# SPIN: A Data-Driven Model to Reduce Large Chemical Reaction Networks

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### Abstract

The behavior and chemical reactivity of a group of molecules are typically illustrated using intricate and extensive chemical reaction networks. These networks consist of a group of species and a series of reactions that detail their evolution. Although recent years have seen a surge in efforts to create numerical algorithms that generate dense chemical reaction networks with thousands of reactions and molecules, the simulation of these networks is a computationally demanding task, even for reaction mechanisms that describe the combustion of hydrocarbons. This paper introduces an innovative and unbiased approach to data-driven model reduction of extensive reaction networks called the SParse IdeNtification (SPIN) algorithm. SPIN combines tools from different domains to identify a set of crucial reactions using species concentrations and reaction rates, all while maintaining minimal computational costs and without requiring extra data or simulations. SPIN is successfully tested for large combustion networks of propane and *n*-heptane. The study demonstrates that, despite containing only one-fifth of the reactions found in the full mechanism, the SPIN reduced mechanism for *n*-heptane combustion serves as a highly accurate approximation of the original mechanism, with an average deviation of only 8.4% in ignition delay. Notably, this outstanding performance is achieved without bias towards any particular target property, such as ignition delay, as the reduction and model parameters are optimized to obtain the best possible results. We demonstrate that SPIN can operate as a standalone method or be hybridized with existing species-based reduction methods to further enhance its ability to identify the most significant reactions. This capability is particularly beneficial in comprehending the intricate mechanisms of combustion.

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### 1. Introduction

At the heart of energy lies a fundamental principle: its continual transformation. From the radiant glow of stars to the con-3 trolled combustion of renewable fuels, energy undergoes intricate exchanges governed by the delicate dance of molecules. 24 5 This intricate network of possibilities, where molecules col-6 lide, split, and rearrange, is what we call reaction mechanisms. 26 7 Understanding these mechanisms is crucial for unlocking en-27 8 ergy secrets, from optimizing fuel production and engine per-28 9 formance to designing sustainable solutions for a cleaner fu-10 ture [1]. 11

The sheer number and intricate dependencies of elementary reactions in fuel combustion, influenced by varying temperature, pressure, and species concentrations, present a formidable obstacle to fully understanding and optimizing these networks. However, deciphering this chemical dance is key to unlocking these energy sources' full potential and efficient utilization. Numerical modeling has proven to be a valuable tool in analyzing <sup>36</sup>

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reactive systems. For instance, computational fluid dynamics (CFD) simulations [2] that combine mass, momentum, and energy equations with a chemical mechanism have become essential for designing combustion systems and have facilitated improvements in efficiency and emissions. Despite the potential benefits of these computational techniques, the excessive computational expense caused by the complexity of chemical mechanisms remains a challenge. While the chemical mechanism with more species and reactions is generally better able to capture kinetic behaviors across a wider range of conditions, it comes at the cost of increased computational burden. As a result, the detailed version of chemical mechanisms for large hydrocarbons relevant to real transportation fuels is practically not applicable to CFD simulations of practical combustion systems. Numerous algorithms have been proposed to address this issue, creating skeletal or reduced mechanisms from a parent detailed mechanism.

These algorithms aim to replicate the desired properties of the reaction network while allowing for a tolerable level of deviation, using only the most significant species and reactions [3]. Previous methods, such as quasi-steady state analysis [4] and sensitivity analysis [5, 6], have been employed to reduce mechanisms. However, these techniques either require prior knowl-

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edge of the system or are computationally expensive and do 99 42 not scale well with the size of the system. Alternative reduc-100 43 tion techniques, such as the method proposed by Bhattachar-101 44 jee et al. [7], have approached the system as an integer linear<sup>102</sup> 45 programming problem. However, this method requires many<sub>103</sub> 46 reduced models, which can be computationally cumbersome.104 47 Direct relational graph (DRG) methods [8] view the reaction<sub>105</sub> 48 network as a graph and evaluate the influence of each species<sub>106</sub> 49 on a set of target species (e.g., major products and reactants).107 50 While DRG and related techniques, such as DRG with error<sub>108</sub> 51 propagation [9], have been successful reduction tools, their re-109 52 liance on prior knowledge of important species poses a chal-110 53 lenge for some reaction networks that are not well-understood111 54 outside combustion chemistry. Graph theoretic methods based112 55 purely on the graph structure have also been applied as a highly<sub>113</sub> 56 efficient reduction tool. However, these methods cannot cap-114 57 ture condition-specific phenomena such as negative tempera-115 58 ture coefficient chemistry [10]. Recently, a class of data-driven<sub>116</sub> 59 techniques based on machine learning have emerged as tools117 60 to model reduced chemistry [11, 12]. These include meth-118 61 ods to cluster reactions and species with principal component119 62 analyses [13], to optimize reduced mechanisms with genetic al-120 63 gorithms [14, 15], and to represent non-linear chemical rela-121 64 tionships using artificial neural networks and a small sub-set of122 65 species [16]. Challenges still exist for this class of methods as123 66 machine learning methods typically generalize poorly on data124 67 that falls outside the training distribution, and not all methods<sub>125</sub> 68 necessarily enforce physically meaningful solutions such as ad-126 69 herence to conservation laws [17]. 70

Our group has recently presented a novel approach called,127 71 the sparse-learning (SL) [18] to identify important reactions 72 in combustion networks. This approach has a significant ad-128 73 vantage over other methods as it is entirely data-driven and re-129 74 quires no prior knowledge of the reaction system. The proposed<sup>130</sup> 75 algorithm is an optimization problem to minimize the number131 76 of reactions while ensuring that the concentration deviation re-132 77 mains within a predefined threshold. The discrete form of the133 78 chemical rate equation was utilized to solve for the concentra-134 79 tions and identify the error in concentrations. As this technique 80 is applied to larger, more realistic fuels, the non-linear nature<sup>135</sup> 81 and noise in the reaction system become increasingly problem-136 82 atic. The authors of [18] noted that for the reaction mecha-<sup>137</sup> 83 nisms describing the combustion of *n*-heptane or complex hy-138 84 drocarbons, a forward-Euler discretization of the continuous-139 85 time mass-action kinetics was significantly imprecise in regions<sup>140</sup> 86 with sudden changes in concentration. 87

