrix function and $\mathbf{P}(s)$ is a polynomial matrix function, then the finite eigenvalues are the poles of the proper rational part, while infinite eigenvalues belong to the polynomial part.

In the following, a matrix with orthonormal columns spanning the right nullspace of the matrix $\mathbf{M}$ is denoted by $S_\infty(\mathbf{M})$ and a matrix with orthonormal columns spanning the left nullspace of $\mathbf{M}$ by $T_\infty(\mathbf{M})$. Although these matrices are not uniquely determined, we speak of these matrices as the corresponding spaces.

Regular pencils can be analyzed via the Weierstraß Canonical Form; see, e.g., [13].

Theorem 1 *If $\lambda\mathbf{E} - \mathbf{A}$ is a regular pencil, then there exist nonsingular matrices $\mathbf{U} = [\mathbf{U}_f, \mathbf{U}_\infty] \in \mathbb{R}^{n\times n}$ and $\mathbf{Y} = [\mathbf{V}_f, \mathbf{V}_\infty] \in \mathbb{R}^{n\times n}$ for which*

$$\mathbf{U}^T\mathbf{E}\mathbf{V} = \begin{bmatrix} \mathbf{U}_f^T \\ \mathbf{U}_\infty^T \end{bmatrix} \mathbf{E} \begin{bmatrix} \mathbf{V}_f & \mathbf{V}_\infty \end{bmatrix} = \begin{bmatrix} \mathbf{I} & 0 \\ 0 & \mathbf{N}_\infty \end{bmatrix}, \tag{4}$$

and

$$\mathbf{U}^T\mathbf{A}\mathbf{V} = \begin{bmatrix} \mathbf{U}_f^T \\ \mathbf{U}_\infty^T \end{bmatrix} \mathbf{A} \begin{bmatrix} \mathbf{V}_f & \mathbf{V}_\infty \end{bmatrix} = \begin{bmatrix} \mathbf{J}_f & 0 \\ 0 & \mathbf{I} \end{bmatrix}, \tag{5}$$

where $\mathbf{J}_f$ *is a matrix in Jordan canonical form whose diagonal elements are the finite eigenvalues of the pencil and* $\mathbf{N}_\infty$ *is a nilpotent matrix, also in Jordan form.* $\mathbf{J}_f$ *and* $\mathbf{N}_\infty$ *are unique up to permutation of Jordan blocks.*

The *index* ν of the pencil $\lambda\mathbf{E} - \mathbf{A}$ is the index of nilpotency of the matrix $\mathbf{N}_\infty$ in (4), and if $\mathbf{E}$ is nonsingular, then the pencil has index 0. A pencil $\lambda\mathbf{E} - \mathbf{A}$ has index less than or equal to 1 iff $T_\infty(\mathbf{E})^T \mathbf{A} S_\infty(\mathbf{E})$ is square and nonsingular.

2.1 Controllability and observability

To analyze general DAE systems and also to understand the properties of the transfer function, some controllability and observability conditions are needed, see e.g. [7, 10]. Consider the conditions

$$\text{C1}: \ \operatorname{rank}[\lambda\mathbf{E} - \mathbf{A}, \mathbf{B}] = n \text{ for all } \lambda \in \mathbb{C}, \qquad \text{C2}: \ \operatorname{rank}[\mathbf{E}, \mathbf{A}S_\infty(\mathbf{E}), \mathbf{B}] = n. \tag{6}$$

(C1) characterizes controllability of the dynamical system, while systems that satisfy condition (C2) are *controllable at infinity* or *impulse controllable* [10]. If both (C1) and (C2) hold, the system is *strongly controllable* [7]. Analogous observability conditions dual to (C1) and (C2) appear as

$$\text{O1}: \ \operatorname{rank}\begin{bmatrix} \lambda\mathbf{E} - \mathbf{A} \\ \mathbf{C} \end{bmatrix} = n \text{ for all } \lambda \in \mathbb{C}, \qquad \text{O2}: \ \operatorname{rank}\begin{bmatrix} \mathbf{E} \\ T_\infty^T(\mathbf{E})\mathbf{A} \\ \mathbf{C} \end{bmatrix} = n. \tag{7}$$

Condition (O1) characterizes observability of the dynamical system, and systems that satisfy both (O1) and (O2) are called *strongly observable*. Condition (O2) is *observability at infinity* or *impulse observability*. If a system is strongly controllable and strongly observable then the underlying dynamical system is *minimal*.

(C1) and (C2) are preserved under non-singular equivalence transformations as well as under state and output feedback, i.e., if the system satisfies (C1) or (C2), then for any non-singular $\mathbf{U} \in \mathbb{R}^{n\times n}$, $\mathbf{V} \in \mathbb{R}^{n\times n}$, and any $\mathbf{F}_1 \in \mathbb{R}^{m\times n}$ and $\mathbf{F}_2 \in \mathbb{R}^{m\times p}$, the system $(\tilde{\mathbf{E}}, \tilde{\mathbf{A}}, \tilde{\mathbf{B}}, \tilde{\mathbf{C}})$ satisfies the same condition for all of the following three choices:

$$\text{System 1:} \quad \tilde{\mathbf{E}} = \mathbf{UEV}, \quad \tilde{\mathbf{A}} = \mathbf{UAV}, \quad \tilde{\mathbf{B}} = \mathbf{UB}, \tag{8}$$

$$\text{System 2:} \quad \tilde{\mathbf{E}} = \mathbf{E}, \quad \tilde{\mathbf{A}} = \mathbf{A} + \mathbf{BF}_1, \quad \tilde{\mathbf{B}} = \mathbf{B}, \tag{9}$$

$$\text{System 3:} \quad \tilde{\mathbf{E}} = \mathbf{E}, \quad \tilde{\mathbf{A}} = \mathbf{A} + \mathbf{BF}_2\mathbf{C}, \quad \tilde{\mathbf{B}} = \mathbf{B}, \tag{10}$$

Analogous properties hold for (O1) and (O2).

Note, however, that regularity or non-regularity of the pencil, the index, and the polynomial part of the transfer function are in general not preserved under state or output feedback. For systems that satisfy (C2), there exists a suitable linear state feedback matrix $\mathbf{F}_1$ that such that $\lambda\mathbf{E} - (\mathbf{A} + \mathbf{BF}_1))$ is regular and of index at most one. Also if conditions (C2) and (O2) hold, then there exists a linear output feedback

matrix $\mathbf{F}_2$ so that the pencil $\lambda\mathbf{E} - (\mathbf{A} + \mathbf{B}\mathbf{F}_2\mathbf{C})$ has this property, see [7]. In practical control design it is therefore common, see [21], to first perform a regularization procedure that we will briefly discuss in the next subsection.

3 Regularization of PHDAE Systems

In general, it cannot be guaranteed that a system, generated either from a realization procedure or an automated modeling procedure, has a regular pencil $\lambda\mathbf{E} - \mathbf{A}$. Therefore, typically a regularization procedure has to be applied, see [6,8,21]. For pHDAEs the structure helps simplify theses general regularization procedures significantly.

The pencil $\lambda\mathbf{E} - (\mathbf{J} - \mathbf{R})$ associated with a free *dissipative Hamiltonian* DAE system (i.e., $\mathbf{u} = 0$) has many nice properties [24]: The index of the system is at most two; all eigenvalues are in the closed left half plane; and all eigenvalues on the imaginary axis are semi-simple (except for possibly the eigenvalue 0, which may have Jordan blocks of size at most two). Furthermore, a singular pencil can only occur when $\mathbf{E}, \mathbf{J}, \mathbf{R}$ have a common nullspace; see [23]. Therefore, if one is able to efficiently compute this common nullspace, it is possible to remove the singular part.

Lemma 1 *For the pHDAE in* (1)*, there exists an orthogonal basis transformation matrix* $\mathbf{V} \in \mathbb{R}^{n\times n}$ *such that in the new variable* $\widetilde{\mathbf{x}} = \begin{bmatrix} \widetilde{\mathbf{x}}_1^T & \widetilde{\mathbf{x}}_2^T T & \widetilde{\mathbf{x}}_3^T \end{bmatrix}^T = \mathbf{V}^T\mathbf{x}$*, the system has the form*

$$\begin{bmatrix} \mathbf{E}_1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \dot{\widetilde{\mathbf{x}}}_1 \\ \dot{\widetilde{\mathbf{x}}}_2 \\ \dot{\widetilde{\mathbf{x}}}_3 \end{bmatrix} = \begin{bmatrix} \mathbf{J}_1 - \mathbf{R}_1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \widetilde{\mathbf{x}}_1 \\ \widetilde{\mathbf{x}}_2 \\ \widetilde{\mathbf{x}}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{B}_1 - \mathbf{P}_1 \\ \mathbf{B}_2 \\ 0 \end{bmatrix} \mathbf{u}, \tag{11}$$

$$\mathbf{y} = \begin{bmatrix} (\mathbf{B}_1 + \mathbf{P}_1)^T & \mathbf{B}_2^T & 0 \end{bmatrix} \begin{bmatrix} \widetilde{\mathbf{x}}_1 \\ \widetilde{\mathbf{x}}_2 \\ \widetilde{\mathbf{x}}_3 \end{bmatrix} + (\mathbf{S} + \mathbf{N})\mathbf{u}, \tag{12}$$

where $\lambda\mathbf{E}_1 - (\mathbf{J}_1 - \mathbf{R}_1)$ *is a regular pencil and* $\mathbf{B}_2$ *has full row rank. Also, the subsystem*

$$\begin{bmatrix} \mathbf{E}_1 & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \dot{\widetilde{\mathbf{x}}}_1 \\ \dot{\widetilde{\mathbf{x}}}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{J}_1 - \mathbf{R}_1 & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \widetilde{\mathbf{x}}_1 \\ \widetilde{\mathbf{x}}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{B}_1 - \mathbf{P}_1 \\ \mathbf{B}_2 \end{bmatrix} \mathbf{u}, \tag{13}$$

$$\mathbf{y} = \begin{bmatrix} (\mathbf{B}_1 + \mathbf{P}_1)^T & \mathbf{B}_2^T \end{bmatrix} \begin{bmatrix} \widetilde{\mathbf{x}}_1 \\ \widetilde{\mathbf{x}}_2 \end{bmatrix} + (\mathbf{S} + \mathbf{N})\mathbf{u}, \tag{14}$$

that is obtained by removing the third equation and the variable $\mathbf{x}_3$ *is still a pHDAE.*

