Optimization-Based Structured Reduced Order Modeling from Frequency Samples ⋆

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1. INTRODUCTION

We consider the computation of low-order *port-Hamiltonian* (pH) surrogate models of the form

$$\Sigma_{\mathrm{pH}} : \begin{cases} \dot{x}(t) = (J-R)Qx(t) + Bu(t), \\ y(t) = B^{\mathsf{T}}Qx(t), \end{cases}$$

where J, R, $Q \in \mathbb{R}^{r\times r}$ and $B \in \mathbb{R}^{r\times m}$ with $J = -J^{\mathsf{T}}$, $R \geq 0$, and $Q \geq 0$. We call $x : \mathbb{R} \to \mathbb{R}^r$, $u : \mathbb{R} \to \mathbb{R}^m$, and $y : \mathbb{R} \to \mathbb{R}^m$ the *state*, *input*, and *output* of the system, respectively. The state dimension r is also called the model order of the system. We compute surrogate models in the sense that Σ_{pH} is not derived by first-principle modeling but is instead obtained by approximating the input-to-output mapping of a given system.

For linear dynamical systems, the input-to-output mapping is characterized by the *transfer function* in the frequency domain. The transfer function of Σ_{pH} is given by

$$H_{\mathrm{pH}}(s) := B^{\mathsf{T}}Q(sI_r - (J-R)Q)^{-1}B.$$

In this work, we aim at determining matrices J, R, Q, and B such that H_{pH} approximates the transfer function H_{g} of a given (possibly unstructured) system Σ_{g} with respect to the $\mathcal{H}_\infty$ norm. Let $\mathcal{RH}_\infty^{m\times m}$ denote the normed space of all real-rational and proper $m \times m$ transfer functions that have no poles in the set $\overline{\mathbb{C}^+} := \{\lambda \in \mathbb{C} \mid \mathrm{Re}(\lambda) \geq 0\}$. Then the $\mathcal{H}_\infty$ norm of a function $H \in \mathcal{RH}_\infty^{m\times m}$ is given by

$$\|H\|_{\mathcal{H}_\infty} := \sup_{\lambda\in\mathbb{C}^+} \|H(\lambda)\|_2 = \sup_{\omega\in\mathbb{R}} \sigma_1(H(\mathrm{i}\omega)),$$

where $\sigma_1(\cdot)$ denotes the largest singular value of its matrix argument.

Two use cases for the construction of low-order surrogate models that approximate a given input-to-output mapping are *model order reduction* (MOR) and *system identification*. MOR is used when a given model has a high complexity (e. g., a large state-dimension), which makes its repeated simulation or model-based control computationally prohibitively expensive. Therefore, MOR is applied to construct a low-order surrogate model that is then used in place of the high-complexity model. On the other hand, system identification is applied when no mathematical model of a given system is available, and instead a model must be constructed from experimental data. Our method can be applied in both situations. However, in this note, we only explain our method in the context of MOR and refer to Schwerdtner (2021) for a related system identification algorithm.

The main features of our method are as follows:

- We construct surrogate models with pH structure, which are automatically passive. Passivity leads to several benefits for simulation and controller design.
- We only use transfer function evaluations to construct our low-order model. In this way, no particular model structure of the original model is required for our computation of a pH surrogate model. Therefore, our method can be applied to a wide range of dynamical systems.
- Our experiments show that our algorithm can determine pH surrogate models that are as accurate as models found by well-established (and unstructured) MOR routines such as *balanced truncation* (BT).

2. OUR METHOD

In Schwerdtner and Voigt (2020) we pose MOR as a parameter optimization problem. For that, we define a parametrized pH system as follows.