This paper presents a new SParse IdeNtification (SPIN) algo-88 rithm to identify influential reactions in a combustion network<sup>141</sup> 89 and create a smaller representative network. The SPIN algo-142 90 rithm improves upon existing approaches in three ways. First,<sup>143</sup> 91 it employs a Wiener filter-based system identification technique<sup>144</sup> 92 to obtain an accurate approximation of the discretized mass-145 93 action kinetics. The Wiener filter is a linear least-squares fil-146 94 ter, ensuring that the identified system is also linear. This is<sup>147</sup> 95 important as it was observed in [18] that a simple discretized<sup>148</sup> 96 mass-action kinetic equation may not accurately approximate 97 reaction kinetics in regions near ignition, with sharp changes

in chemical concentrations. By making appropriate modifications to the discretized mass-action kinetics, the Wiener filter addresses this issue while retaining its linearity. Although our work focuses on demonstrating the benefits of the Wiener filter in our sparse-learning reduction technique, we anticipate that this system identification approach can be applied to other computational strategies, such as multi-scale fluid simulations [19], which require a numerical representation of a complex evolution mechanism. Second, SPIN significantly reduces complex chemical reactions by removing many non-influential reactions. The automatic elimination of non-influential reactions during optimization results from using a Wiener filter. The filter coefficients tend to suppress inactive or moderately active modes in the dynamical system, reducing the number of noninfluential reactions. Lastly, we demonstrate that our sparselearning method can be used in conjunction with directed relational graph (DRG) techniques [9] to achieve an additional level of reduction in skeletal mechanisms for numerical simulations.

Our reduction technique provides a completely data-driven approach to analyzing reaction networks while upholding the underlying chemical relationships. The results demonstrate that we can accurately reconstruct the underlying reaction network for various fuels with different complexities without prior assumptions about the significance of species or reactions. Therefore, our sparse-learning method can effectively reduce a chemical mechanism while maintaining reasonable accuracy. This can be useful in chemical exploration and analysis, especially in cases where expert knowledge is not readily available.

### 2. The SParse IdeNtification (SPIN) Method

### 2.1. Preliminaries

The proposed SPIN algorithm leverages tools from multiple domains. Below, we review some useful definitions and properties of Wiener filters, mixed-integer linear programs and their linear programming (LP) relaxations, and fundamental differences between the SPIN algorithm and other network reduction methods.

#### 2.1.1. Mass-action kinetic equations & Wiener filter

Mass-action kinetic equations are often used to model the time evolution of chemical reaction networks using a set of coupled ordinary differential equations (ODEs) [20, 21, 22, 23]. A simple forward-Euler discretization of these coupled ODEs can be expressed as:

$$\mathbf{x}_{t+1} - \mathbf{x}_t = \mathbf{M}\mathbf{r}_t \Delta_t + \boldsymbol{\omega}_t, \text{ for all } t = 1, 2, \dots, T - 1, \quad (1)$$

where  $\mathbf{x}_t$  is an  $N_s \times 1$  vector representing chemical concentrations of all  $N_s$  species at any time *t*. The quantity  $\mathbf{M}$  is an  $N_s \times N_r$ matrix of stoichiometric coefficients of the associated reactions with reaction rates  $\mathbf{r}_t$ , an  $N_r \times 1$  vector. Here,  $\Delta_t$  represents the sampling time used for discretization, while  $\boldsymbol{\omega}_t$  captures modeling error and process noise, which is typically assumed to be small. The reaction rate associated with the *i*<sup>th</sup>-reaction is obtained as:

$$\mathbf{r}_t(i) = k_i \prod_{j=1}^{N_{\rm s}} \mathbf{x}_t(j)^{\nu_{ij}},$$

where  $k_i$  is the rate constant for the *i*<sup>th</sup> reaction and  $v_{ij}$  is the 186 149 stoichiometric coefficient of the  $j^{\text{th}}$  species involved in the  $i^{\text{th}}_{187}$ 150 reaction and zero otherwise. Typical linear discretized models<sub>188</sub> 151 for mass-action kinetics tend to ignore the modeling and pro-189 152 cess noise term  $\omega_t$  under assumptions on small modeling and 190 153 discretization errors, as is the case with our earlier work [18].<sub>191</sub> 154 However, these assumptions are grossly inaccurate if the sam-192 155 pling time  $\Delta_t$  is sufficiently large or in the regions near the igni-193 156 tion that are characterized by sudden changes in concentrations<sub>194</sub> 157 of species. Consequently, it was observed that model-based re-195 158 duction methods that consider (1) as the underlying discretized  $_{196}$ 159 model do not scale well for more complex mechanisms. In this<sub>197</sub> 160 paper, we alleviate this drawback by considering generalized<sub>198</sub> 161 mass-action kinetic equations expressed as: 162 199

$$\mathbf{x}_{t+1} = \mathbf{A}\mathbf{x}_t + \mathbf{B}\mathbf{M}\mathbf{r}_t\Delta_t + \tilde{\boldsymbol{\omega}}_t, \text{ for all } t = 1, 2, \dots, T-1, \quad (2)_{20}$$

where **A**, **B** are  $N_s \times N_s$  matrices obtained using Wiener fil-203 163 ters. Wiener theory was formulated by Norbert Wiener [24],204 164 and it forms the foundation of data-dependent system identifi-205 165 cation using linear least square error filters. A finite-duration<sub>206</sub> 166 impulse response (FIR) Wiener filter uses multiple linear re-207 167 gression to predict the output from multiple time bins of the 168 input. In particular, for a block of N samples of the in-169 put signal  $[\mathbf{u}_0, \mathbf{u}_1, \cdots, \mathbf{u}_{N-1}]$  and the desired output signal 170  $[\mathbf{y}_0, \mathbf{y}_1, \cdots, \mathbf{y}_{N-1}]$ , the corresponding Wiener filter input-output<sup>2</sup> 171 relationship is described as: 172 210

$$\begin{pmatrix} \hat{\mathbf{y}}_{0} \\ \hat{\mathbf{y}}_{1} \\ \vdots \\ \hat{\mathbf{y}}_{N-1} \end{pmatrix} = \begin{pmatrix} \hat{\mathbf{u}}_{0} & \hat{\mathbf{u}}_{-1} & \cdots & \hat{\mathbf{u}}_{1-P} \\ \hat{\mathbf{u}}_{1} & \hat{\mathbf{u}}_{0} & \cdots & \hat{\mathbf{u}}_{2-P} \\ \vdots & \vdots & \ddots & \vdots \\ \hat{\mathbf{u}}_{N-1} & \hat{\mathbf{u}}_{N-2} & \cdots & \hat{\mathbf{u}}_{N-P} \end{pmatrix} \begin{pmatrix} w_{0} \\ w_{1} \\ \vdots \\ w_{P-1} \end{pmatrix},$$
(3)

