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Symmetry-Based Structural Identifiability and Observability Analysis of PDE and ODE Models in STRIKE-GOLDD

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Resumen

La identificabilidad y la observabilidad estructurales son propiedades que describen la capacidad de determinar los parámetros y estados de un modelo a partir del conocimiento de sus ecuaciones, entradas y salidas. Un modelo es estructuralmente inidentificable si diferentes conjuntos de parámetros producen salidas idénticas. En este trabajo adoptamos un enfoque, al que denominamos SIM, para analizar la identificabilidad y la observabilidad en sistemas dinámicos mediante la búsqueda de sus simetrías de escala. El método propuesto se basa en el análisis de la invariancia del sistema bajo transformaciones de escala de parámetros y estados, y puede aplicarse sistemáticamente independientemente de la dimensionalidad del modelo. Este método evalúa una condición suficiente pero no necesaria para la no-identificabilidad; por tanto, no puede asegurar identificabilidad. Presentamos la implementación del método SIM para modelos de ecuaciones diferenciales ordinarias (EDOs) en la *toolbox* de MATLAB STRIKE-GOLDD, y lo extendemos a modelos de ecuaciones diferenciales parciales (EDPs) mediante el nuevo algoritmo SIM-PDE. Este enfoque es sencillo de implementar y computacionalmente eficiente, lo que lo hace adecuado incluso para modelos altamente no lineales y a gran escala.

Palabras clave: Identificabilidad estructural, Observabilidad, Escalado, Simetría, EDOs (ecuaciones diferenciales ordinarias), EDPs (ecuaciones en derivadas parciales)

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Abstract

Structural identifiability and observability are properties that describe the ability to determine the parameters and states of a model from knowledge of its equations, inputs, and outputs. A model is structurally unidentifiable if different parameter sets produce identical outputs. In this work, we follow an approach, to which we refer as the SIM algorithm, to analyse identifiability and observability in dynamical systems based on finding its scaling symmetries. The method relies on analysing the invariance of the system under parameter and state scaling transformations and can be systematically applied regardless of the model's dimensionality. This method evaluates a sufficient but not necessary condition for unidentifiability; hence, it cannot ensure identifiability. We report the implementation of the SIM method for ODE models in the STRIKE-GOLDD MATLAB toolbox, and extend it to partial differential equation (PDE) models through the newly introduced SIM-PDE algorithm. The approach is straightforward to implement and computationally efficient, making it suitable even for highly nonlinear and large-scale models.

Keywords: Structural Identifiability, Observability, Scaling, Symmetry, ODEs (Ordinary Differential Equations), PDEs (Partial Differential Equations).

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1. Introduction

Mathematical models play a central role in understanding biological systems, enabling quantitative descriptions of complex mechanisms and providing a framework for interpreting experimental data. In many cases, these models are formulated as dynamical systems, where unknown parameters must be estimated from observational data. These parameters typically represent constant biological rates or mechanisms that govern system behavior (DiStefano III, 2015). Even if abundant and noise-free data is available, it is not always possible to uniquely determine all parameters. This fundamental limitation is known as lack of structural identifiability. Structural identifiability is distinct from practical identifiability, which depends on noise, sampling, and experimental design (Holmberg, 1982; Raue et al., 2009; Wieland et al., 2021). In contrast, structural identifiability is an intrinsic property of the model itself and cannot be resolved by improving data quality. Ensuring structural identifiability is a necessary step before parameter estimation, since a good fit to data does not guarantee that parameter estimates are unique or physically meaningful. Structural identifiability is typically classified as global or local, depending on whether uniqueness holds over the entire parameter space or only in a neighborhood of the true values (Ljung and Glad, 1994). A related property, observability, informs about the possibility of inferring the state variables – rather than the parameters – from knowledge of the input and output. While many works have focused only on structural identifiability (particularly in the area of mathematical biology), here we are interested in both properties, to which we refer as SIO. However, we may still use the phrase “structural identifiability” in parts of the text.