Proof First determine an orthogonal matrix $\mathbf{V}_1$ (via SVD) such that

$$\mathbf{V}_1^T(\lambda\mathbf{E} - (\mathbf{J} - \mathbf{R}))\mathbf{V}_1 = \lambda \begin{bmatrix} \mathbf{E}_1 & 0 \\ 0 & 0 \end{bmatrix} - \begin{bmatrix} \mathbf{J}_1 - \mathbf{R}_1 & 0 \\ 0 & 0 \end{bmatrix}, \ \mathbf{V}_1^T(\mathbf{B} - \mathbf{P}) = \begin{bmatrix} \mathbf{B}_1 - \mathbf{P}_1 \\ \tilde{\mathbf{B}}_2 - \tilde{\mathbf{P}}_2 \end{bmatrix}.$$

Such $\mathbf{V}_1$ exists, since $\mathbf{E}, \mathbf{J}, \mathbf{R}$ have a common nullspace when the pencil $\lambda\mathbf{E} - (\mathbf{J} - \mathbf{R})$ is singular [23]. Then a row compression of $\tilde{\mathbf{B}}_2 - \tilde{\mathbf{P}}_2$ via an orthogonal matrix $\tilde{\mathbf{V}}_2$ and a congruence transformation with $\mathbf{V}_2 = \mathsf{diag}(\mathbf{I}, \tilde{\mathbf{V}}_2)$ is performed, so that with $\mathbf{V} = \mathsf{diag}(\mathbf{V}_1, \mathbf{V}_2)$, we obtain the zero pattern in (11). Updating the output equation accordingly and using the fact that the transformed passivity matrix

$$\tilde{\mathbf{W}} = \begin{bmatrix} \mathbf{V}^T\mathbf{R}\mathbf{V} & \mathbf{V}^T\mathbf{P} \\ \mathbf{P}^T\mathbf{V}^T & \mathbf{S} \end{bmatrix} \in \mathbb{R}^{(n+m)\times(n+m)}$$

is still semidefinite; it follows that $\mathbf{P}_2 = 0$ and $\mathbf{P}_3 = 0$, giving the desired form. □

The next result presents a condensed form and shows that the controllability conditions (C2) and (O2) are equivalent and hold for (13)-(14).

Lemma 2 *For the pHDAE in (13)-(14), there exists an orthogonal basis transformation $\widehat{\mathbf{V}}$ such that in the new variable $\widehat{\mathbf{x}} = \begin{bmatrix} \widehat{\mathbf{x}}_1^T & \widehat{\mathbf{x}}_2^T & \widehat{\mathbf{x}}_3^T & \widehat{\mathbf{x}}_4^T & \widehat{\mathbf{x}}_5^T \end{bmatrix}^T = \widehat{\mathbf{V}}^T \begin{bmatrix} \widetilde{\mathbf{x}}_1^T & \widetilde{\mathbf{x}}_2^T \end{bmatrix}^T$, the system has the form*

$$\begin{bmatrix} \mathbf{E}_{11} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \dot{\widehat{\mathbf{x}}}_1 \\ \dot{\widehat{\mathbf{x}}}_2 \\ \dot{\widehat{\mathbf{x}}}_3 \\ \dot{\widehat{\mathbf{x}}}_4 \\ \dot{\widehat{\mathbf{x}}}_5 \end{bmatrix} = \begin{bmatrix} \mathbf{J}_{11} - \mathbf{R}_{11} & \mathbf{J}_{12} - \mathbf{R}_{12} & \mathbf{J}_{13} & \mathbf{J}_{14} & 0 \\ \mathbf{J}_{21} - \mathbf{R}_{21} & \mathbf{J}_{22} - \mathbf{R}_{22} & \mathbf{J}_{23} & \mathbf{J}_{24} & 0 \\ \mathbf{J}_{31} & \mathbf{J}_{32} & \mathbf{J}_{33} & 0 & 0 \\ \mathbf{J}_{41} & \mathbf{J}_{42} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \widehat{\mathbf{x}}_1 \\ \widehat{\mathbf{x}}_2 \\ \widehat{\mathbf{x}}_3 \\ \widehat{\mathbf{x}}_4 \\ \widehat{\mathbf{x}}_5 \end{bmatrix} + \begin{bmatrix} \mathbf{B}_1 - \mathbf{P}_1 \\ \mathbf{B}_2 - \mathbf{P}_2 \\ \mathbf{B}_3 \\ \mathbf{B}_4 \\ \mathbf{B}_5 \end{bmatrix} \mathbf{u}, \quad (15)$$

$$\mathbf{y} = \begin{bmatrix} (\mathbf{B}_1 + \mathbf{P}_1)^T & (\mathbf{B}_2 + \mathbf{P}_2)^T & \mathbf{B}_3^T & \mathbf{B}_4^T & \mathbf{B}_5^T \end{bmatrix} \begin{bmatrix} \widehat{\mathbf{x}}_1 \\ \widehat{\mathbf{x}}_2 \\ \widehat{\mathbf{x}}_3 \\ \widehat{\mathbf{x}}_4 \\ \widehat{\mathbf{x}}_5 \end{bmatrix} + (\mathbf{S} + \mathbf{N})\mathbf{u}, \quad (16)$$

where $\mathbf{E}_{11}, \mathbf{R}_{22}, \mathbf{J}_{33}$, and $\begin{bmatrix} \mathbf{J}_{41} & \mathbf{J}_{42} \end{bmatrix} = \begin{bmatrix} -\mathbf{J}_{14}^T & -\mathbf{J}_{24}^T \end{bmatrix}$ have full row rank. Furthermore, the system satisfies (C2) *and equivalently* (O2).

Proof Starting with the form (13)-(14), one first determines an orthogonal matrix $\widetilde{\mathbf{V}}_1$ (via a spectral decomposition of $\mathbf{E}_1$) such $\widetilde{\mathbf{V}}_1^T\mathbf{E}_1\widetilde{\mathbf{V}}_1 = \begin{bmatrix} \mathbf{E}_{11} & 0 \\ 0 & 0 \end{bmatrix}$ with $\mathbf{E}_{11} > 0$, and then forms a congruence transformation with $\widehat{\mathbf{V}}_1 = \mathsf{diag}(\widetilde{\mathbf{V}}_1, \mathbf{I})$ yielding

$$\widehat{\mathbf{V}}_1^T(\mathbf{J} - \mathbf{R})\widehat{\mathbf{V}}_1 = \begin{bmatrix} \tilde{\mathbf{J}}_{11} - \tilde{\mathbf{R}}_{11} & \tilde{\mathbf{J}}_{12} - \tilde{\mathbf{R}}_{12} & 0 \\ \tilde{\mathbf{J}}_{21} - \tilde{\mathbf{R}}_{21} & \tilde{\mathbf{J}}_{22} - \tilde{\mathbf{R}}_{22} & 0 \\ 0 & 0 & 0 \end{bmatrix}, \ \widehat{\mathbf{V}}_1^T(\mathbf{B} - \mathbf{P}) = \begin{bmatrix} \tilde{\mathbf{B}}_1 - \tilde{\mathbf{P}}_1 \\ \tilde{\mathbf{B}}_2 - \tilde{\mathbf{P}}_2 \\ \tilde{\mathbf{B}}_3 - \tilde{\mathbf{P}}_3 \end{bmatrix}.$$

Next compute a spectral decomposition $\widetilde{\mathbf{V}}_2^T\widetilde{\mathbf{R}}_{22}\widetilde{\mathbf{V}}_2 = \begin{bmatrix} \widehat{\mathbf{R}}_{22} & 0 \\ 0 & 0 \end{bmatrix}$, where $\widehat{\mathbf{R}}_{22} > 0$. Then an appropriate congruence transformation with $\widehat{\mathbf{V}}_2 = \mathsf{diag}(\mathbf{I}, \widetilde{\mathbf{V}}_2, \mathbf{I})$ yields

$$\widehat{\mathbf{V}}_2^T\widehat{\mathbf{V}}_1^T\mathbf{E}\widehat{\mathbf{V}}_1\widehat{\mathbf{V}}_2 = \begin{bmatrix} \mathbf{E}_{11} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix},$$

$$\widehat{\mathbf{V}}_2^T\widehat{\mathbf{V}}_1^T(\mathbf{J}-\mathbf{R})\widehat{\mathbf{V}}_1\widehat{\mathbf{V}}_2 = \begin{bmatrix} \widehat{\mathbf{J}}_{11}-\widehat{\mathbf{R}}_{11} & \widehat{\mathbf{J}}_{12}-\widehat{\mathbf{R}}_{12} & \widehat{\mathbf{J}}_{13} & 0 \\ \widehat{\mathbf{J}}_{21}-\widehat{\mathbf{R}}_{21} & \widehat{\mathbf{J}}_{22}-\widehat{\mathbf{R}}_{22} & \widehat{\mathbf{J}}_{23} & 0 \\ \widehat{\mathbf{J}}_{31} & \widehat{\mathbf{J}}_{32} & \widehat{\mathbf{J}}_{33} & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \ \widehat{\mathbf{V}}_2^T\widehat{\mathbf{V}}_1^T(\mathbf{B}-\mathbf{P}) = \begin{bmatrix} \widehat{\mathbf{B}}_1-\widehat{\mathbf{P}}_1 \\ \widehat{\mathbf{B}}_2-\widehat{\mathbf{P}}_2 \\ \widehat{\mathbf{B}}_3-\widehat{\mathbf{P}}_3 \\ \widehat{\mathbf{B}}_4-\widehat{\mathbf{P}}_4 \end{bmatrix}.$$