<sup>173</sup> which can be compactly written as

$$\hat{\mathbf{Y}} = \mathbf{U}\mathbf{w}.$$
 (4)<sup>214</sup>

The Wiener filter error is the difference between the desired<sup>216</sup> signal **Y** and the filter output  $\hat{\mathbf{Y}}$  given by

$$\mathbf{E} = \mathbf{Y} - \hat{\mathbf{Y}},$$
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$$= \mathbf{Y} - \mathbf{U}\mathbf{w}.$$

The Wiener filter minimizes the energy or the sum of the squared elements of the error matrix E. The coefficients **w** are obtained by setting the gradient of the energy function to zero, resulting in 222

$$\mathbf{w} = (\mathbf{U}^{\mathsf{T}}\mathbf{U})^{-1}\,\mathbf{U}^{\mathsf{T}}\mathbf{Y},\tag{5}_{224}$$

where <sup> $\intercal$ </sup> denotes the matrix-transpose. In the context of the<sup>226</sup> proposed modification of the discretized mass-action kinetics<sup>227</sup> described in (2), the Wiener filter coefficients (**A**, **B**) are ob-<sup>228</sup> tained by considering the equivalent block-diagonal formula-<sup>229</sup> tion as shown in (3), with  $P \leftarrow 1$ ,  $\mathbf{y}_t \leftarrow \mathbf{x}_{t+1}$ , and the two input<sup>230</sup> signals  $\mathbf{x}_t$  and  $\mathbf{Mr}_t \Delta_t$ .

#### 2.1.2. Integer programs and LP relaxation

The primary focus of this manuscript is the sparse identification of chemical reaction networks by finding influential reactions that preserve the dominant modes of the underlying full mechanism. We prescribe a quantification of the mismatch between the full reaction mechanism and the reduced mechanism with sparsely selected reactions. The aim is to find the sparsest set of reactions that keeps the mismatch between the two mechanisms below a user-defined threshold. At each time instant, SPIN seeks to select or reject a reaction in the network. The integer programming decision variables corresponding to the selection or rejection of reactions are binary decision variables, where a value of '1' indicates the selection of a reaction and '0' otherwise. On the other hand, the reduction error (mismatch) is a real variable. Such constrained optimization problems with linear objective functions and consisting of binary (integer) decision variables are referred to as integer linear program (ILP) in the literature [25].

To this end, we define a selection/weight vector  $\mathbf{w}_t = [w_{1,t}, w_{2,t}, \dots, w_{N_r,t}]^T$  of size  $N_r \times 1$  which represents the binary weights of all reactions at time *t*. The quantity  $\mathbf{w}_t$  prescribes the evolution of reduced mechanism at time *t* as:

$$\hat{\mathbf{x}}_{t+1} = \mathbf{A}\mathbf{x}_t + \mathbf{B}\mathbf{M}(\mathbf{r}_t \odot \mathbf{w}_t) \Delta_t$$
, for all  $t = 1, 2, \dots, T - 1$ , (6)

where  $\odot$  denotes the element-wise product. Thus, only reactions that are selected at any instant prescribe the evolution of the reduced (approximate) mechanism. Correspondingly, we quantify the mismatch between the original dynamical system (2) and the reduced dynamical system (6) as:

$$\mathcal{E}_{j,t}(\mathbf{w}_t) = |\mathbf{x}_{t+1}(j) - \hat{\mathbf{x}}_{t+1}(j)|,$$
  
=  $|(\mathbf{B}\mathbf{M})_j\mathbf{r}_t - (\mathbf{B}\mathbf{M})_j(\mathbf{r}_t \odot \mathbf{w}_t)|, \quad \forall t, \forall j \in \{1, 2, \dots, N_s\},$   
(7)

where  $\mathcal{E}_{j,t}$  is the error introduced in concentration of the  $j^{\text{th}}$  species at time *t*, and  $(\mathbf{BM})_j$  denotes the  $j^{\text{th}}$  row of the matrixproduct **BM**. We want to constrain this concentration error to be small. However, it must be noted that a reaction is more dominant only at specific intervals, and thus, the magnitude of concentration error varies significantly with time, even if the selection vector  $\mathbf{w}_t$  is kept fixed at all times. Given this limitation, we impose a constraint on the concentration error of each species at all times through appropriate normalization:

$$\mathcal{E}_{j,t}(\mathbf{w}_t) \le \epsilon \mathcal{N}_t(j), \ \forall t, \ \forall j \in \{1, 2, \dots, N_s\},$$
(8)

$$\mathcal{N}_t(j) = |(\mathbf{B}\mathbf{M})_j|\mathbf{r}_t\Delta_t, \quad \forall t, \ \forall j \in \{1, 2, \dots, N_s\}, \tag{9}$$

where  $|\cdot|$  is applied element-wise. The quantity  $N_t(j)$  is the associated normalization constant that enforces relative change in concentration constraint, while  $\epsilon > 0$  is a tuning parameter that indicates the acceptable error tolerance for the normalization constant. For example, a value of 0.10 enforces a maximum of 10% error.

The relative error tolerance constraint (8) effectively limits the *instantaneous* mismatch between the full and the approximate systems. However, the constraint is not ineffective in limiting constant drifts in species concentrations. The effect of not

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<sup>232</sup> selecting a reaction at any time instant *t* is visible at time *t* and <sup>233</sup> at all subsequent times. However, this effect weakens as time <sup>234</sup> evolves. In this work, we account for limiting error propagation<sup>261</sup> <sup>235</sup> by instead considering error in concentration of the  $j^{\text{th}}$  species<sup>262</sup> <sup>236</sup> over a time horizon of length *H* as: <sup>263</sup>

$$\tilde{\mathcal{E}}_{j,t}(\mathbf{w}_t, \dots, \mathbf{w}_{t+H-1}) = |\mathbf{x}_{t+H}(j) - \hat{\mathbf{x}}_{t+H}(j)|,$$

$$= \begin{vmatrix} \mathbf{x}_{t+H}(j) - \mathbf{A}\mathbf{x}_t(j) - \sum_{k=t}^{t+H-1} (\mathbf{B}\mathbf{M})_j (\mathbf{w}_k \odot \mathbf{r}_k) \Delta_{kT}^{266} \\ (10)_{269}^{268} \end{vmatrix}$$

Thus, the constraint on the error term in (8) is suitably modified<sup>270</sup> using the new definition of mismatch error (10) as:

$$\tilde{\mathcal{E}}_{j,t}(\mathbf{w}_t,\ldots,\mathbf{w}_{t+H-1}) \le \epsilon \sum_{k=t}^{t+H-1} \mathcal{N}_k(j), \quad \forall t, \; \forall j \in \{1,2,\ldots,N_s\}, \quad (11)$$

where the normalization constant  $N_k$  is defined as before.