1.1. SIO of ODE models

Lack of structural identifiability or observability can often be traced back to the presence of symmetries in the model equations. It has been shown in the literature that the existence of *scaling* symmetries is equivalent to the existence of similarity transformations, that is, transformations of parameters and state variables that leave the model outputs unchanged. Consequently, the presence of such symmetries implies a lack of structural identifiability and/or observability (Yates et al., 2009; Merkt et al., 2015). In this regard, Castro and de Boer (2020) investigated structural identifiability of ODE models by proposing a simple analytical method based on scaling invariance of system parameters. The core idea is to rescale the parameters and examine whether the model equations remain invariant, which indicates whether different parameter sets can produce the same observed output. This approach allows identifiability conditions to be derived through straightforward algebraic manipulations, avoiding the need for complex computations. In this work, we implement this method within the STRIKE-GOLDD toolbox in MATLAB (Díaz-Seoane et al., 2022). The method (**SIM algorithm**) is illustrated through representative examples and shown to be effective for ODE models, while remaining relatively simple to implement and more practical than many existing techniques.

1.2. SIO of PDE models

Regarding structural identifiability analysis of partial differential equation (PDE), differential algebra approaches have

been extended to this type of systems. Differential algebra converts dynamical systems into input–output polynomial differential equations and assesses identifiability through the injectivity of the coefficient map. However, although this framework has been successfully applied to various ODE and PDE models, it remains computationally intensive and is restricted to polynomial or rational model structures. Recently, Renardy et al. (2022) developed a framework for age-structured PDE models, showing that for constant parameters, identifiability results are consistent with ODE counterparts, while additional identifiable parameter combinations may arise when parameters vary with age or include immigration terms. Browning et al. (2024) extended this approach to linear reaction–advection–diffusion PDEs, showing that spatial effects do not necessarily reduce identifiability, although the method becomes computationally demanding due to large polynomial systems and increasing derivative orders required for state elimination. Further, Byrne et al. (2025) generalized the framework to a broad class of polynomial PDEs and showed that identifiability can be inferred from the input–output coefficient map under generic conditions, though symbolic complexity and dependence on initial and boundary conditions remain significant challenges. Overall, these works demonstrate a progression from age-structured models to more general PDE classes; however, the differential algebra approach remains limited to polynomial or rational structures and is computationally intensive for large-scale systems.

Recently, Wu et al. (2025) proposed a systematic PDE-to-ODE reduction framework for multi-scale infection models, where within-host dynamics are described by ODEs and between-host dynamics are formulated as age-structured PDEs with integral terms. In such cases, unknown parameters can be factored outside integral operators, leading to aggregated variables and enabling standard ODE-based identifiability analysis. However, this reduction is not always valid due to non-separable parameter structures, nonlinear dependence inside integral terms, and convergence requirements. Moreover, in coupled multi-scale systems, identifiability issues may propagate between subsystems depending on observability and available measurements.

1.3. Contribution and outlook

Overall, the existing methods for analysing structural identifiability of PDE models remain computationally intensive and are often restricted to specific model types, which motivates the development of simpler and more general approaches. In this work, the SIM algorithm, which is based on identifying scaling symmetries of differential equations that lead to the detection of unidentifiable parameters and unobservable states, is adapted to PDE models and implemented within a MATLAB framework (**SIM_PDE algorithm**). This method enables a direct analysis of structural identifiability and observability by examining the invariance of the PDE models under scaling transformations of parameters and state variables. Unlike classical differential algebra or symbolic elimination techniques, the proposed approach reduces the problem to solving simple algebraic scaling relations, making it computationally efficient and applicable to large-scale nonlinear ODE and PDE models. In the next section, we present the methodology of both the SIM and SIM_PDE algorithms.

Next, we demonstrate their use by applying them to case studies from the literature. We conclude the paper with a brief discussion and outlook of future research.