Finally performing a spectral decomposition $\widetilde{\mathbf{V}}_3^T\widetilde{\mathbf{J}}_{33}\widetilde{\widetilde{\mathbf{V}}}_3 = \begin{bmatrix} \mathbf{J}_{33} & 0 \\ 0 & 0 \end{bmatrix}$, with $\mathbf{J}_{33}$ non-singular, and an appropriate congruence transformation with $\widehat{\mathbf{V}}_3 = \mathsf{diag}(\mathbf{I}, \mathbf{I}, \widetilde{\widetilde{\mathbf{V}}}_3, \mathbf{I})$ yields the desired form together with the updating of the output equation accordingly. The fact that the blocks $\mathbf{P}_3, \mathbf{P}_4, \mathbf{P}_5$ blocks do not appear follows again from the semidefiniteness of the transformed passivity matrix. By the symmetry structure it follows directly that the condition (C2) holds if and only (O2) holds. Since $\mathbf{E}_{11} > 0$, $\mathbf{R}_{22} > 0$, and $\mathbf{J}_{33}$ is invertible, this holds if and only if the matrix $\begin{bmatrix} \mathbf{J}_{41} & \mathbf{J}_{42} & \mathbf{B}_4 \\ 0 & 0 & \mathbf{B}_5 \end{bmatrix}$ has full rank, which is the case because $\mathbf{B}_5$ (which is the block $\mathbf{B}_2$ in (13)-(14)) has full row rank and the matrices $\mathbf{E}_1, \mathbf{J}_1, \mathbf{R}_1$ were assumed not to have a left nullspace anymore; thus $\begin{bmatrix} \mathbf{J}_{41} & \mathbf{J}_{42} \end{bmatrix}$ has full row rank. □

Note that even though the procedure to compute the condensed form (11)-(12) was used to prove that the controllability conditions (C2) and (O2) hold, it also immediately separates the dynamical part (given by the first block row) the algebraic index-1 conditions (with and without dissipation, given by the second and third block rows), and the index-2 conditions (given by the fourth block row). The last row is the singular part of the free system. However, since the conditions (C2) and (O2) hold, the system can be made regular by output feedback. Note that this is already displayed in the subsystem (13)-(14), so the regularization can be made immediately after creating (13)-(14). Let us denote, for ease of notation, this subsystem by

$$\begin{aligned} \mathbf{E}_r\dot{\mathbf{x}}_r &= (\mathbf{J}_r - \mathbf{R}_r)\,\mathbf{x}_r + (\mathbf{B}_r - \mathbf{P}_r)\,\mathbf{u},\ \mathbf{x}_r(t_0) = 0, \\ \mathbf{y}_r &= (\mathbf{B}_r + \mathbf{P}_r)^T\,\mathbf{x} + (\mathbf{S}_r + \mathbf{N}_r)\,\mathbf{u}. \end{aligned}$$

If we apply an output feedback $\mathbf{u} = -\mathbf{K}_r\mathbf{y}_r$ with $\mathbf{K}_r = \mathbf{K}_r^T > 0$, that makes the (2,2) block in the closed loop system invertible, i.e., it turns the singular part into an index-1 equation. This corresponds to a feedback for the state-to-output map in (13) of the form $\mathbf{y}_r = (\mathbf{I} + (\mathbf{S}_r + \mathbf{N}_r)\mathbf{K}_r)^{-1}((\mathbf{B}_r + \mathbf{P}_r)^T\mathbf{x}_r$, which we can insert into the first equation to obtain

$$\begin{aligned} \mathbf{E}_r\dot{\mathbf{x}}_r &= (\mathbf{J}_r - \mathbf{R}_r)\mathbf{x}_r + (\mathbf{B}_r - \mathbf{P}_r)\mathbf{K}_r\mathbf{y}_r \\ &= \left((\mathbf{J}_r - \mathbf{R}_r) - (\mathbf{B}_r - \mathbf{P}_r)(\mathbf{K}_r^{-1} + (\mathbf{S}_r + \mathbf{N}_r))^{-1}((\mathbf{B}_r + \mathbf{P})^T\right)\mathbf{x}_r. \end{aligned}$$

The negative of the symmetric part of the system matrix is the Schur complement of

$$\tilde{\mathbf{W}}_r = \begin{bmatrix} \mathbf{R}_r & \mathbf{P}_r \\ \mathbf{P}_r^T & \mathbf{K}_r^{-1} + \mathbf{S}_r + \mathbf{N}_r \end{bmatrix} \geq 0.$$

Hence the closed loop system is regular and the closed loop system is still pH.

The regularization procedures described above are computationally demanding, since they typically require large-scale singular value decompositions or spectral decompositions. Fortunately, in many practical cases the condensed form is already available directly from the modeling procedure, so that the transfer function can be formed and the model reduction method can be directly applied. In the following sections we assume that this is the case and extend the tangential interpolation model reduction procedure of [18] to three classes of semi-explicit systems.

4 Interpolatory model reduction of pHDAEs

Given an order-n pHDAE as in (1), we want to construct an order-r reduced pHDAE, with $r \ll n$, having the same structured form

$$\begin{aligned} \widehat{\mathbf{E}}\dot{\mathbf{x}}_r &= (\widehat{\mathbf{J}} - \widehat{\mathbf{R}})\,\mathbf{x}_r + (\widehat{\mathbf{B}} - \widehat{\mathbf{P}})\,\mathbf{u},\ \mathbf{x}_r(t_0) = 0, \\ \mathbf{y}_r &= (\widehat{\mathbf{B}} + \widehat{\mathbf{P}})^T\,\mathbf{x}_r + (\widehat{\mathbf{S}} + \widehat{\mathbf{N}})\,\mathbf{u}, \end{aligned} \tag{17}$$

such that $\widehat{\mathbf{E}}, \widehat{\mathbf{J}}, \widehat{\mathbf{R}} \in \mathbb{R}^{r\times r}$, $\widehat{\mathbf{B}}, \widehat{\mathbf{P}} \in \mathbb{R}^{r\times m}$, $\widehat{\mathbf{S}} = \widehat{\mathbf{S}}^T$, $\widehat{\mathbf{N}} = -\widehat{\mathbf{N}}^T \in \mathbb{R}^{m\times m}$ satisfy the same requirements as in Definition 1 and that the output $\mathbf{y}_r(t)$ of (17) is an accurate approximation to the original output $\mathbf{y}(t)$ over a wide range of admissible inputs $\mathbf{u}(t)$. We will enforce accuracy by constructing the reduced model (17) via interpolation.

Let $\mathbf{H}(s) = \mathcal{C}(s\mathbf{E} - \mathbf{A})^{-1}\mathcal{B} + \mathbf{D}$ and $\widehat{\mathbf{H}}(s) = \widehat{\mathcal{C}}(s\widehat{\mathbf{E}} - \widehat{\mathbf{A}})^{-1}\widehat{\mathcal{B}} + \widehat{\mathbf{D}}$ denote the transfer functions of (1) and (17), where $\mathcal{C} = (\mathbf{B} + \mathbf{P})^T$, $\mathbf{A} = \mathbf{J} - \mathbf{R}$, $\mathcal{B} = \mathbf{B} - \mathbf{P}$, $\mathbf{D} = \mathbf{S} + \mathbf{N}$, and similarly for the reduced-order ("hat") quantities. Given the right-interpolation points $\{\sigma_1, \sigma_2, \ldots, \sigma_r\} \in \mathbb{C}$ together with the corresponding left-tangent directions $\{\boldsymbol{b}_1, \boldsymbol{b}_2, \ldots, \boldsymbol{b}_r\} \in \mathbb{C}^m$ and the left-interpolation points $\{\mu_1, \mu_2, \ldots, \mu_r\} \in \mathbb{C}$ together with the corresponding right-tangent directions $\{\boldsymbol{\ell}_1, \boldsymbol{\ell}_2, \ldots, \boldsymbol{\ell}_r\} \in \mathbb{C}^m$, we would like to construct $\widehat{\mathbf{H}}(s)$ such that it tangentially interpolates $\mathbf{H}(s)$, i.e.,

$$\mathbf{H}(\sigma_i)\boldsymbol{b}_i = \widehat{\mathbf{H}}(\sigma_i)\boldsymbol{b}_i \quad \text{and} \quad \boldsymbol{\ell}_i^T\mathbf{H}(\mu_i) = \boldsymbol{\ell}_i^T\widehat{\mathbf{H}}(\mu_i), \ \text{ for } i = 1, 2, \ldots, r. \tag{18}$$

These tangential interpolation conditions can be easily enforced via a Petrov-Galerkin projection [1, 3, 12]. Construct $\mathbf{V} \in \mathbb{C}^{n\times r}$ and $\mathbf{Z} \in \mathbb{C}^{n\times r}$ using

$$\mathbf{V} = \left[(\sigma_1\mathbf{E} - \mathbf{A})^{-1}\mathcal{B}\boldsymbol{b}_1,\ (\sigma_2\mathbf{E} - \mathbf{A})^{-1}\mathcal{B}\boldsymbol{b}_2,\ \cdots (\sigma_r\mathbf{E} - \mathbf{A})^{-1}\mathcal{B}\boldsymbol{b}_r\right] \text{ and} \tag{19}$$

$$\mathbf{Z} = \left[(\mu_1\mathbf{E} - \mathbf{A})^{-T}\mathcal{C}^T\boldsymbol{\ell}_1,\ (\mu_2\mathbf{E} - \mathbf{A})^{-T}\mathcal{C}^T\boldsymbol{\ell}_2,\ \cdots (\mu_r\mathbf{E} - \mathbf{A})^{-1}\mathcal{C}^T\boldsymbol{\ell}_r\right]. \tag{20}$$

Then the interpolatory reduced model can be obtained via projection:

$$\widehat{\mathbf{E}} = \mathbf{Z}^T\mathbf{E}\mathbf{V},\ \ \widehat{\mathbf{A}} = \mathbf{Z}^T\mathbf{A}\mathbf{V},\ \ \widehat{\mathcal{B}} = \mathbf{Z}^T\mathcal{B},\ \ \widehat{\mathcal{C}} = \mathcal{C}\mathbf{V},\ \text{ and }\ \widehat{\mathbf{D}} = \mathbf{D}. \tag{21}$$

In the setting of pHDAEs two fundamental issues arise: First, the reduced quantities in (21) are no longer guaranteed to have the pH structure. This is easiest to see in the reduced quantity $\widehat{\mathcal{A}} = \mathbf{Z}^T\mathcal{A}\mathbf{V} = \mathbf{Z}^T\mathbf{J}\mathbf{V} - \mathbf{Z}^T\mathbf{R}\mathbf{V}$. If we decompose $\widehat{\mathcal{A}}$ into its symmetric and skew-symmetric parts, we can no longer guarantee that the symmetric part is positive semi-definite. This could be resolved by using a Galerkin projection, i.e., with $\mathbf{Z} = \mathbf{V}$. In this case one only satisfies the interpolation conditions associated with right interpolation data. However, this does not resolve the second issue since in the generic case when $r < \text{rank}(\mathbf{E})$, the reduced quantity $\widehat{\mathbf{E}}$ is expected to be a nonsingular matrix; thus the reduced system will be an ODE. This means that the polynomial parts of $\mathbf{H}(s)$ and $\widehat{\mathbf{H}}(s)$ do not match, leading to unbounded errors.