Another important objective of the reduction process is to en-<sup>276</sup> sure that if a reaction is selected at any time instant *t*, it must<sup>277</sup> remain selected for all future times since the reduced mecha-<sup>278</sup> nism would simulate all the selected reactions in the final mech-<sup>279</sup> anism. To address this, we impose another constraint on the<sup>280</sup> selection vector  $\mathbf{w}_t$  as <sup>281</sup>

$$\mathbf{w}_t \le \mathbf{w}_{t+1}, \ \forall t \in \{1, 2, \dots, T-2\},$$
 (12)<sub>24</sub>

where *T* is the total number of discretization time points. Note that the above set of linear inequality constraints ensures that if  $\mathbf{w}_t(i) = 1$  for some  $i \in \{1, ..., N_r\}$ , then  $\mathbf{w}_{t'}(i) = 1$  for all  $t' \in \{t + 1, t + 2, ..., T - 1\}$ .

Finally, we add another set of constraints to ensure that the reduction process does not eliminate many reactions from the complete mechanism for scenarios where significant concentration changes are not observed at sampled time instants. We address this constraint using the following linear inequality:

$$\sum_{i=1}^{N_{\rm r}} \mathbf{w}_{T-1}(i) \ge \beta N_{\rm r},\tag{13}$$

where  $0 \le \beta \le 1$  is a user-specified parameter. For instance,  $\beta = 0.2$  indicates that the reduced mechanism must include at least 20% reactions in the final (reduced) set. Thus, the resulting ILP for each horizon window of length *H* can be described as:

$$\underset{\{\mathbf{w}_k\}_{k=t}^{t+H-1}}{\text{minimize}} \sum_{k=t}^{t+H-1} \sum_{i=1}^{N_t} \mathbf{w}_k(I) \qquad (P_{\text{ILP}})$$

s.t. 
$$\mathbf{w}_k(i) \in \{0, 1\}, \ \forall k \in \{t, \dots, t+H-1\}, \forall i \in \{1, \dots, N_r\}$$
  
(P<sub>ILP</sub>-1)

$$\tilde{\mathcal{E}}_{j,t} \le \epsilon \sum_{k=t}^{t+H-1} \mathcal{N}_k(j), \ \forall j \in \{1, 2, \dots, N_s\}$$
(P<sub>ILP</sub>-2)<sup>287</sup><sub>288</sub>

$$\mathbf{w}_k \le \mathbf{w}_{k+1}, \ \forall k \in \{t-1, t, \dots, t+H-2\}$$
  $(\mathbf{P}_{\text{ILP}}-3)_{290}$ 

$$\sum_{i=1}^{N_{\rm T}} \mathbf{w}_{T-1}(i) \ge \beta N_{\rm r}, \quad \text{if } t \ge T - H. \tag{P_{\rm ILP}-4}_{293}$$

The primary objective of the proposed ILP is to minimize the total number of reactions in the reduced mechanism while ensuring that the corresponding constraints  $(P_{ILP}-1)-(P_{ILP}-4)$  are met. The binary (or integer) aspect of decision variables makes solving an ILP combinatorially complex. For an ILP, the worstcase computational complexity is exponential in the number of decision variables. This makes the proposed ILP for mechanism reduction computationally prohibitive to handle. However, the solution to the above ILP can be closely approximated using linear programming (LP) relaxation [26]. Here, we replace the integer constraint (P<sub>ILP</sub>-2) with its convex relaxation  $0 \leq \mathbf{w}_k(i) \leq 1$ . LP relaxations to ILPs are computationally tractable, and the worst-case time complexity is still polynomial in the number of decision variables. The exact formulation of the relaxed LP and recovering the original weight selection vector  $\mathbf{w}_t$  is described in detail in Sec. 2.2.

### 2.1.3. Species vs reactions selection

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The proposed SPIN algorithm for mechanism reduction works primarily by finding influential reactions in the mechanism. If all reactions corresponding to a given species are eliminated in the reduction process, that particular species is also removed from the final reduced mechanism. Thus, a reactionbased reduction methodology, such as SPIN, targets the elimination of reactions. This is illustrated in Fig. 1. On the other hand, state-of-the-art species reduction approaches, such as directed relation graph (DRG) [27] or directed relation graph with error propagation (DRGEP) [28] are efficient at reducing the number of species in the skeletal mechanism.



Figure 1: An illustration of working methodology of species-based reduction vs reaction-based reduction. The red arrows indicate weak reaction coupling, while the red node indicates unimportant species. Since species E is connected with the rest of the combustion network through weak coupling, a reaction-based reduction eliminates species E and all other weak reactions. On the other hand, species-based reduction only targets species while retaining all the reactions associated with an important species.

One of the significant advantages of the proposed SPIN algorithm is its lower runtime relative to other reaction reduction methods, which allows hybridization with existing speciesbased approaches to further reduce the skeletal mechanism to even fewer species and reactions while ensuring a tight approximation to the original full mechanism. Hybridization of SPIN with other algorithms is discussed in detail in Section 3.

#### 294 2.2. Proposed SPIN algorithm

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s.t.