2. Methodology

2.1. SIM: scaling invariance method for structural identifiability and observability analysis of ODE models

Structural Identifiability and Observability (SIO) analysis is a theoretical framework used to determine whether the state variables and unknown parameters of a dynamic model can be uniquely detected from the available output. A model is said to be structurally locally identifiable (SLI) when only a finite number of parameter vectors can produce the same input–output behaviour (DiStefano III, 2015). Since unknown parameters may be considered as constant state variables, structural identifiability can be treated as a particular case of observability. Consequently, both concepts are investigated together within a unified SIO analysis.

The scaling symmetry-based method is based on introducing unknown scaling factors for all model parameters and for unobserved state variables. Each parameter and unobserved variable is multiplied by an independent scaling factor, which represents a possible symmetry transformation of the system. These scaled quantities are then substituted into the original model equations. To ensure consistency with the original system, we impose the condition that the transformed model must preserve its structure. In other words, the equations must remain invariant under the scaling transformation. This invariance is applied separately to each functionally independent component of the model, leading to a set of algebraic equations in terms of the scaling factors. These algebraic relations capture the intrinsic scaling symmetry structure of the model. Solving these equations provides direct information about parameter dependencies and observable quantities.

To illustrate the concepts, consider a simple death model:

$$\frac{dx}{dt} = -p_1 p_2 x \quad (1)$$

To establish the proposed approach, we first relate SIO to sensitivity analysis. It should be noted that identifiability can also be determined without explicitly computing sensitivities.

It follows from the solution $x(t) = x_0 e^{-p_1 p_2 t}$ that only the product $p_1 p_2$ can be inferred from observations of $x(t)$, rather than the individual parameters. This lack of uniqueness is associated with the linear dependence of the sensitivity functions. In general, structural identifiability can be analysed through the sensitivity matrix S , whose elements are defined as:

$$S_{ij}(x_1, \dots, x_n, p_1, \dots, p_m) \equiv \frac{\partial x_i}{\partial p_j} \quad (2)$$

A necessary condition for identifiability is that the columns of this matrix are linearly independent (Walter and Pronzato, 1997; Stigter and Molenaar, 2015). To provide a more interpretable and dimensionless measure, we use the relative sensitivity (or elasticity) matrix K , defined as:

$$K_{ij}(x_1, \dots, x_n, p_1, \dots, p_m) \equiv \frac{p_j}{x_i} \frac{\partial x_i}{\partial p_j} \equiv \frac{p_j}{x_i} S_{ij} \quad (3)$$

This formulation quantifies the sensitivity of each state variable to variations in the model parameters. Specifically, a value of $K_{ij} = 1$ implies that the state x_i responds proportionally to changes in the parameter p_j , so both quantities vary at the same relative rate. In contrast, a value of $K_{ij} = 0.5$ reflects a damped response, indicating that x_i changes at only half the relative rate of p_j . For the considered death model, the elasticity matrix reduces to a (1×2) vector:

$$K = (K_{11}, K_{12}) \quad (4)$$

with:

$$K_{11} = \frac{p_1}{x} \frac{\partial x}{\partial p_1}, \quad K_{12} = \frac{p_2}{x} \frac{\partial x}{\partial p_2} \quad (5)$$

Let us now introduce independent scaling factors, u_i :

$$p_1 \rightarrow u_1 \cdot p_1, \quad p_2 \rightarrow u_2 \cdot p_2 \quad (6)$$

Substituting into the model gives:

$$\frac{dx}{dt} = -u_1 \cdot p_1 \cdot u_2 \cdot p_2 \cdot x \quad (7)$$

To preserve invariance, this expression must coincide with the original equation:

$$p_1 \cdot p_2 \cdot x = u_1 \cdot p_1 \cdot u_2 \cdot p_2 \cdot x \quad (8)$$

which leads to the condition:

$$u_1 \cdot u_2 = 1 \quad (9)$$

Since u_1 and u_2 cannot be uniquely determined, the individual parameters p_1 and p_2 are unidentifiable, although their product remains identifiable. If e.g. $u_1 = 1$, no scaling symmetry involving p_1 would exist. While such a result might be interpreted as a suggestion that p_1 is structurally identifiable, this method does not rule out the possible existence of other symmetries. Hence, it provides a necessary condition for identifiability (and, equivalently, a sufficient condition for non-identifiability), but not a sufficient and necessary condition for neither property (Villaverde and Massonis, 2021).