Structure-preservation interpolatory reduction of pH systems in the most general setting of tangential interpolation has been studied in [16,17]. However, this work focused on the ODE case. On the other hand, [18] developed the tangential interpolation framework for reducing *unstructured* DAEs with guaranteed polynomial matching. Only recently in [11, 19], the combined problem has been investigated. We now develop a treatment of structure-preserving interpolatory model reduction problem for index-1 and index-2 pHDAEs in the general setting of tangential interpolation.

In the rest of this section, in some instances we will use the generic transfer function notations $\mathbf{H}(s) = \mathcal{C}(s\mathbf{E} - \mathbf{A})^{-1}\mathcal{B} + \mathbf{D}$ and $\widehat{\mathbf{H}}(s) = \widehat{\mathcal{C}}(s\widehat{\mathbf{E}} - \widehat{\mathbf{A}})^{-1}\widehat{\mathcal{B}} + \widehat{\mathbf{D}}$ for full and reduced pHDAEs. It will be clear from the context what the matrices $\mathbf{E}$, $\mathbf{A}$, $\mathcal{B}$, $\mathcal{C}$, $\mathbf{D}$, and their reduced counter-parts are in terms of the pH structure.

4.1 Semi-explicit index-1 pHDAE systems

The simplest class of pHDAEs are *semi-explicit index*-1 pHDAEs of the form

$$\begin{aligned}\begin{bmatrix} \mathbf{E}_{11} & 0 \\ 0 & 0 \end{bmatrix}\dot{\mathbf{x}}(t) &= \begin{bmatrix} \mathbf{J}_{11} - \mathbf{R}_{11} & \mathbf{J}_{12} - \mathbf{R}_{12} \\ -\mathbf{J}_{12}^T - \mathbf{R}_{12}^T & \mathbf{J}_{22} - \mathbf{R}_{22} \end{bmatrix}\mathbf{x}(t) + \begin{bmatrix} \mathbf{B}_1 - \mathbf{P}_1 \\ \mathbf{B}_2 - \mathbf{P}_2 \end{bmatrix}u(t), \\ \mathbf{y}(t) &= \begin{bmatrix} \mathbf{B}_1^T + \mathbf{P}_1^T & \mathbf{B}_2^T + \mathbf{P}_2^T \end{bmatrix}\mathbf{x}(t) + (\mathbf{S} + \mathbf{N})\mathbf{u}(t).\end{aligned} \tag{22}$$

where $\mathbf{E}_{11}$ and $\mathbf{J}_{22} - \mathbf{R}_{22}$ are nonsingular. We have the following interpolation result.

Theorem 2 *Consider the pHDAE system in* (22)*. Let the interpolation points* $\{\sigma_1, \sigma_2, \ldots, \sigma_r\} \in \mathbb{C}$ *and the corresponding tangent directions* $\{\boldsymbol{b}_1, \boldsymbol{b}_2, \ldots, \boldsymbol{b}_r\} \in \mathbb{C}^m$ *be given. Construct the interpolatory model reduction basis* $\mathbf{V}$ *as*

$$\mathbf{V} = \begin{bmatrix} \mathbf{V}_1 \\ \mathbf{V}_2 \end{bmatrix} = \left[(\sigma_1\mathbf{E} - \mathbf{A})^{-1}\mathcal{B}\boldsymbol{b}_1,\ \ \cdots,\ \ (\sigma_r\mathbf{E} - \mathbf{A})^{-1}\mathcal{B}\boldsymbol{b}_r\right] \in \mathbb{C}^{n\times r}, \tag{23}$$

where $\mathbf{V}$ *is partitioned conformably with the system, and define the matrices*

$$\mathbb{B} = \left[\boldsymbol{b}_1\ \boldsymbol{b}_2\ \cdots\ \boldsymbol{b}_r\right] \in \mathbb{C}^{m\times r} \text{ and } \mathcal{D} = \mathbf{D} - (\mathbf{B}_2^T + \mathbf{P}_2^T)(\mathbf{J}_{22} - \mathbf{R}_{22})^{-1}(\mathbf{B}_2 - \mathbf{P}_2) \in \mathbb{C}^{m\times m}.$$

Let $\mathbf{A} = \begin{bmatrix} \mathbf{A}_{11} & \mathbf{A}_{12} \\ \mathbf{A}_{21} & \mathbf{A}_{22} \end{bmatrix} = \mathbf{J} - \mathbf{R}$, *partitioned accordingly to* (22). *Then the transfer function* $\widehat{\mathbf{H}}(s)$ *of the reduced model*

$$\widehat{\mathbf{E}}\dot{\mathbf{x}}_r(t) = (\widehat{\mathbf{J}} - \widehat{\mathbf{R}})\mathbf{x}_r(t) + \widehat{\mathcal{B}}\mathbf{u}(t), \qquad \mathbf{y}_r(t) = \widehat{\mathcal{C}}\mathbf{x}_r(t) + \widehat{\mathbf{D}}\mathbf{u}(t) \tag{24}$$

with

$$\begin{aligned} \widehat{\mathbf{E}} &= \mathbf{V}_1^T\mathbf{E}_{11}\mathbf{V}_1 & \widehat{\mathcal{C}} &= \mathcal{C}\mathbf{V} + (\mathbf{B}_2^T + \mathbf{P}_2^T)\mathbf{A}_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2)\mathbb{B}, \\ \widehat{\mathbf{A}} &= \mathbf{V}^T\mathcal{A}\mathbf{V} + \mathbb{B}^T(\mathcal{D} - \mathbf{D})\mathbb{B}, & \widehat{\mathbf{D}} &= \mathcal{D} = \mathbf{D} - (\mathbf{B}_2^T + \mathbf{P}_2^T)\mathbf{A}_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2) \\ \widehat{\mathcal{B}} &= \mathbf{V}^T\mathcal{B} + \mathbb{B}^T(\mathbf{B}_2^T + \mathbf{P}_2^T)\mathbf{A}_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2), \end{aligned}$$

matches the polynomial part of $\mathbf{H}(s)$ *and tangentially interpolates it, i.e.,*

$$\mathbf{H}(\sigma_i)\boldsymbol{b}_i = \widehat{\mathbf{H}}(\sigma_i)\boldsymbol{b}_i, \ \text{for } i = 1, 2, \ldots, r.$$

Define $\widehat{\mathbf{P}} = \frac{1}{2}(-\widehat{\mathcal{G}} + \widehat{\mathcal{C}})$, *and decompose* $\widehat{\mathbf{D}} = \widehat{\mathbf{S}} + \widehat{\mathbf{N}}$, $\widehat{\mathbf{A}} = \widehat{\mathbf{J}} - \widehat{\mathbf{R}}$ *into their symmetric and skew-symmtric part. Then, the reduced model* (24) *is a* pHDAE *system if the reduced passivity matrix* $\widehat{\mathbf{W}} = \begin{bmatrix} \widehat{\mathbf{R}} & \widehat{\mathbf{P}} \\ \widehat{\mathbf{P}}^T & \widehat{\mathbf{S}} \end{bmatrix}$ *is positive seimdefinite.*

Proof We employ a Galerkin projection using the interpolatory model reduction basis $\mathbf{V}$ to obtain the *intermediate* reduced model

$$\widetilde{\mathbf{E}} = \mathbf{V}_1^T\mathbf{E}_{11}\mathbf{V}_1, \ \widetilde{\mathbf{A}} = \widetilde{\mathbf{J}} - \widetilde{\mathbf{R}} = \mathbf{V}^T\mathbf{J}\mathbf{V} - \mathbf{V}^T\mathbf{R}\mathbf{V}, \ \widetilde{\mathcal{B}} = \mathbf{V}^T\mathcal{B}, \ \widetilde{\mathcal{C}} = \mathcal{C}\mathbf{V} \text{ and } \widetilde{\mathbf{D}} = \mathbf{D}.$$

Even though this reduced model is a pHDAE system due to the one-sided Galerkin model reduction and it satisfies the tangential interpolation conditions, it will *not* match the transfer $\mathbf{H}(s)$ function at $s = \infty$, i..e, its polynomial part, given by

$$\lim_{s\to\infty} \mathbf{H}(s) = \mathcal{D} = \mathbf{D} - (\mathbf{B}_2^T + \mathbf{P}_2^T)\mathbf{A}_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2).$$