The SParse IdeNtification (SPIN) algorithm proposed in this 295 manuscript combines tools from multiple domains for princi-296 pled reduction of the full mechanism. It first leverages a linear 297 least-squared filter (Wiener filter) for data-based identification 298 of sampled linear system that describes the evolution of concen-299 trations of species in a chemical reaction network. The identi-300 fied generalized mass-action kinetic equations are described in 301 (2). The filter coefficients (**A**, **B**) are obtained using (5). 302

The sampled linear system is then subjected to an integral 303 optimization problem over a moving horizon of length H, as 304 shown in (P<sub>ILP</sub>), to obtain an optimal weight selection vector 305  $\{\mathbf{w}_t\}$  that best approximates the full mechanism up to a user-306 defined error tolerance. However, integer constraints make 307 the optimization problem computationally prohibitive to han-308 dle. Hence, a linear programming (LP) relaxation is suggested, 309 and the following equivalent optimization problem is consid-310 ered over each horizon of length *H*: 311

$$\mathbf{w}_{k}^{*}\}_{k=t}^{l+H-1} \coloneqq \underset{\{\mathbf{w}_{k}\}_{k=t}^{l+H-1}}{\arg\min} \sum_{k=t}^{t+H-1} \sum_{i=1}^{N_{r}} \mathbf{w}_{k}(I)$$
(P<sub>SPIN</sub>)333

$$0 \le \mathbf{w}_k(i) \le 1, \ \forall k \in \{t, \dots, t + H - 2\}, \forall i \in \{1, \dots, N_r\}$$
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(P<sub>SPIN</sub>-1)336

$$\tilde{\mathcal{E}}_{j,t} \le \epsilon \sum_{k=t}^{t+H-1} \mathcal{N}_k(j), \ \forall j \in \{1, 2, \dots, N_{\mathrm{s}}\}$$
 (P<sub>SPIN</sub>-2)<sup>338</sup>
<sub>339</sub>

$$\mathbf{w}_k \le \mathbf{w}_{k+1}, \ \forall k \in \{t-1, t, \dots, t+H-2\}$$
 (P<sub>SPIN</sub>-3)<sup>340</sup>

$$\sum_{i=1}^{N_{\rm r}} \mathbf{w}_{T-1}(i) \ge \beta N_{\rm r}, \quad \text{if } t \ge T - H. \tag{P_{\rm SPIN}-4}_{_{343}}^{_{342}}$$

The optimal solution  $\{\mathbf{w}_k^*\}_{k=t}^{t+H-1}$  to  $(P_{SPIN})$  is not necessarily  $bi_{345}^{-345}$ nary. However, including or excluding a reaction in the reduced mechanism is a binary decision. Consequently, we perform  $LP_{347}^{-315}$ rounding of the optimal solution vector based on a pre-specified threshold  $0 \le \alpha < 1$  as:

$$\tilde{\mathbf{w}}_{t}^{*}(i) = \begin{cases} 0, & \text{if } \mathbf{w}_{t}^{*}(i) \leq \alpha \\ 1, & \text{if } \mathbf{w}_{t}^{*}(i) > \alpha \end{cases}$$
(16)<sup>350</sup>

352 Algorithm 1 describes the proposed SPIN methodology for re-353 317 ducing the full mechanism for specified reaction conditions,354 318 namely temperature  $\tilde{T}$ , equivalence ratio  $\phi$ , and pressure  $\tilde{P}$  (*i.e.*, 355 319  $\theta = [\tilde{T}; \phi; \tilde{P}]$ ). The computational complexity of SPIN and the 320 choice of various hyperparameters is discussed in the next sec-321 tion. The output of the algorithm is a binary weight selection<sub>358</sub> 322 matrix  $\theta$  of size  $N_r \times T - 1$ , with columns indicating the selected 323 reactions at each time instance under specific initial conditions. 324 The algorithm is executed once for each reaction condition  $\theta_{361}^{360}$ 325 and thus, the final reduced mechanism consists of the union-326 sum of selected reactions at each condition and the species in- $\frac{302}{383}$ 327 volved in those reactions, *i.e.*, 328

$$\mathbf{w}_{\text{red}} = \bigcup_{\theta} \mathbf{W}_{T-1}(\theta), \qquad (17)_{_{364}}$$

where  $\mathbf{w}_{red}$  is the vector consisting of all reactions in the re-<sup>365</sup> duced mechanism, and  $\mathbf{W}_{T-1}(\theta)$  denotes the last column of the<sup>366</sup> matrix  $\mathbf{W}(\theta)$ .

## Algorithm 1 The SParse IdeNtification (SPIN) Algorithm

**Input:**  $\{\mathbf{x}_t\}_{t=1}^T, \{\mathbf{r}_t\}_{t=1}^T, \{\Delta_t\}_{t=1}^T, \epsilon, \alpha, \beta, \mathbf{M}, H, \theta \leftarrow [\tilde{T}; \phi; \tilde{P}]$  **Output:** Optimal weight selection vector  $\mathbf{W}(\theta) \coloneqq \{\tilde{\mathbf{w}}_t^*(\theta)\}_{t=1}^{T-1}$ *Initialization*:  $t \leftarrow 1; \mathbf{w}_0(i) \leftarrow 0, \forall i \in \{1, \dots, N_r\}$ 

- 1: Find Wiener filter coefficients (**A**, **B**) using (5)
- 2: while  $t \le T 1$  do
- 3:  $W \leftarrow \min(H, T t 1)$
- 4: Set the time horizon to  $\{t, t+1, \dots, t+W\}$
- 5: Solve the relaxed optimization problem (P<sub>SPIN</sub>) to obtain  $\mathbf{w}_t^*(\theta), t \in \{t, t+1, \dots, t+W-2\}$
- 6: Binarize  $\mathbf{w}_t^*(\theta)$  using (16)
- 7: Assign  $\tilde{\mathbf{w}}_{t}^{*}, t \in \{t, t+1, ..., t+W-1\}$  to columns  $\{t, t+1, ..., t+W-1\}$  of  $\mathbf{W}(\theta)$
- 8:  $t \leftarrow t + W$
- 9: end while
- 10: return  $W(\theta)$

### 2.3. Computational Complexity of SPIN

The original problem (P<sub>ILP</sub>) is an ILP whose worst-case computational complexity is exponential in the number of integer decision variables. For a horizon of length *H*, the number of binary decision variables is  $N_rH$ . While efficient ILP solvers that involve heuristics, such as branch and bound [29], and branch and cut [30], are empirically shown to exhibit polynomial-time convergence, the worst case complexity may still be exponential. For each condition  $\theta$  with total number of samples *T*, the worst-case computational complexity of the original ILP (P<sub>ILP</sub>) is  $O(\lceil T/H \rceil 2^{N_rH})$ .

The choice of H determines the trade-off between the quality of solutions and computational complexity. Note that the worstcase complexity is exponential in H. Thus, a smaller H is preferred because it involves fewer decision variables. On the other hand, a larger value of H enforces error toleration bound for a longer time. While it may result in a relatively large number of reactions in the reduced mechanism, the effect of excluding a reaction at a given time instant is minimal at future instants. Thus, the resulting reduced mechanism is a tight approximation of the original mechanism. It is observed empirically that a value of H = 10 balances this trade-off.