Lemma 1. (Schwerdtner and Voigt (2020)). Let $\theta \in \mathbb{R}^{n_\theta}$ be a vector with $n_\theta := r\left(\frac{3r+1}{2} + m\right)$. Furthermore, let θ be partitioned as $\theta := \left[\theta_J^{\mathsf{T}}, \theta_R^{\mathsf{T}}, \theta_Q^{\mathsf{T}}, \theta_B^{\mathsf{T}}\right]^{\mathsf{T}}$ with $\theta_J \in \mathbb{R}^{r(r-1)/2}$, $\theta_R \in \mathbb{R}^{r(r+1)/2}$, $\theta_Q \in \mathbb{R}^{r(r+1)/2}$, and $\theta_B \in \mathbb{R}^{rm}$. Further define the matrices

$$\begin{aligned} J(\theta) &= \mathrm{vtsu}(\theta_J)^{\mathsf{T}} - \mathrm{vtsu}(\theta_J), \\ R(\theta) &= \mathrm{vtu}(\theta_R)^{\mathsf{T}}\,\mathrm{vtu}(\theta_R), \\ Q(\theta) &= \mathrm{vtu}(\theta_Q)^{\mathsf{T}}\,\mathrm{vtu}(\theta_Q), \\ B(\theta) &= \mathrm{vtf}_{r,m}(\theta_B), \end{aligned}$$

where the function $\mathrm{vtu} : \mathbb{R}^{r(r+1)/2} \to \mathbb{R}^{r\times r}$ maps a vector of length $r(r+1)/2$ to an upper triangular matrix, the

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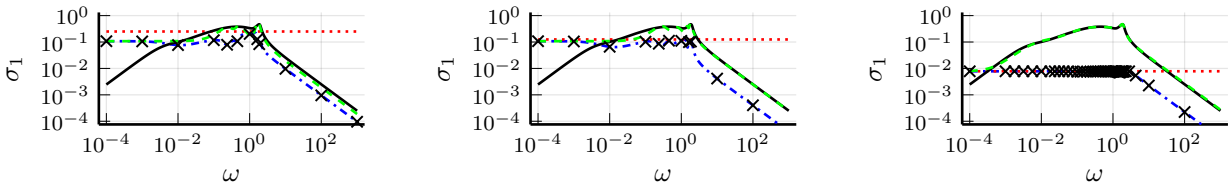

(a) $\gamma = 2.5 \cdot 10^{-1}$ (b) $\gamma = 1.25 \cdot 10^{-1}$ (c) $\gamma = 7.81 \cdot 10^{-3}$

Fig. 1. The progress of our method for reduced model order of $r = 8$ is depicted for decreasing levels γ. The given transfer function is illustrated as black solid line, the low-order surrogate transfer function is depicted as green dashed line, and the error is shown as blue dash-dotted line. The sample points are depicted as black crosses.

function vtsu : $\mathbb{R}^{r(r-1)/2} \to \mathbb{R}^{r\times r}$ maps a vector of length $r(r-1)/2$ to a strictly upper triangular matrix, and the function $\mathrm{vtf}_{r,m} : \mathbb{R}^{rm} \to \mathbb{R}^{r\times m}$ reshapes a vector of length rm to an $r \times m$ matrix. Then, to each $\theta \in \mathbb{R}^{n_\theta}$ one can assign the pH system

$$\Sigma_{\mathrm{pH}}(\theta) : \begin{cases} \dot{x}(t) = (J(\theta) - R(\theta))\, Q(\theta)x(t) + B(\theta)u(t), \\ y(t) = B(\theta)^{\mathsf{T}} Q(\theta)x(t). \end{cases} \tag{1}$$

Conversely, to each pH system Σ_{pH} with r states and m inputs and outputs one can assign a vector $\theta \in \mathbb{R}^{n_\theta}$ such that $\Sigma_{\mathrm{pH}} = \Sigma_{\mathrm{pH}}(\theta)$ with $\Sigma_{\mathrm{pH}}(\theta)$ as in (1).

For details of the construction, we refer the reader to Schwerdtner and Voigt (2020). In the following, we denote the transfer function of $\Sigma_{\mathrm{pH}}(\theta)$ by $H_{\mathrm{pH}}(\cdot, \theta)$.