A remedy to this problem, proposed in [4,22] and employed in the general DAE setting in [18], is to modify the $\mathbf{D}$-term in the reduced model to match the polynomial part and at the same time *to shift* the other reduced quantities appropriately so as to keep the tangential interpolation property. Using this, we obtain a modified reduced model

$$\begin{aligned} \widehat{\mathbf{E}} &= \widetilde{\mathbf{E}} = \mathbf{V}_1^T\mathbf{E}_{11}\mathbf{V}_1, \\ \widehat{\mathbf{A}} &= \widetilde{\mathbf{A}} + \mathbb{B}^T(\mathcal{D} - \mathbf{D})\mathbb{B} = \mathbf{V}^T\mathbf{J}\mathbf{V} - \mathbf{V}^T\mathbf{R}\mathbf{V} - \mathbb{B}^T(\mathbf{B}_2^T + \mathbf{P}_2^T)A_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2)\mathbb{B}, \\ \widehat{\mathcal{B}} &= \widetilde{\mathcal{B}} + \mathbb{B}^T(\mathbf{B}_2^T + \mathbf{P}_2^T)A_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2) \\ &= \mathbf{V}_1^T(\mathbf{B}_1 - \mathbf{P}_1) + \mathbf{V}_2^T(\mathbf{B}_2 - \mathbf{P}_2) + \mathbb{B}^T(\mathbf{B}_2^T + \mathbf{P}_2^T)A_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2), \\ \widehat{\mathcal{C}} &= \widetilde{\mathcal{C}} + (\mathbf{B}_2^T + \mathbf{P}_2^T)A_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2)\mathbb{B} \\ &= (\mathbf{B}_1^T + \mathbf{P}_1^T)\mathbf{V}_1^T + (\mathbf{B}_2^T + \mathbf{P}_2^T)\mathbf{V}_2^T + (\mathbf{B}_2^T + \mathbf{P}_2^T)A_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2)\mathbb{B}, \quad \text{and} \\ \widehat{\mathbf{D}} &= \mathcal{D} = \mathbf{D} - (\mathbf{B}_2^T + \mathbf{P}_2^T)A_{22}^{-1}(\mathbf{B}_2 - \mathbf{P}_2), \end{aligned} \tag{25}$$

which satisfies the original tangential interpolation conditions, and matches the polynomial part due to the modified $\widehat{\mathbf{D}}$-term. However, for this system to be pH we need to check that the associated passivity matrix is still positive semidefinite, which after rewriting the input and output matrix in the usual way is exactly the condition on $\widehat{\mathbf{W}}$ in the assertion. We then have that the reduced model not only satisfies the interpolation conditions and matches the polynomial part at $s = \infty$, but also is pH.□

Remark 1 Note that if the input does not influence the algebraic equations, i.e., if $\mathbf{B}_2 = \mathbf{P}_2 = 0$, then the shift of the constant term is not necessary, and the formulas simplify significantly, i.e., $\widehat{\mathbf{A}} = \mathbf{V}^T\mathcal{A}\mathbf{V}$, $\widehat{\mathcal{B}} = \widetilde{\mathcal{B}} = \mathbf{V}^T\mathcal{B}$, $\widehat{\mathcal{C}} = \mathcal{C}\mathbf{V}$, and $\widehat{\mathbf{D}} = \mathcal{D} = \mathbf{D}$.

Remark 2 It should be noted that if one eliminates the algebraic conditions from the system by solving for $\mathbf{x}_2(t)$, then this conditions shows up in the resulting dynamical part. Furthermore, by constructing an appropriate output feedback as in Lemma 1, this condition can always be guaranteed.

Another solution to preserving pH structure via interpolation can be obtained through the following theorem.

Theorem 3 *Consider a full-order pHDAE system of the form* (22)*. Let interpolation points* $\{\sigma_1, \sigma_2, \ldots, \sigma_r\} \in \mathbb{C}$ *and the corresponding tangent directions* $\{\boldsymbol{b}_1, \boldsymbol{b}_2, \ldots, \boldsymbol{b}_r\} \in \mathbb{C}^m$ *be given. Construct the interpolatory model reduction basis* $\mathbf{V}$ *as in* (23)*. Then the reduced model*

$$\begin{aligned}\begin{bmatrix} \widehat{\mathbf{V}}_1^T\mathbf{E}_{11}\widehat{\mathbf{V}}_1 & 0 \\ 0 & 0 \end{bmatrix}\dot{\mathbf{x}}(t) &= \begin{bmatrix} \mathbf{V}_1^T(\mathbf{J}_{11}-\mathbf{R}_{11})\mathbf{V}_1 & \mathbf{V}_1^T(\mathbf{J}_{12}-\mathbf{R}_{12}) \\ (-\mathbf{J}_{12}^T-\mathbf{R}_{12}^T)\mathbf{V}_1 & \mathbf{J}_{22}-\mathbf{R}_{22} \end{bmatrix}\mathbf{x}(t) + \begin{bmatrix} \mathbf{V}_1^T(\mathbf{B}_1-\mathbf{P}_1) \\ \mathbf{B}_2-\mathbf{P}_2 \end{bmatrix}\mathbf{u}(t) \\ \mathbf{y}_r(t) &= \begin{bmatrix} (\mathbf{B}_1^T+\mathbf{P}_1)^T\mathbf{V}_1 & \mathbf{B}_2+\mathbf{P}_2^T \end{bmatrix}\mathbf{x}(t) + \mathbf{D}\mathbf{u}(t)\end{aligned} \tag{26}$$

retains the pH structure, tangentially interpolates the original model, and matches the polynomial part.

Proof We first note that the subspace spanned by the columns of $\mathbf{V} = \begin{bmatrix}\mathbf{V}_1^T & \mathbf{V}_2^T\end{bmatrix}^T$ is contained in the subspace spanned by the columns of $\widehat{\mathbf{V}} := \mathsf{diag}(\mathbf{V}_1, \mathbf{I})$. Then the system in (26) results from reducing the original system in (22) via $\widehat{\mathbf{V}}$. Since $\mathsf{span}(\mathbf{V}) \subseteq \mathsf{span}(\widehat{\mathbf{V}})$, this reduced DAE automatically satisfies the interpolation conditions and since $\widehat{\mathbf{V}}$ does not alter the matrix $\mathbf{J}_{22} - \mathbf{R}_{22}$ and the matrices $\mathbf{B}_2, \mathbf{P}_2$, the polynomial part of the transfer function is $\mathbf{D}-(\mathbf{B}_2^T+\mathbf{P}_2^T)(\mathbf{J}_{22}-\mathbf{R}_{22})^{-1}(\mathbf{B}_2-\mathbf{P}_2)$, matching that of the original model. The reduced system in (26) is pH as this one-sided projection retains the original pH structure. □

Remark 3 Theorem 3 presents a seemingly easy solution to structure-preserving interpolatory model reduction of index-1 pHDAEs compared to Theorem 2. However, in this way the dimension reduction is restricted solely to the dynamic equations, which may not be the maximal reduction that is possible because redundant algebraic conditions cannot be removed; see [26].

4.2 Semi-explicit pHDAE systems with index-2 constraints

Another large class of pHDAE systems that arise directly in applications is that of semi-explicit index-2 systems. We first consider the case that the input does not affect the algebraic equations.

Theorem 4 *Consider an index-2 pHDAE system of the form*

$$\begin{aligned}\begin{bmatrix}\mathbf{E}_{11} & 0\\ 0 & 0\end{bmatrix}\begin{bmatrix}\dot{\mathbf{x}}_1(t)\\ \dot{\mathbf{x}}_2(t)\end{bmatrix} &= \begin{bmatrix}\mathbf{J}_{11}-\mathbf{R}_{11} & \mathbf{J}_{12}\\ -\mathbf{J}_{12}^T & \mathbf{0}\end{bmatrix}\begin{bmatrix}\mathbf{x}_1(t)\\ \mathbf{x}_2(t)\end{bmatrix}+\begin{bmatrix}\mathbf{B}_1-\mathbf{P}_1\\ \mathbf{0}\end{bmatrix}\mathbf{u}(t)\\ \mathbf{y}(t) &= \begin{bmatrix}\mathbf{B}_1^T+\mathbf{P}_1^T & \mathbf{0}\end{bmatrix}\begin{bmatrix}\mathbf{x}_1(t)\\ \mathbf{x}_2(t)\end{bmatrix}+\mathbf{D}\mathbf{u}(t),\end{aligned} \tag{27}$$

with $\mathbf{E}_{11} > 0$ *and set* $\mathbf{A}_{11} = \mathbf{J}_{11}-\mathbf{R}_{11}$. *Given interpolation points* $\{\sigma_1,\sigma_2,\ldots,\sigma_r\}$ *and associated tangent directions* $\{\boldsymbol{b}_1,\boldsymbol{b}_2,\ldots,\boldsymbol{b}_r\}$, *let the vectors* $\mathbf{v}_i$, *for* $i = 1,2,\ldots,r$, *be the first block of the solution of*

$$\begin{bmatrix}\mathbf{A}_{11}-\sigma_i\mathbf{E}_{11} & \mathbf{J}_{12}\\ -\mathbf{J}_{12}^T & \mathbf{0}\end{bmatrix}\begin{bmatrix}\mathbf{v}_i\\ \mathbf{z}\end{bmatrix} = \begin{bmatrix}(\mathbf{B}_1-\mathbf{P}_1)\boldsymbol{b}_i\\ \mathbf{0}\end{bmatrix}. \tag{28}$$

Define $\mathbf{V} = [\mathbf{v}_1,\mathbf{v}_2,\ldots,\mathbf{v}_r]$. *Then the reduced model*

$$\widehat{\mathbf{E}}\dot{\mathbf{x}}_r = (\widehat{\mathbf{J}}-\widehat{\mathbf{R}})\mathbf{x}_r+\widehat{\mathcal{B}}\mathbf{u}(t),\quad \mathbf{y}_r = \widehat{\mathcal{C}}\mathbf{x}_r+\widehat{\mathbf{D}}, \tag{29}$$

with

$$\begin{aligned}&\widehat{\mathbf{E}} = \mathbf{V}^T\mathbf{E}_{11}\mathbf{V},\ \widehat{\mathbf{J}} = \mathbf{V}^T\mathbf{J}_{11}\mathbf{V},\ \widehat{\mathbf{R}} = \mathbf{V}^T\mathbf{R}_{11}\mathbf{V},\\ &\widehat{\mathcal{B}} = \mathbf{V}^T\mathbf{B}_1-\mathbf{V}^T\mathbf{P}_1,\ \widehat{\mathcal{C}} = \mathbf{B}_1^T\mathbf{V}^T+\mathbf{P}^T\mathbf{V}_1^T,\quad \textit{and}\quad \widehat{\mathbf{D}} = \mathbf{D},\end{aligned} \tag{30}$$

is still pH, matches the polynomial part of the original transfer function, and satisfies the tangential interpolation conditions, i.e.,

$$\mathbf{H}(\sigma_i)\boldsymbol{b}_i = \widehat{\mathbf{H}}(\sigma_i)\boldsymbol{b}_i,\ \textit{for}\ i = 1,2,\ldots,r.$$