The same procedure can be applied to state variables, thus providing a result about their (non-)observability.

2.2. Extending the approach to PDE models: SIM_PDE

The relationship between scaling invariance, structural identifiability, and observability for partial differential equations (PDE) models follows the same principles discussed previously for ODE systems. In particular, the existence of scaling transformations that preserve the model equations implies parameter dependencies and lack of uniqueness in the identification problem. Therefore, the theoretical foundation of the proposed SIM approach remains unchanged when extending the analysis from ODEs to PDEs. Based on these considerations, we propose to apply the same scaling invariance framework to PDE models. Consider a model described by a set of n PDEs:

$$\frac{\partial x_i(t, s)}{\partial t} = f_i \left(x_i(t, s), \frac{\partial x_i(t, s)}{\partial s}, \frac{\partial^2 x_i(t, s)}{\partial s^2}, \frac{\partial^2 x_i(t, s)}{\partial t^2}, \frac{\partial^2 x_i(t, s)}{\partial s \partial t}, p_j \right), \quad (10)$$

where $x_i(t, s)$ denotes the state variables of the model, which depend on time t and an additional independent variable (e.g., space; here, we have used the letter s). The methodology for analysing PDE systems can be summarized as follows:

1. Scale all parameters and all unobserved state variables by unknown scaling factors u :

$$p_i \rightarrow u_{p_i} p_i, \quad i = 1, \dots, m, \quad (11)$$

$$x_j \rightarrow u_{x_j} x_j, \quad j = r + 1, \dots, n, \quad (12)$$

and substitute them into Eq. 10.

2. Enforce invariance of each functionally independent term in the model equations.

$$f_i(x_1, \dots, x_n, p_1, \dots, p_m) = \sum_{k=1}^M f_{ik}(\tilde{x}, \tilde{p}), \quad (13)$$

Specifically, each term f_{ik} must satisfy:

$$f_{ik}(\tilde{x}, \tilde{p}) = \frac{1}{u_{x_i}} f_{ik}(u_{\tilde{x}} \tilde{x}, u_{\tilde{p}} \tilde{p}), \quad (14)$$

where $u_{x_i} = 1$ for observed states, since they are not scaled. The prefactor arises from the scaling of the time derivative:

$$\frac{\partial x_i}{\partial t} \rightarrow u_{x_i} \frac{\partial x_i}{\partial t}.$$

Additionally, from the initial/boundary conditions

$$x_i(0, s) = x_{i,0}(s), \quad i = 1, \dots, n,$$

it follows that $u_{x_i} = u_{x_{i,0}}$, ensuring consistency between the observability of the state variables and the identifiability of their corresponding initial conditions. Following Browning et al. (2024), we do not consider boundary conditions explicitly; we assume that we have no information about the system at the boundaries.

3. Solve the resulting algebraic equations obtained from Eq.14 to determine combinations of scaling factors that leave the system invariant. These relations define the identifiability equations of the model:

$$u_k = F_k(u_{m_1}, u_{m_2}, \dots).$$

Based on the solutions of the scaling equations, the SIO of both ODE and PDE models can be characterized as follows:

- A parameter p_i may be structurally identifiable if its associated scaling factor is uniquely equal to one (i.e., $u_{p_i} = 1$). This indicates that no non-trivial scaling transformation can leave the system invariant while modifying that parameter independently. However, this result does not rule out the existence of other types of symmetries, and therefore it does not guarantee identifiability.
- A parameter p_i is structurally unidentifiable if its scaling factor admits non-trivial solutions different from one. In this case, multiple parameter values can produce identical system behavior, making independent estimation impossible.

- Similarly, a state variable x_i may be observable if its corresponding scaling factor is constrained to one (i.e., $u_{x_i} = 1$). If the scaling factor admits non-trivial solutions different from one, the state is unobservable.
- If two or more parameters (and/or state variables) are associated with coupled scaling factors, they may form an identifiable (and/or observable) group. Such parameters and states cannot be estimated independently, but their combinations could.