The proposed SPIN algorithm is computationally efficient since it further relaxes the original ILP into an equivalent LP (P<sub>SPIN</sub>) with convex constraints. Unlike ILPs, LPs are polynomial-time solvable in the number of decision variables. For the LP described in (P<sub>SPIN</sub>), the worst-case computational complexity for  $\delta$ -approximation is  $O\left(\left\lceil \frac{T}{H} \rceil n^{\omega} \log(n/\delta)\right)$ , where  $\omega = 2.38$  is the constant of matrix multiplication and *n* is the number of decision variables. In the context of (P<sub>SPIN</sub>), the number of decision variables is  $2N_rH$  since the convexrelaxation introduces additional  $N_rH$  slack variables.

### 3. Primary Results

### 3.1. Analysis of Propane Combustion

In this section, we aim to evaluate the performance of SPIN in reducing a propane combustion mechanism and showcase

Table 1: Comparison of different propane mechanisms. Size is described as the number of species  $N_{spe}$  and reactions  $N_{rea}$ , and for each reduced mechanism, accuracy is measured as the average,  $ID_{avg}$ , and maximum,  $ID_{max}$ , % error in the ignition delay, and as the mean absolute deviations in peak concentrations for three species. Error is measured relatively to the full mechanism for all the 216 conditions.

	$N_{spe}$	N <sub>rea</sub>	$ID_{avg}, \%$	$ID_{max}, \%$	$C_2H_4,\%$	$H_2,\%$	CO, %
Full Mechanism	117	1270	-	-	-	-	-
SPIN	111	484	3.3	37.1	4.3	3.1	0.5
DRGEP	80	885	7.2	22.4	2.7	7.0	5.8
DRGEP + SPIN	79	501	7.5	21.4	3.7	6.8	5.7
SPIN + DRGEP	76	342	5.5	25.7	8.4	10.7	6.8

its effectiveness. The propane mechanism adopted in our 368 study [31] consists of 117 species and 1270 reactions. We uti-369 lized the time history of species concentration derived from 0-D 370 homogeneous reactor [32] simulations (with constant volume 371 and internal energy) as the input for SPIN. We chose a 0-D 372 homogeneous reactor for our simulation environment since au-373 toignition behavior captured by the 0-D system provides the 374 most influential combustion characteristics governed by oxida-375 tion chemistry. 376

A comprehensive assessment was performed on 216 cases 377 that spanned temperatures from 700 to 1500 K, pressures be-378 tween 1 and 50 atm, and equivalence ratios from 0.5 to 2. To 379 contrast SPIN with prevalent reduction techniques, we tested 380 the DRGEP method [9], as implemented in CHEMKIN [32]. 381 The thermodynamic conditions (temperature, pressure, equiv-382 alence ratio) utilized for the DRGEP execution were identical 383 to those used for SPIN. The selection threshold for DRGEP re-384 duction was the maximum error in ignition delay of no more 385 than 40%, which is roughly equivalent to the maximum error 386 of the SPIN-reduced mechanism. Moreover, we declared sig-387 nificant reactants and products, including C<sub>3</sub>H<sub>8</sub>, O<sub>2</sub>, N<sub>2</sub>, CO<sub>2</sub>, 388 and H<sub>2</sub>O as species that should not be removed by the DRGEP 389 algorithm. For a consistent comparison, we discarded from all mechanisms any inert gases except for N<sub>2</sub>, specifically He and 391 Ar. The reduction levels for SPIN and DRGEP are presented in 392 Table 1. 393

Although species reduction is typically prioritized in mechanism reductions [33], DRGEP also includes a method for removing reactions [9]. For consistency in error, we only present the results of DRGEP species reduction.

Additionally, we explore the potential for further reduction 398 by combining SPIN and DRGEP methodologies, which has413 399 been successful in previous reduction frameworks [9, 34, 35].414 400 To achieve higher levels of reduction, we implement a two-415 401 stage reduction approach, where we first reduce the propane416 402 mechanism with SPIN, prioritizing the removal of reactions417 403 over species. We then apply DRGEP for species reduction, tar-418 404 geting major products and reactants, CO<sub>2</sub>, O<sub>2</sub>, C<sub>3</sub>H<sub>8</sub>, N<sub>2</sub>, and<sub>419</sub> 405 H<sub>2</sub>O, with a 40% error tolerance from the reduced SPIN mech-420 406 anism. Both SPIN + DRGEP and DRGEP + SPIN reduction<sub>421</sub> 407 orders are considered, and the results of these combined re-422 408 duction methods are presented in Table 1. By utilizing these<sub>423</sub> 409 two-stage reduction frameworks, we can obtain a mechanism<sub>424</sub> 410 with fewer reactions and species than the individual reduction425 411 methodologies. 426 412



Figure 2: Comparison of ignition delay for propane mechanisms as % deviation from the full mechanism.

To begin with, we examine how accurately the reduced mechanism can replicate the combustion behavior of the full mechanism. Specifically, we calculate the ignition delay, which is defined as the time when the temperature increases by 400 K, for each of the 216 conditions and compare it with that of the full system. The results for the performance of the reduction methodologies in predicting the ignition delay of the full mechanism are presented in Fig. 2. We observe that, for most conditions, the SPIN and SPIN + DRGEP mechanisms have an ignition delay within 10% of the full mechanism. Only in six of the 216 conditions does SPIN have an error of greater than 10%. While the combined SPIN + DRGEP mechanism increases the mean deviation compared to SPIN, its mean error is still lower than that of DRGEP, and there are some conditions where it

performs similarly or better than DRGEP and SPIN. This in-452 427 dicates that it may be useful when a high degree of reduction453 428 is required. Despite having fewer species and reactions in the454 429 mechanism, SPIN + DRGEP also outperforms DRGEP + SPIN455 430 regarding mean absolute deviation. This suggests that remov-456 431 ing unimportant reactions with SPIN before removing species457 432 may result in a more effective reduction strategy. Interestingly, 458 433 the mechanism reduced with DRGEP + SPIN has similar er-459 434 rors to the mechanism reduced with DRGEP with an identi-460 435 cal number of species and significantly fewer reactions. This<sub>461</sub> 436 demonstrates that SPIN can identify additional unimportant re-462 437 actions that were not identified in the first DRGEP step, result-463 438 ing in further reduction. All three methodologies, SPIN, SPIN464 439 + DRGEP, and DRGEP + SPIN, outperform the published per-465 440 formance of SL [18] in both accuracy and level of reduction,466 441 highlighting the advantages of this new methodology. 442 467



Figure 3: Time evolution of  $C_2H_4$ ,  $H_2$ , and CO mole fractions for propane com-497 bustion at 1 atm, 1000 K and equivalence ratio of 1.