Proof Note first that the regularity of $\lambda\mathbf{E}-(\mathbf{J}-\mathbf{R})$ and the index-2 condition imply that $-\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12}$ is invertible, see [5, 21]. Following [18], we write (27) as

$$\begin{aligned}\mathbf{\Pi}_l\mathbf{E}_{11}\mathbf{\Pi}_r\dot{\mathbf{x}}_1(t) &= \mathbf{\Pi}_l\mathbf{A}_{11}\mathbf{\Pi}_r\mathbf{x}_1(t)+\mathbf{\Pi}_l\mathbf{B}_1\mathbf{u}(t),\\ \mathbf{y}(t) &= \mathbf{C}_1\mathbf{\Pi}_r\mathbf{x}_1(t)+\mathbf{D}\mathbf{u}(t),\end{aligned} \tag{31}$$

together with the algebraic equation

$$\mathbf{x}_2(t) = -(\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12})^{-1}\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{A}_{11}\mathbf{x}_1(t)-(\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12})^{-1}\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{B}_1\mathbf{u}(t),$$

where $\mathbf{\Pi}_l$ and $\mathbf{\Pi}_l$ are projectors defined as

$$\mathbf{\Pi}_l = \mathbf{I}-\mathbf{E}_{11}^{-1}\mathbf{J}_{12}(\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12})^{-1}\mathbf{J}_{21}^T\quad\text{and}\quad \mathbf{\Pi}_r = \mathbf{I}-\mathbf{J}_{12}(\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12})^{-1}\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}.$$

The equivalent system (31) is now an implicit ODE pH system that can be reduced with standard model reduction techniques. However, this would require computing the projectors $\mathbf{\Pi}_l$ and $\mathbf{\Pi}_l$ explicitly, see [26]. For general index-2 DAE systems one can avoid this computational step in interpolatory model reduction; i.e., theoretically reducing (31) via interpolation but without computing $\mathbf{\Pi}_l$ and $\mathbf{\Pi}_l$ explicitly; see [18].

To adapt this idea to pHDAE systems, we construct $\mathbf{V}$ using (28) and then compute the reduced-order quantities via one-sided projection as in (30). This construction of $\mathbf{V}$, as in [18], guarantees that the reduced model in (29) tangentially interpolates the original pHDAE system in (31) and the polynomial part of the transfer function in (27) is given by $\mathbf{D} = \mathbf{S} + \mathbf{N}$ partitioned in its symmetric and skew-symmetric part. Since (29) is an implicit ODE pH system with the exact $\mathbf{D}$-term, it matches the polynomial part of the original transfer function $\mathbf{H}(s)$.

It remains to show that (29) is pH. By construction in (30), $\widehat{\mathbf{J}}$ is skew-symmetric, $\widehat{\mathbf{R}}$ is symmetric positive semidefinite, and $\mathbf{E}_{11}$ is symmetric positive definite. Moreover,

$$\begin{bmatrix} \mathbf{V}^T\mathbf{R}_{11}\mathbf{V} & \mathbf{V}^T\mathbf{P}_1 \\ \mathbf{P}_1^T\mathbf{V} & \mathbf{S} \end{bmatrix} = \begin{bmatrix} \mathbf{V}^T & 0 \\ 0 & \mathbf{I} \end{bmatrix} \begin{bmatrix} \mathbf{R}_{11} & \mathbf{P}_1 \\ \mathbf{P}_1^T & \mathbf{S} \end{bmatrix} \begin{bmatrix} \mathbf{V} & 0 \\ 0 & \mathbf{I} \end{bmatrix} \geq 0,$$

since the original model is PH, and therefore the pH-structure is retained. □

The situation becomes more complicated when the second block in $\mathcal{B}$ is nonzero, i.e., the system has the form

$$\begin{aligned} \begin{bmatrix} \mathbf{E}_{11} & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \dot{\mathbf{x}}_1(t) \\ \dot{\mathbf{x}}_2(t) \end{bmatrix} &= \begin{bmatrix} \mathbf{J}_{11} - \mathbf{R}_{11} & \mathbf{J}_{12} \\ -\mathbf{J}_{12}^T & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{x}_1(t) \\ \mathbf{x}_2(t) \end{bmatrix} + \begin{bmatrix} \mathbf{B}_1 - \mathbf{P}_1 \\ \mathbf{B}_2 - \mathbf{P}_2 \end{bmatrix} \mathbf{u}(t), \\ \mathbf{y}(t) &= \begin{bmatrix} \mathbf{B}_1^T + \mathbf{P}_1^T & \mathbf{B}_2 + \mathbf{P}_2^T \end{bmatrix} \begin{bmatrix} \mathbf{x}_1(t) \\ \mathbf{x}_2(t) \end{bmatrix} + \mathbf{D}\mathbf{u}(t). \end{aligned} \tag{32}$$

The polynomial part of the transfer function of the pHDAE in (32) is given by [18]

$$\begin{aligned} \mathbf{P}(s) = \mathbf{D} &+ (\mathbf{B}_2^T + \mathbf{P}_2^T)(\mathbf{J}_{21}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12})^{-1}\mathbf{J}_{12}\mathbf{E}_{11}^{-1}(\mathbf{B}_1 - \mathbf{P}_1) \\ &+ s(\mathbf{B}_2^T + \mathbf{P}_2^T)(\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12})^{-1}(\mathbf{B}_2 - \mathbf{P}_2). \end{aligned} \tag{33}$$

We have the following theorem.

Theorem 5 *Consider a pHDAE system of the form* (32) *and define the matrices*

$$\begin{aligned} \mathbf{Z} &= -(\mathbf{A}_{21}\mathbf{E}_{11}^{-1}\mathbf{A}_{12})^{-1} = \left(\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}\mathbf{J}_{12}\right)^{-1} \\ \mathcal{C} &= (\mathbf{B}_1^T - \mathbf{P}_1^T) - (\mathbf{B}_2^T - \mathbf{P}_2^T)\mathbf{Z}\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}(\mathbf{J}_{11} - \mathbf{R}_{11}), \\ \mathcal{B} &= (\mathbf{B}_1 - \mathbf{P}_1) + (\mathbf{J}_{11} - \mathbf{R}_{11})\mathbf{E}_{11}^{-1}\mathbf{J}_{12}\mathbf{Z}(\mathbf{B}_2 - \mathbf{P}_2), \\ \mathcal{D}_0 &= \mathbf{D} - (\mathbf{B}_2^T + \mathbf{P}_2^T)\mathbf{Z}\mathbf{J}_{12}^T\mathbf{E}_{11}^{-1}(\mathbf{B}_1 - \mathbf{P}_1), \quad \textit{and} \\ \mathcal{D}_1 &= -(\mathbf{B}_2^T + \mathbf{P}_2^T)\mathbf{Z}(\mathbf{B}_2 - \mathbf{P}_2). \end{aligned}$$

Given interpolation points $\{\sigma_1, \sigma_2, \ldots, \sigma_r\}$ *and associated tangent directions* $\{\boldsymbol{b}_1, \boldsymbol{b}_2, \ldots, \boldsymbol{b}_r\}$, *let the vectors* $\mathbf{v}_i$ *be the first blocks of the solutions of*

$$\begin{bmatrix} \mathbf{J}_{11} - \mathbf{R}_{11} - \sigma_i \mathbf{E}_{11} & \mathbf{J}_{12} \\ -\mathbf{J}_{12}^T & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{v}_i \\ \mathbf{z} \end{bmatrix} = \mathbf{B}\boldsymbol{b}_i, \ \textit{for} \ i = 1, 2, \ldots, r, \tag{34}$$

and set $\mathbf{V} := [\mathbf{v}_1, \mathbf{v}_2, \ldots, \mathbf{v}_r]$, $\mathbf{u}_1 := \mathbf{u}$, $\mathbf{u}_2 := \dot{\mathbf{u}}$, *and* $\widehat{\mathbf{D}} := \begin{bmatrix} \mathcal{D}_0 & \mathcal{D}_1 \end{bmatrix} = \widehat{\mathbf{S}} + \widehat{\mathbf{N}}$. *Then, the reduced model*

$$\widehat{\mathbf{E}}\dot{\mathbf{x}}_r = (\widehat{\mathbf{J}} - \widehat{\mathbf{R}})\mathbf{x}_r + \begin{bmatrix} \widehat{\mathbf{B}} - \widehat{\mathbf{P}} & 0 \end{bmatrix} \begin{bmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \end{bmatrix}, \ \mathbf{y}_r = (\widehat{\mathbf{B}} + \widehat{\mathbf{P}})^T \mathbf{x}_r + \widehat{\mathbf{D}} \begin{bmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \end{bmatrix}, \tag{35}$$

with

$$\begin{aligned} &\widehat{\mathbf{E}} = \mathbf{V}^T \mathbf{E}_{11} \mathbf{V}, \ \widehat{\mathbf{J}} = \mathbf{V}^T \mathbf{J}_{11} \mathbf{V}, \ \widehat{\mathbf{R}} = \mathbf{V}^T \mathbf{R}_{11} \mathbf{V}, \\ &\widehat{\mathbf{B}} = \frac{1}{2}\left(\mathbf{V}^T \mathcal{B} + \mathbf{V}^T \mathcal{C}^T\right), \ \textit{and} \ \widehat{\mathbf{P}} = \frac{1}{2}\left(\mathbf{V}^T \mathcal{C}^T - \mathbf{V}^T \mathcal{B}\right), \end{aligned} \tag{36}$$

satisfies the interpolation conditions, matches the polynomial part of the transfer function, and preserves the pH structure, provided that the reduced passivity matrix $\widehat{\mathbf{W}} = \begin{bmatrix} \widehat{\mathbf{R}} & \widehat{\mathbf{P}} \\ \widehat{\mathbf{P}}^T & \widehat{\mathbf{S}} \end{bmatrix}$ *is positive semidefinite.*