We remark that the SIM algorithm provides a necessary but not sufficient condition for structural identifiability and observability. Therefore, any conclusions regarding identifiability or observability obtained through this approach should be interpreted as indications rather than definitive guarantees. However, non-identifiability and non-observability results are conclusive.

3. Case Studies

To demonstrate the applicability and effectiveness of the proposed approach, this section presents two representative case studies: one based on an ordinary differential equation (ODE) model and another based on a partial differential equation (PDE) model. These examples are selected from the literature, where their structural identifiability properties have been previously analysed using established methods.

3.1. gLV model

The generalized Lotka–Volterra (gLV) model is a widely used framework in ecology and systems biology for describing species–species interactions through coupled nonlinear differential equations. In this approach, the growth of each species is modeled as a combination of its intrinsic growth rate and the cumulative effects of pairwise interactions with other species. The SIO of gLV models was analysed by Díaz-Seoane et al. (2023) in the context of microbial community modeling.

We use as case study a model with three state variables (x_1, x_2, x_3) and 12 parameters, including intrinsic growth rates (r_1, r_2, r_3) and interaction coefficients (β_{ij}). The system equations are given by:

$$gLV = \begin{cases} \dot{x}_1 = r_1 x_1 + \beta_{11} x_1^2 + \beta_{12} x_1 x_2 + \beta_{13} x_1 x_3 \\ \dot{x}_2 = r_2 x_2 + \beta_{21} x_1 x_2 + \beta_{22} x_2^2 + \beta_{23} x_2 x_3 \\ \dot{x}_3 = r_3 x_3 + \beta_{31} x_1 x_3 + \beta_{32} x_2 x_3 + \beta_{33} x_3^2 \end{cases} \quad (15)$$

In this configuration, only x_2 and x_3 are directly measurable outputs, but not x_1 . We introduce scaling factors for all parameters and unobserved states:

$$\begin{aligned} r_1 &\rightarrow u_{r_1} r_1, & r_2 &\rightarrow u_{r_2} r_2, & r_3 &\rightarrow u_{r_3} r_3, \\ \beta_{ij} &\rightarrow u_{\beta_{ij}} \beta_{ij}, & x_1 &\rightarrow u_{x_1} x_1. \end{aligned} \quad (16)$$

while, since x_2 and x_3 are observed outputs, their scaling factors are fixed as

$$u_{x_2} = 1, \quad u_{x_3} = 1.$$

The scaling equations obtained from the SIM procedure are:

$$\begin{aligned} u_{\beta_{12}} &= 1, & u_{\beta_{13}} &= 1, & u_{\beta_{22}} &= 1, & u_{\beta_{23}} &= 1, \\ u_{\beta_{31}} &= 1, & u_{\beta_{32}} &= 1, & u_{r_1} &= 1, & u_{r_2} &= 1, \\ u_{r_3} &= 1, & u_{\beta_{11}} u_{x_1} &= 1, & u_{\beta_{21}} u_{x_2} &= 1, & u_{\beta_{31}} u_{x_3} &= 1. \end{aligned}$$

Based on the SIM method, the (possibly) identifiable parameters are:

$$\{r_1, r_2, r_3, \beta_{12}, \beta_{13}, \beta_{22}, \beta_{23}, \beta_{32}, \beta_{33}\}$$

and the (definitely) non-identifiable parameters are:

$$\{\beta_{11}, \beta_{21}, \beta_{31}\}$$

Regarding the state variables, x_2 and x_3 are directly measured, whereas x_1 is unobservable. The results obtained from the SIM method are further validated through comparison with other established structural identifiability and observability tools, including the FISPO and Prob.Obs.Test algorithms included in STRIKE-GOLDD (Díaz-Seoane et al., 2022). All three approaches consistently identify the same unidentifiable parameters and unobservable state, confirming the reliability of the obtained classification.