We also evaluate how SPIN reproduces important species<sub>500</sub> 443 concentrations. Here, we consider the concentrations of  $C_2H_{4,501}$ 444 H<sub>2</sub>, and CO. We select these intermediates as they have been 445 considered in previous reduction studies [28] and are impor-446 tant parts of the propane combustion chemistry [36, 37] and the 447 formation of other chemical byproducts [38]. The concentra-503 448 tion profiles of these species for a single reaction condition are504 449 shown in Fig. 3. The concentrations of these molecules in the 505 450 full mechanism increase rapidly and reach a peak concentration506 451

during ignition. While overall, the reduced mechanisms follow this behavior, deviations are observed in the time in which this concentration increases, the concentration at the endpoint of the simulation, and the magnitude of the increase. The difference in time when the increase in concentration occurs can largely be characterized by the ignition delay discussed above. When considering the endpoint concentration, all mechanisms reproduce this value well. Except for  $C_2H_4$ , where the endpoint concentration is approximately zero, the mean deviation of all other endpoint concentrations is below 0.1%, showing that the chemical equilibrium of the mechanism is still intact. To evaluate how well these reduction models reproduce the ideal gas peak concentrations of species across all conditions, we assess the maximum concentration observed during combustion relative to the full propane mechanism. We calculate the mean absolute deviation in maximum concentration between each condition's full and reduced mechanisms, presented in Table 1. The data shows that, except for  $C_2H_4$ , SPIN performs better than the other mechanisms in reproducing the peak concentrations. This is likely because SPIN optimizes the full combustion chemistry within an error tolerance, while the graph-based methods used in our study identify species importance relative to target species and set a tolerance to maintain the ignition delay below a specific threshold, which does not necessarily correspond to accurately reproducing the concentrations of other combustion intermediates.

Finally, we compare the species removed from each of the mechanisms. SPIN removes six species from the full mechanism. These species consist primarily of dimethyl ether peroxides and dimethyl ether peroxy radicals. This suggests that the mechanism where dimethyl ether adds peroxides and undergoes  $\beta$ -scission [39] is not relevant under these propane combustion conditions. Interestingly, this is supported by other works [40], which suggest that propane mechanisms could be considered separately from dimethyl ether mechanisms for many conditions as there is minimal cross-over. Further removing species with DRGEP, SPIN + DRGEP, and DRGEP + SPIN produces very similar sets of species. When considering the effects of two-stage reduction (SPIN and DRGEP) on species removal, DRGEP and DRGEP + SPIN have identical species sets as the species removal step is performed with an identical methodology. Of the 41 species removed by SPIN + DRGEP, all but one are oxygenated. Many of the species removed are alkyl peroxy radicals, which are a part of low-temperature propane combustion pathways [37]. Of the 37 compounds DRGEP removes, there is an overlap with SPIN + DRGEP on all but 3 of these compounds. This suggests that the SPIN reaction removal step does not significantly alter the importance coefficients. SPIN + DRGEP removes ethanol and four similar alcohol compounds, while DRGEP retains these species.

### 3.2. n-Heptane Combustion

We then move on to analyze the combustion mechanism of n-heptane [41], which is a larger and more complex fuel compared to the previous mechanism. To compare the reduction methods, we consider a DRGEP-reduced mechanism, a

Table 2: Comparison of different *n*-heptane mechanisms. Size is described as the number of species  $N_{spe}$  and reactions  $N_{rea}$ , and for each reduced mechanism, accuracy is measured as the average,  $ID_{avg}$ , and maximum,  $ID_{max}$ , % error in the ignition delay, and as the mean absolute deviations in peak concentrations for three species. Error is measured relatively to the full mechanism for all 144 conditions.

	$N_{spe}$	N <sub>rea</sub>	$ID_{avg}, \%$	$ID_{max}, \%$	$C_2H_4,\%$	$H_2,\%$	CO, %
Full Mechanism	629	5478	-	-	-	-	-
SPIN	454	1092	9.5	31.9	4.2	13.2	5.0
DRGEP	236	2283	13.7	32.3	3.8	4.3	1.5
DRGEP + SPIN	234	1814	13.5	28.3	15.2	6.6	4.9
SPIN + DRGEP	222	934	14.4	42.1	7.8	11.1	4.4

507 SPIN-reduced mechanism, a SPIN+DRGEP-reduced mecha-508 nism, and a DRGEP+SPIN-reduced mechanism. Our analysis 509 is based on a total of 144 conditions, with temperatures ranging 510 from 700 K to 1300 K, pressures ranging from 1 atm to 40 atm, 511 and equivalence ratios between 0.5 and 2.

To maintain uniformity, the 40% maximum error tolerance 512 employed for propane is utilized for the DRGEP species re-513 duction and the combined SPIN and DRGEP methods as well. 514 Table 2 displays the reductions, while Fig. 4 depicts the per-515 formance of each approach. In most cases, the SPIN-reduced 516 mechanism's ignition delay deviates by less than 20% from 517 the full mechanism, demonstrating its efficiency in reducing 518 the larger mechanism to approximately one-fifth of the original 519 reactions. Using the SPIN + DRGEP approach generates the 520 fewest species and reactions in the mechanism. Implementing 521 DRGEP + SPIN eliminates 469 reactions and 2 species from 522 the DRGEP mechanism, with minimal change in ignition delay 523 deviation. However, performing SPIN and then DRGEP results 524 in a significantly greater level of reduction. 525

Interestingly, while SPIN did not significantly reduce the 526 number of species in the propane mechanism, many species 527 were eliminated during the reduction of *n*-heptane. Since SPIN 528 only removes a species if it no longer participates in reactions 529 and eliminates reactions, more species are likely to be elim-530 inated in a sparse reaction network. To determine this spar-531 sity, we computed the median number of reactions (separately 532 counting forward and reverse reactions) involving a species for 533 each mechanism. The full n-heptane mechanism has a me-534 dian number of 8 reactions, whereas the median for propane 535 is 28, suggesting that fewer reactions would have to be re-536 moved to eliminate species in the *n*-heptane mechanism. Of 537 the 198 species eliminated during the initial SPIN reduction, 538 186 contain four or more carbons, indicating that this sparsity 539 is due to larger species participating in fewer pathways. These 540 observations suggest that SPIN can eliminate many species<sub>552</sub> 541 for larger mechanisms by removing all the reactions involving553 542

Next, we examine the effectiveness of the mechanisms in555 544 reproducing the concentrations of C<sub>2</sub>H<sub>4</sub>, H, and CO. Fig-556 545 ure 5 displays the concentration profiles, and the mean devi-557 546 ation for peak concentrations is shown in Tab. 2. Compared<sub>558</sub> 547 to propane, SPIN performs slightly worse, on average, in re-559 548 producing peak concentrations relative to other reduction meth-560 549 ods. This difference can be attributed to the much higher reduc-561 550 tion offered by SPIN, which involves roughly 20% of the reac-562 551

those species.