Proof The proof follows similar to the proof of Theorem 4. Following [18], the state $\mathbf{x}_1$ can be decomposed as $\mathbf{x}_1 = \mathbf{x}_c + \mathbf{x}_g$, where $\mathbf{x}_g = \mathbf{E}_{11}^{-1}\mathbf{A}_{12}(\mathbf{J}_{12}^T \mathbf{E}_{11}^{-1} \mathbf{J}_{12})^{-1}(\mathbf{B}_2 - \mathbf{P}_2)\mathbf{u}(t)$ and $\mathbf{x}_c(t)$ satisfies $\mathbf{J}_{12}^T \mathbf{x}_c = 0$. Then, one can rewrite (32) as

$$\begin{aligned} \boldsymbol{\Pi}_l \mathbf{E}_{11} \boldsymbol{\Pi}_r \dot{\mathbf{x}}_0(t) &= \boldsymbol{\Pi}_l \mathbf{A}_{11} \boldsymbol{\Pi}_r \mathbf{x}_0(t) + \boldsymbol{\Pi}_l \mathbf{B}_1 \mathbf{u}(t) \\ \mathbf{y}(t) &= \mathbf{C}\boldsymbol{\Pi}_r \mathbf{x}_1(t) + \mathcal{D}_0 \mathbf{u}(t) + \mathcal{D}_1 \dot{\mathbf{u}}(t). \end{aligned} \tag{37}$$

As before, the ODE part can be reduced with usual model reduction techniques. Following [18], however, we achieve this without computing the projectors $\boldsymbol{\Pi}_l$ and $\boldsymbol{\Pi}_l$ explicitly, instead by constructing $\mathbf{V}$ using (34) and then applying one-sided model reduction with $\mathbf{V}$ to obtain the reduced model

$$\widehat{\mathbf{E}}\dot{\mathbf{x}}_r = (\widehat{\mathbf{J}} - \widehat{\mathbf{R}})\mathbf{x}_r + \widetilde{\mathbf{B}}\mathbf{u}(t), \ \mathbf{y}_r = \widetilde{\mathbf{C}}^T \mathbf{x}_r + \mathcal{D}_0 \mathbf{u}(t) + \mathcal{D}_1 \dot{\mathbf{u}}(t), \tag{38}$$

where $\widehat{\mathbf{E}} = \mathbf{V}^T \mathbf{E}_{11} \mathbf{V}$, $\widehat{\mathbf{J}} = \mathbf{V}^T \mathbf{J}_{11} \mathbf{V}$, $\widehat{\mathbf{R}} = \mathbf{V}^T \mathbf{R}_{11} \mathbf{V}$, $\widetilde{\mathbf{B}} = \mathbf{V}^T \mathcal{B}$, and $\widetilde{\mathbf{C}} = \mathcal{C}\mathbf{V}$. This reduced model, by construction, satisfies the tangential interpolation conditions. Note that the reduced model in (38) has exactly the same realization as the reduced model in (35) except for the reduced $\widetilde{\mathbf{B}}$ and $\widetilde{\mathbf{C}}$ terms. The reduced terms in (38) already have the desired pH structure. To recover the desired symmetry in (37), we need to find matrices $\widehat{\mathbf{B}}$ and $\widehat{\mathbf{P}}$ such that

$$\widetilde{\mathbf{B}} = \mathbf{V}^T \mathcal{B} = \widehat{\mathbf{B}} - \widehat{\mathbf{P}} \quad \text{and} \quad \widetilde{\mathbf{C}} = \mathcal{C}\mathbf{V} = (\widehat{\mathbf{B}} + \widehat{\mathbf{P}})^T.$$

This can be achieved by defining $\widehat{\mathbf{B}}$ and $\widehat{\mathbf{P}}$ as

$$\widehat{\mathbf{B}} = \frac{1}{2}\left(\widetilde{\mathbf{B}} + \widetilde{\mathbf{C}}^T\right) = \frac{1}{2}\mathbf{V}^T\left(\mathcal{B} + \mathcal{C}^T\right) \quad \text{and} \quad \widehat{\mathbf{P}} = \frac{1}{2}\left(\widetilde{\mathbf{C}}^T - \widetilde{\mathbf{B}}\right) = \frac{1}{2}\mathbf{V}^T\left(\mathcal{C}^T - \mathcal{B}\right),$$

recovering (36). The final requirement to retain the pH structure is, then, again that $\begin{bmatrix} \widehat{\mathbf{R}} & \widehat{\mathbf{P}} \\ \widehat{\mathbf{P}}^T & \frac{1}{2}\left(\mathbf{D}+\mathbf{D}^T\right) \end{bmatrix} \geq 0$, which is the final condition in the statement of the theorem.□

The approach for the case that the input influences the index-2 constraint has the disadvantage that one has to introduce the derivative of $\mathbf{u}$ as an extra input, which may lead to difficulties when applying standard control and optimization methods. For this reason it is usually preferable to first perform an index reduction via an appropriate output feedback, see Section 3, and then apply the results from Section 4.1. But note that this changes the polynomial part of the transfer function.

4.3 Semi-explicit pHDAE systems with index-1 and index-2 constraints

Finally we consider semi-explicit index-2 systems which also have an index-1 part, [11, 19, 26]. In this case we only consider the special case

$$\begin{bmatrix} \mathbf{E}_{11} & \mathbf{E}_{22} & 0 \\ \mathbf{E}_{21} & \mathbf{E}_{22} & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \dot{\mathbf{x}}_1 \\ \dot{\mathbf{x}}_2 \\ \dot{\mathbf{x}}_3 \end{bmatrix} = \begin{bmatrix} \mathbf{J}_{11}-\mathbf{R}_{11} & \mathbf{J}_{12}-\mathbf{R}_{12} & \mathbf{J}_{13} \\ \mathbf{J}_{21}-\mathbf{R}_{21} & \mathbf{J}_{22}-\mathbf{R}_{22} & 0 \\ \mathbf{J}_{31} & 0 & 0 \end{bmatrix} \begin{bmatrix} \mathbf{x}_1 \\ \mathbf{x}_2 \\ \mathbf{x}_3 \end{bmatrix} + \begin{bmatrix} \mathbf{B}_1-\mathbf{P}_1 \\ \mathbf{B}_2-\mathbf{P}_2 \\ 0 \end{bmatrix} \mathbf{u}, \quad (39)$$

$$\mathbf{y} = \begin{bmatrix} (\mathbf{B}_1+\mathbf{P}_1)^T & (\mathbf{B}_2+\mathbf{P}_2)^T & 0 \end{bmatrix} \begin{bmatrix} \mathbf{x}_1 \\ \mathbf{x}_2 \\ \mathbf{x}_3 \end{bmatrix} + (\mathbf{S}+\mathbf{N})\mathbf{u}, \quad (40)$$

where $\begin{bmatrix} \mathbf{E}_{11} & \mathbf{E}_{22} \\ \mathbf{E}_{21} & \mathbf{E}_{22} \end{bmatrix} > 0$, $\mathbf{J}_{22}-\mathbf{R}_{22}$, and $\mathbf{J}_{31}$ are nonsingular. This implies that the index-2 constraint is given by $\mathbf{x}_1 = 0$, and this constraint is easy to enforce in the model reduction procedure. We then have the following theorem.

Theorem 6 *Consider an index-2 pHDAE system of the form (39)–(40). Construct an interpolatory model reduction basis*

$$\mathbf{V} = \begin{bmatrix} \mathbf{V}_1 \\ \mathbf{V}_2 \\ \mathbf{V}_3 \end{bmatrix} = \left[(\sigma_1\mathbf{E}-\mathbf{A})^{-1}\mathcal{B}\boldsymbol{b}_1, \quad \cdots \ (\sigma_r\mathbf{E}-\mathbf{A})^{-1}\mathcal{B}\boldsymbol{b}_r \right] \in \mathbb{C}^{n\times r}, \quad (41)$$

partitioned as the system. Define $\widehat{\mathbf{V}} := \mathit{diag}(\mathbf{I}, \mathbf{V}_2, \mathbf{I})$. *Then the reduced system*

$$\widehat{\mathbf{E}}\dot{\mathbf{x}}_r = (\widehat{\mathbf{J}}-\widehat{\mathbf{R}})\mathbf{x}_r + \widehat{\mathcal{B}}\mathbf{u}(t), \quad \mathbf{y}_r = \widehat{\mathcal{C}}\mathbf{x}_r + \widehat{\mathbf{D}}, \quad (42)$$

with $\widehat{\mathbf{E}} = \widehat{\mathbf{V}}^T\mathbf{E}\widehat{\mathbf{V}}$, $\widehat{\mathbf{J}} = \widehat{\mathbf{V}}^T\mathbf{J}\widehat{\mathbf{V}}$, $\widehat{\mathbf{R}} = \widehat{\mathbf{V}}^T\mathbf{R}\widehat{\mathbf{V}}$,

$$\widehat{\mathcal{B}} = \widehat{\mathbf{V}}^T\mathcal{B} = \widehat{\mathbf{V}}^T\mathbf{B} - \widehat{\mathbf{V}}^T\mathbf{P}, \quad \widehat{\mathcal{C}} = \mathbf{C}\widehat{\mathbf{V}} = \mathbf{B}^T\widehat{\mathbf{V}}^T + \mathbf{P}^T\widehat{\mathbf{V}}^T, \quad \textit{and} \quad \widehat{\mathbf{D}} = \mathbf{D}, \quad (43)$$

is still pH, matches the polynomial part of the transfer function, and satisfies the tangential interpolation conditions, i.e., $\mathbf{H}(\sigma_i)\boldsymbol{b}_i = \widehat{\mathbf{H}}(\sigma_i)\boldsymbol{b}_i$, *for* $i = 1, 2, \ldots, r$.