A significant difference among the algorithms is observed in computational efficiency. The SIM method required approximately one second to analyse the model in our computers, making it the fastest approach among the considered methods. In contrast, the Prob.Obs.Test required 7 seconds, and the FISPO method required 482 seconds. Furthermore, the SIM algorithm is generally applicable, i.e., unlike Prob.Obs.Test it does not require the model to be rational. This generality, as well as its good scalability with problem size, is the main advantage of SIM.

3.2. Age-structured PDE model with density-dependent transmission and constant parameters

In this case study, a simplified mathematical model of tuberculosis (TB) epidemiology is considered (Renardy et al., 2022). TB is transmitted via the aerosolized bacterium *Mycobacterium tuberculosis*, which spreads between individuals through lung inhalation. A key feature of TB is the frequent development of a latent infection, during which individuals are asymptomatic and non-infectious, and the infection may persist for a long period.

The population is divided into three compartments: Susceptible (S), Exposed/latent (E), and Infectious (I). Susceptible individuals become infected through contact with infectious individuals and may either progress directly to the infectious class or first enter the exposed class, extending the classical SEI framework. In this work, the SEI PDE model is analysed using the SIM_PDE method. The system can be written as:

$$SEI = \begin{cases} \frac{\partial S}{\partial t} + \frac{\partial S}{\partial s} = -\beta S \frac{y_I}{k_I} - \mu_S S, \\ \frac{\partial y_E}{\partial t} + \frac{\partial y_E}{\partial s} = (1 - \epsilon)\beta S \frac{k_E}{k_I} y_I - (\delta + \mu_E) y_E, \\ \frac{\partial y_I}{\partial t} + \frac{\partial y_I}{\partial s} = \epsilon\beta S y_I + \delta \frac{k_I}{k_E} y_E - \mu_I y_I, \end{cases} \quad (17)$$

All state variables depend on both time and age. The parameters $\beta, \mu_S, \epsilon, \delta, \mu_E, \mu_I, k_E$, and k_I are assumed constant, while y_E and y_I are considered as measured outputs. We introduce scaling factors for all parameters and unobserved states:

$$\begin{aligned} \beta &\rightarrow u_\beta \beta, & \mu_S &\rightarrow u_{\mu_S} \mu_S, & \epsilon &\rightarrow u_\epsilon \epsilon, \\ \delta &\rightarrow u_\delta \delta, & \mu_E &\rightarrow u_{\mu_E} \mu_E, & \mu_I &\rightarrow u_{\mu_I} \mu_I, \\ k_E &\rightarrow u_{k_E} k_E, & k_I &\rightarrow u_{k_I} k_I, & S &\rightarrow u_S S, \end{aligned} \quad (18)$$

while, since y_E and y_I are observed outputs, their scaling factors are fixed as

$$u_{y_E} = 1, \quad u_{y_I} = 1.$$

Imposing invariance of the system under these transformations leads to the following identifiability equations:

$$\begin{aligned} u_{\mu_S} &= 1, & u_\beta &= u_{k_I}, & (1 - u_\epsilon) u_S &= (1 - \epsilon), \\ u_{\mu_I} &= 1, & u_\delta &= \frac{u_{k_E}}{u_{k_I}}, & u_\delta \delta + u_{\mu_E} \mu_E &= \delta + \mu_E, \\ u_\epsilon u_\beta u_S &= 1, \end{aligned} \quad (19)$$

From these relations, it follows that only the parameters μ_S and μ_I can be structurally identifiable.