Using this parametrization, we minimize the objective function

$$\mathsf{L}\left(\gamma, H, H_{\mathrm{pH}}(\cdot,\theta), S\right) := \frac{1}{\gamma} \sum_{s_i \in S} \left(\left[\left\| H_{\mathrm{g}}(s_i) - H_{\mathrm{pH}}(s_i, \theta) \right\|_2 - \gamma \right]_+ \right)^2, \tag{2}$$

with respect to θ for decreasing values of $\gamma > 0$, where

$$[\cdot]_+ : \mathbb{R} \to [0, \infty), \quad x \mapsto \begin{cases} x & \text{if } x \geq 0, \\ 0 & \text{if } x < 0 \end{cases}$$

and $S \subset \mathrm{i}\mathbb{R} := \{\lambda \in \mathbb{C} \mid \mathrm{Re}(\lambda) = 0\}$. Minimizing this objective function for decreasing values of γ effectively reduces the $\mathcal{H}_\infty$ error between H_{g} and H_{pH}. Furthermore, using L comes with several benefits compared to a direct minimization of $\|H_{\mathrm{g}} - H_{\mathrm{pH}}\|_{\mathcal{H}_\infty}$. These are discussed in Schwerdtner and Voigt (2020).

To obtain a good approximation of H_{g} by minimizing L, the sample points $s_i \in S$ must capture the error transfer function $H_{\mathrm{g}} - H_{\mathrm{pH}}$ with sufficient accuracy, such that

$$\max_{s_i \in S} \|H_{\mathrm{g}}(s_i) - H_{\mathrm{pH}}(s_i)\|_2$$

is close to $\|H_{\mathrm{g}} - H_{\mathrm{pH}}\|_{\mathcal{H}_\infty}$. However, each new sample point also increases the computational demand of the optimization, since both the large-scale transfer function and our surrogate transfer function (and gradient of the their difference with respect to θ) must be evaluated at each sample point. This speed/accuracy trade-off is circumvented by a recently developed adaptive sampling strategy, which adds new sample points at those locations where the discrepancy between $H_{\mathrm{g}}(s)$ and $H_{\mathrm{pH}}(s)$ is larger than a tolerance which is automatically adjusted by the algorithm. For implementation details we refer to Schwerdtner and Voigt (2021).

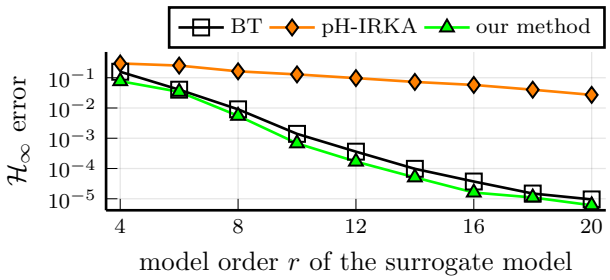

Fig. 2. $\mathcal{H}_\infty$ error comparison for different MOR methods

3. EXPERIMENTAL RESULTS

We assess the performance of our described optimization-based MOR by computing low-order approximations to a large-scale mass-spring-damper model from Gugercin et al. (2012). Fig. 1 illustrates how the minimization of L for decreasing values of γ leads to increasingly accurate surrogate models. Furthermore, it can be observed that the number of sample points is increased as γ is reduced to capture the error transfer function with sufficient accuracy.

In Fig. 2, we report the $\mathcal{H}_\infty$ errors that are obtained when using our method in comparison with another structure-preserving as well as an unstructured MOR method. The key observation is that using our method, we can obtain pH structured surrogate models that are as accurate as models obtained from unstructured MOR routines (such as BT), while other structured MOR methods (such as pH-IRKA developed in Gugercin et al. (2012)) typically lead to a decrease in accuracy. All reported results are obtained with the setup described in Schwerdtner and Voigt (2021).

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