Proof It follows from the definitions of $\mathbf{V}$ and $\widehat{\mathbf{V}}$ that $\mathsf{span}(\mathbf{V}) \subseteq \mathsf{span}(\widehat{\mathbf{V}})$. Therefore, the resulting reduced system automatically satisfies the interpolation conditions. Since $\widehat{\mathbf{V}}$ does not alter the algebraic constraints, the polynomial part of its transfer function is still $\mathbf{D}$, matching that of the original model. The reduced system in (43) is a pHDAE as this one-sided projection retains the original pH structure. □

5 Algorithmic Considerations

The preceding analysis presumed that interpolation points and tangent directions were specified beforehand. We consider now how one might make choices that generally produce effective approximations with respect to the $\mathcal{H}_2$ system measure and propose an algorithm to accomplish this. We then illustrate the performance of this approach on a numerical test case.

5.1 $\mathcal{H}_2$-inspired structure-preserving interpolation

The $\mathcal{H}_2$ *distance* between the full model $\mathbf{H}(s)$ and the reduced model $\mathbf{H}_r(s)$ is

$$\left\|\mathbf{H}-\mathbf{H}_r\right\|_{\mathcal{H}_2} = \left(\frac{1}{2\pi}\int_{-\infty}^{\infty}\left\|\mathbf{H}(\imath\omega)-\mathbf{H}_r(\imath\omega)\right\|_F^2 d\omega\right)^{1/2}, \tag{44}$$

where $\imath^2 = -1$ and $\|\mathbf{M}\|_F$ denote the Frobenius norm of a matrix $\mathbf{M}$. To have a finite $\mathcal{H}_2$ error norm the polynomial parts of $\mathbf{H}_r(s)$ and $\mathbf{H}(s)$ need to match. To make this precise, write $\mathbf{H}(s) = \mathbf{G}(s)+\mathbf{P}(s)$ and $\mathbf{H}_r(s) = \mathbf{G}_r(s)+\mathbf{P}_r(s)$ as where $\mathbf{G}(s)$ and $\mathbf{G}_r(s)$ are strictly proper transfer functions, and $\mathbf{P}(s)$ and $\mathbf{P}_r(s)$ are the polynomial parts. Therefore, if $\mathbf{H}_r(s)$ is the $\mathcal{H}_2$-optimal approximation to $\mathbf{H}(s)$, then $\mathbf{P}_r(s) = \mathbf{P}(s)$ and $\mathbf{G}_r(s)$ is the $\mathcal{H}_2$-optimal approximation to $\mathbf{G}(s)$. This suggests that one decomposes $\mathbf{H}(s)$ into its rational and polynomial parts $\mathbf{H}(s) = \mathbf{G}(s) + \mathbf{P}(s)$ and then applies $\mathcal{H}_2$ optimal reduction to $\mathbf{G}(s)$. However, this requires the explicit construction of $\mathbf{G}(s)$. This problem was resolved in [18] for *unstructured* index-1 and index-2 DAEs. On the other hand, for the ODE case, [17] proposed a structure preserving algorithm for minimizing the $\mathcal{H}_2$ norm while retaining the pH structure. In this section, we aim to unify these two approaches.

First, we briefly revisit the interpolatory $\mathcal{H}_2$ optimality conditions; for details we refer the reader to [1, 3, 15] and the references therein. Since $\mathcal{H}_2$ optimality for the DAE case boils down to optimality for the ODE part, we focus on the latter. Let $\mathbf{G}_r(s) = \sum_{i=1}^{r}\frac{\mathbf{c}_i\mathbf{b}_i^T}{s-\lambda_i}$ be the pole-residue decomposition of $\mathbf{G}_r(s)$. For simplicity we assume simple poles. If $\mathbf{G}_r(s)$ is an $\mathcal{H}_2$ optimal approximation to $\mathbf{G}(s)$, then

$$\mathbf{G}(-\lambda_i)\mathbf{b}_i = \mathbf{G}_r(-\lambda_i)\mathbf{b}_i,\ \ \mathbf{c}_i^T\mathbf{G}(-\lambda_i) = \mathbf{c}_i^T\mathbf{G}_r(-\lambda_i),\ \text{ and }\ \mathbf{c}_i^T\mathbf{G}'(-\lambda_i)\mathbf{b}_i = \mathbf{c}_i^T\mathbf{G}_r'(-\lambda_i)\mathbf{b}_i \tag{45}$$

for $i = 1, 2, \ldots, r$ where $'$ denotes the derivate with respect to s. Therefore an $\mathcal{H}_2$ optimal reduced model is a bitangential Hermite interpolant where the interpolation points are the mirror images of its poles and the tangent directions are the residue directions. Since the optimality conditions depend on the reduced model to be computed, this requires an iterative algorithm. This is precisely what the Iterative Rational Krylov Algorithm [15] achieves and we will use this framework in our formulation. For other approaches in $\mathcal{H}_2$ optimal approximation, see, e.g., [1, 3].

Following [17], in order to preserve the structure, we will satisfy only a subset of these conditions. We will make sure that the interpolation points will be the mirror images of the reduced order poles and enforce either left or right-tangential interpolation conditions without the derivate conditions. However, intuitively, one might expect that in the pH setting this may not cause too much deviation from true optimality. Dropping the Hermite condition means that one chooses a Galerkin projection, i.e., $\mathbf{Z} = \mathbf{V}$. However, due to the pH structure, the input-to-state matrix $\mathbf{B}$ and the state-to-output matrix $\mathbf{C}$ are related. Therefore, the model reduction basis $\mathbf{V}$ can be thought to contain some information involving $\mathbf{C}$, and thus involving $\mathbf{Z}$.

As an example for the algorithmic approach, consider the semi-explicit index-2 case uncontrolled at ∞ studied in Section 4.2.

Starting with an initial selection of interpolation points $\{\sigma_1, \sigma_2, \ldots, \sigma_r\}$ and the tangent directions $\{\boldsymbol{b}_1, \boldsymbol{b}_2, \ldots, \boldsymbol{b}_r\}$, construct the interpolatory reduced pHDAE $\widehat{\mathbf{H}}(s)$ as in Theorem 4. Let $\widehat{\mathbf{H}}(s) = \sum_{i=1}^{r} \frac{\widehat{\boldsymbol{\ell}}_i \widehat{\boldsymbol{b}}_i^T}{s-\lambda_i} + \mathbf{D}$ be the pole-residue decomposition. Since initially the optimality condition $\sigma_i = -\lambda_i(\widehat{\mathbf{J}}-\widehat{\mathbf{R}}, \widehat{\mathbf{E}})$ is not (generally) satisfied, choose $-\lambda_i(\widehat{\mathbf{J}} - \widehat{\mathbf{R}}, \widehat{\mathbf{E}})$ as the next set of interpolation points and $\widehat{\boldsymbol{b}}_i$ as the next set of tangent directions. This is repeated until convergence upon which the reduced model $\mathbf{H}_r(s)$ is not only a structure-preserving pHDAE, but also satisfies $\sigma_i = -\lambda_i(\widehat{\mathbf{J}} - \widehat{\mathbf{R}}, \widehat{\mathbf{E}})$.

We illustrate the discussed procedure with a numerical example. Consider the incompressible fluid flow model of the Oseen equations, taken from [19, §4.1]

$$\begin{aligned} \partial_t v &= -(a \cdot \nabla)v + \mu \Delta v - \nabla p + f \quad \text{in } \Omega \times (0,T], & v &= 0, \quad \text{on } \partial\Omega \times (0,T], \\ 0 &= -\mathrm{div} v, \qquad\qquad\qquad\quad \text{in } \Omega \times (0,T], & v &= v^0, \qquad\quad \text{in } \Omega \times 0. \end{aligned}$$

where v and p are the velocity and pressure variables, $\mu > 0$ is the viscosity, and $\Omega = (0,1)^2$ with boundary $\partial\Omega$. f is an externally imposed body force that for simplicity is assumed to be separable: $f(x,t) = b(x)u(t)$. A finite-difference discretization on a staggered rectangular grid leads to a single-input/single-output index-2 pHDAE of the form (27); for details, see [19]. In our model, we used a uniform grid with 50 grid points yielding a pHDAE of order $n = 7399$, of which $n_1 = 4900$ degrees of freedom are for velocity and $n_2 = 2499$ for pressure. We apply our approach to reduce the order to $r = 1, 2, \ldots, 10$ with logarithmically spaced initialization for interpolation points in the interval $[10^{-2}, 10^4]$. For every r value, we compute the relative $\mathcal{H}_\infty$ error between the full and reduced transfer functions, i.e., $\|\mathbf{H} - \widehat{\mathbf{H}}\|_\infty / \|\mathbf{H}\|_\infty$ where $\|\mathbf{H}\|_\infty = \sup_{\omega \in \mathbb{R}} \mid \mathbf{H}(\imath\omega) \mid$. The results in Figure 1 show that the reduced pHDAE accurately approximates the original one; for the reduction from $n = 7399$ to order $r = 10$, the relative error is around 10^{-5}, illustrating the success of the proposed framework.

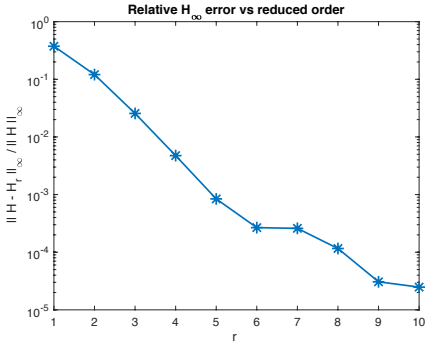

Fig. 1 Evolution of the model reduction error for Oseen example as r varies

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