If the additional condition $\mu_S = \mu_E$ is imposed, the system simplifies and yields:

$$\begin{aligned} u_{\mu_I} &= u_{\mu_E} = 1, & u_\delta &= 1, & u_S u_{k_E} &= 1, \\ u_{k_E} &= u_{k_I} = u_\beta, & u_\epsilon &= 1. \end{aligned} \quad (20)$$

In this case, the (possibly) identifiable parameters are:

$$\{\mu_S, \mu_I, \mu_E, \delta, \epsilon\}.$$

The identifiable parameter combinations are:

$$\left\{ \frac{\beta}{k_I}, \frac{\beta}{k_E}, \frac{k_I}{k_E}, \frac{k_I \delta}{k_E}, \frac{\beta \mu_I}{k_I} \right\}.$$

According to Renardy et al. (2022), the polynomial coefficients obtained from input output equations via the differential algebra approach include:

$$\left\{ \frac{\beta}{k_I}, \frac{k_I \delta}{k_E}, \frac{k_I \epsilon}{k_E(\epsilon - 1)}, \frac{k_I(\delta + \mu_E \epsilon)}{k_E(\epsilon - 1)}, \frac{\beta \mu_I}{k_I}, \mu_I, \mu_S, -\frac{\delta k_I \mu_S}{k_E}, \mu_I \mu_S - \frac{\beta \delta}{k_E} \right\}$$

while μ_S and μ_I are structurally identifiable.

Furthermore, under the condition $\mu_S = \mu_E$, the parameters δ and ϵ become identifiable, together with the combinations:

$$\left\{ \frac{\beta}{k_E}, \frac{\beta}{k_I} \right\}.$$

so the identifiable parameters are:

$$\{\mu_S, \mu_I, \mu_E, \delta, \epsilon\}.$$

Thus, the results obtained using the scaling symmetry-based algorithm are fully consistent with those reported in the literature using differential algebra approaches for the analysis of PDE models, while requiring only 0.3322 seconds to analyse this model. These findings suggest that the proposed method provides a computationally efficient framework for the structural analysis of PDE models with low computational cost.

4. Conclusions

In this work, we have reported the implementation of the SIM method – a simple approach based on scaling symmetries for the analysis of structural identifiability and observability of ODE models – within the MATLAB toolbox STRIKE-GOLDD. The method is applicable to a wide range of biological models, such as the ones available in the STRIKE-GOLDD GitHub repository (which can be accessed here).

Furthermore, as the main contribution of this study we have extended the SIM framework to partial differential equation (PDE) models, leading to the development of the SIM.PDE algorithm. This approach enables the analysis of structural identifiability and observability in PDE models by exploiting scaling invariance properties, without requiring model transformation or symbolic elimination. The proposed method has been successfully applied to a PDE model from the literature, demonstrating its practical applicability.

As illustrated in the case studies section, the results obtained using the proposed approach are fully consistent with those reported using established methods, such as differential algebra approaches and other algorithms available in the literature. In particular, the method reliably identifies unidentifiable parameters, observable and unobservable states, and parameter combinations arising from scaling symmetries – which may be identifiable in the absence of other symmetries. That said, it should be remarked that the method evaluates a condition for unidentifiability that is sufficient, but not necessary. In other words, the method can determine that a parameter is unidentifiable with certainty, but it cannot guarantee that it is identifiable. The same is valid for the observability of a state variable.

A key advantage of the proposed framework is its simplicity and computational efficiency. The method reduces the identifiability problem to the solution of algebraic scaling relations, thereby avoiding the complexity typically associated with alternative approaches, such as differential algebra methods for PDE models and differential geometry methods such as FISPO, Prob.Obs.Test, and Lie.Symmetry for ODE models. Consequently, the framework is particularly well suited for the analysis of large-scale and highly nonlinear ODE and PDE models involving a large number of states and parameters.

Overall, the integration of the SIM and SIM.PDE algorithms within STRIKE-GOLDD provides a practical and efficient tool for identifiability and observability analysis in both ODE and PDE systems.