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Figure 4: Comparison of ignition delay for propane mechanisms as % deviation from the full mechanism.

tions in the full mechanism and less than 50% of the reactions in DRGEP. Additionally, the data illustrate how significantly SPIN enhances overall computational time when implemented in a two-step algorithm, beginning with SPIN and culminating with DRGEP. This combination not only yields a significant, statistically noteworthy decrease in computational time but also streamlines the reaction network regarding both reactions and species. Explicitly, when compared to the reduction realized through DRGEP, this two-step method diminishes the number of species from 236 to 222 and reactions from 2283 to 934, as detailed in Tab. 2.



Figure 5: Time evolution of  $C_2H_4$ ,  $H_2$ , and CO mole fractions for *n*-heptane combustion at 1 atm, 1000 K and equivalence ratio of 1.

### 563 3.3. Computational Cost

When it comes to the performance gained by removing re-604 564 actions and species, several factors vary with the computing605 565 framework (e.g., instructions per cycle, cache, language opti-606 566 mization), and therefore general statements that hold the test607 567 of time are hard to make, beyond the complexity analysis out-608 568 lined before. For example, we considered two classes of sys-609 569 tems to demonstrate the potential reduction in computational<sub>610</sub> 570 cost when using a reduced mechanism. The first was 0-D homo-611 571 geneous reactor simulations, reflecting the computational cost612 572 when combustion chemistry is solved in each cell during 3D<sub>613</sub> 573 CFD simulations. The second class comprised 1-D reactors614 574 that are used for premixed burners and opposed flow flames.615 575 These flame models are expected to potentially reduce compu-616 576 tational costs when CFD simulations involve creating lookup617 577 tables based on flame calculations. However, as an example,618 578 we considered two classes of systems: 0-D homogenous reac-619 579 tors, since CFD simulations rely on these model types, and 1-D<sub>620</sub> 580 reactors, as they highlight different dependencies of the execu-621 581 tion time. 582 622

The results for the 0-D reactors, which span the same con-623 ditions used to create the reduced models, are shown in Ta-624 ble 3. The values are reported as the average relative execution625 time compared to the full mechanism, which is 0.7 s for the626 propane and 280 s for the heptane, truncating the ratio to the627

Table 3: Relative mean time of execution for a 0-D homogeneous reactor model (Propane and Heptane), burner stabilized flame (Burner), and opposite flow flame (Opposed, as the average of 3 conditions) are reported. Additional details for these systems can be found in the text.

	0	D	1 D		
	Propane	Heptane	Burner	Opposed	
Full	1.00	1.00	1.00	1.00	
SPIN	0.90	0.64	0.31	0.25	
DRGEP	0.93	0.53	0.10	0.09	
DRGEP + SPIN	0.90	0.52	0.10	0.11	
SPIN + DRGEP	0.83	0.45	0.08	0.07	

last significant digit. For the 1-D systems, reported in Tab. 2, we considered only heptane combustion since it has the largest mechanism and ran a premixed and three opposed flow flames. We established the inlet condition for the premixed flame to stoichiometric *n*-heptane/air at 373 K and 1 atm. For the opposed flow flame, we set the fuel-sided stream to *n*-heptane/Ar at 300 K, and the oxidizer stream to air  $(O_2 + 3.76 N_2)$  at the same temperature for three *n*-heptane/Ar ratio to attain stoichiometric, lean, or rich equivalence ratios. For these simulations, given the smaller sample size, the time should be considered to have an uncertainty of about 15%.

### 4. Conclusions

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In this paper, we present a cutting-edge, data-driven algorithm named SPIN. This algorithm has been designed to discern the most impactful reactions within a combustion network by utilizing species concentrations and reaction rates at a specific moment. This allows SPIN to provide an optimal reaction set that can accurately approximate the concentration of the species, all within a pre-set error-bearing tolerance.

SPIN's distinctive strengths are manifold. Its unique singleshot, non-iterative nature allows for a direct approach to problem-solving. The algorithm also promotes unbiased results towards any predetermined target, not including post-reduction parameter fine-tuning. The performance of SPIN can be accredited to the fusion of tools from multiple domains. Initially, SPIN utilizes Wiener filters for network identification, applying least-squared error minimization and suppression techniques for non-dominant reaction modes. The sparse identification problem is then effectively formulated as a MILP, thus simplifying computational challenges through the use of convex LP relaxation. Lastly, DRGEP's optional application for species reduction further diminishes the overall combustion network size.

We validated SPIN's effectiveness through applications on the reaction networks resulting from propane and *n*-heptane combustion. The algorithm notably exceeds the performance of our preceding sparse learning approach, especially in reducing propane mechanisms. Impressively, even with the intricacies inherent to *n*-heptane fuel, the mechanism reduced by SPIN presents a mere 9.5% average deviation in ignition delay, even after more than 80% of the original mechanism's reactions have
 been disposed of.

This performance, devoid of biases towards any specific tar-630 get property, highlights the immense potential of SPIN. Op-631 timized model parameters and reduction have facilitated the893 632 best possible outcome, further reinforcing the fact that SPIN<sup>694</sup> 633 can function as either a standalone method or a supplemental 634 tool to extant species-based reduction methods. This amplifies<sub>697</sub> 635 SPIN's strength in identifying crucial reactions and, thus, map-698 636 ping complex combustion processes. In conclusion, the unpar-699 637 alleled potential of this data-driven approach for scrutinizing<sup>701</sup> 638 intricate reaction networks and facilitating catalytic mechanism702 639 reduction in a computationally effective manner is clear. The703 640 results underscore the potential impact SPIN may hold for the<sup>704</sup> 641 future progress of combustion network analysis. 642 706

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