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Referencias

- Browning, A. P., Taşcă, M., Falcó, C., Baker, R. E., 2024. Structural identifiability analysis of linear reaction–advection–diffusion processes in mathematical biology. *Proceedings of the Royal Society A* 480 (2286), 20230911.
URL: <https://arxiv.org/abs/2309.15326>
- Byrne, H., Harrington, H., Ovchinnikov, A., Pogudin, G., Rahkooy, H., Soto, P., 01 2025. Algebraic identifiability of partial differential equation models. *Nonlinearity* 38.
DOI: 10.1088/1361-6544/ada510
- Castro, M., de Boer, R. J., 11 2020. Testing structural identifiability by a simple scaling method. *PLOS Computational Biology* 16 (11), 1–15.
URL: <https://doi.org/10.1371/journal.pcbi.1008248>
DOI: 10.1371/journal.pcbi.1008248
- Díaz-Seoane, S., Rey Barreiro, X., Villaverde, A., 11 2022. Strike-goldd 4.0: user-friendly, efficient analysis of structural identifiability and observability. *Bioinformatics* 39.
DOI: 10.1093/bioinformatics/btac748
- Díaz-Seoane, S., Sellán, E., Villaverde, A. F., 2023. Structural identifiability and observability of microbial community models. *Bioengineering* 10 (4).
URL: <https://www.mdpi.com/2306-5354/10/4/483>
DOI: 10.3390/bioengineering10040483
- DiStefano III, J., 2015. *Dynamic systems biology modeling and simulation*. Academic Press.
- Holmberg, A., 1982. On the practical identifiability of microbial growth models incorporating michaelis-menten type nonlinearities. *Mathematical Biosciences* 62 (1), 23–43.
- Ljung, L., Glad, T., 1994. On global identifiability for arbitrary model parametrizations. *Automatica* 30 (2), 265–276.
URL: <https://www.sciencedirect.com/science/article/pii/0005109894900299>
DOI: [https://doi.org/10.1016/0005-1098\(94\)90029-9](https://doi.org/10.1016/0005-1098(94)90029-9)
- Merkt, B., Timmer, J., Kascsek, D., 07 2015. Higher-order lie symmetries in identifiability and predictability analysis of dynamic models. *Physical review. E, Statistical, nonlinear, and soft matter physics* 92, 012920.
DOI: 10.1103/PhysRevE.92.012920
- Raue, A., Kreutz, C., Maiwald, T., Bachmann, J., Schilling, M., Klingmüller, U., Timmer, J., 2009. Structural and practical identifiability analysis of partially observed dynamical models by exploiting the profile likelihood. *Bioinformatics* 25 (15), 1923–1929.
- Renardy, M., Kirschner, D., Eisenberg, M., 01 2022. Structural identifiability analysis of age-structured pde epidemic models. *Journal of Mathematical Biology* 84.
DOI: 10.1007/s00285-021-01711-1
- Stigter, J. D., Molenaar, J., 2015. A fast algorithm to assess local structural identifiability. *Automatica* 58, 118–124.
- Villaverde, A. F., Massonis, G., 10 2021. On testing structural identifiability by a simple scaling method: Relying on scaling symmetries can be misleading. *PLOS Computational Biology* 17 (10), 1–8.
URL: <https://doi.org/10.1371/journal.pcbi.1009032>
DOI: 10.1371/journal.pcbi.1009032
- Walter, E., Pronzato, L., 1997. *Identification of parametric models: from experimental data*. Springer.
- Wieland, F.-G., Hauber, A. L., Rosenblatt, M., Tönsing, C., Timmer, J., 2021. On structural and practical identifiability. *Current Opinion in Systems Biology* 25, 60–69.
URL: <https://www.sciencedirect.com/science/article/pii/S245231002100007X>
DOI: <https://doi.org/10.1016/j.coisb.2021.03.005>
- Wu, H., Zhao, Y., Xu, X., Lou, J., 2025. Global stability and identifiability of the immuno-epidemiological model. *Advances in Continuous and Discrete Models* 2025 (1), 131.
URL: <https://doi.org/10.1186/s13662-025-03983-z>
DOI: 10.1186/s13662-025-03983-z
- Yates, J. W., Evans, N. D., Chappell, M. J., 2009. Structural identifiability analysis via symmetries of differential equations. *Automatica* 45 (11), 2585–2591.
URL: <https://www.sciencedirect.com/science/article/pii/S0005109809003550>
DOI: <https://doi.org/10.1016/j.automatica.2009.07.009>