Fundamental limitations of network reconstruction

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Abstract

Network reconstruction is the first step towards understanding, diagnosing and controlling the dynamics of complex networked systems. It allows us to infer properties of the interaction matrix, which characterizes how nodes in a system directly interact with each other. Despite a decade of extensive studies, network reconstruction remains an outstanding challenge. The fundamental limitations governing which properties of the interaction matrix (e.g., adjacency pattern, sign pattern and degree sequence) can be inferred from given temporal data of individual nodes remain unknown. Here we rigorously derive necessary conditions to reconstruct any property of the interaction matrix. These conditions characterize how uncertain can we be about the coupling functions that characterize the interactions between nodes, and how informative does the measured temporal data need to be; rendering two classes of fundamental limitations of network reconstruction. Counterintuitively, we find that reconstructing any property of the interaction matrix is generically as difficult as reconstructing the interaction matrix itself, requiring equally informative temporal data. Revealing these fundamental limitations shed light on the design of better network reconstruction algorithms, which offer practical improvements over existing methods.
Networks are central to the functionality of complex systems in a wide range of fields, from physics to engineering, biology and medicine [1–3]. When these networks serve as conduit to the system dynamics, their properties fundamentally affect the dynamic behavior of the associated system; examples include epidemic spreading [4, 5], synchronization phenomena [6, 7], controllability [8, 9] and observability [10]. For many complex networked systems, measuring the temporal response of individual nodes (such as proteins, genes and neurons) is becoming more accessible [11]. Yet, the network reconstruction (NR) problem—that is, recovering the underlying interconnection network of the system from temporal data of its nodes—remains a challenge [11–13]. Consider a networked system of \( n \) nodes.

Each node is associated with a state variable \( x_i(t) \in \mathbb{R}, \ i = 1, \cdots, n \), at time \( t \) that may represent the concentration of certain biomolecule in a biochemical system, the abundance of certain species in an ecological system, etc. The time evolution of the state variables is governed by a set of ordinary differential equations:

\[
\dot{x}_i(t) = \sum_{j=1}^{n} a_{ij} f_{ij}(x_i(t), x_j(t)) + u_i(t), \quad i = 1, \cdots, n. \tag{1}
\]

Here the coupling functions \( f_{ij} : \mathbb{R} \times \mathbb{R} \to \mathbb{R} \) specify the interactions between nodes—self interactions when \( i = j \), or pairwise interactions between nodes when \( i \neq j \). The term \( u_i(t) \in \mathbb{R} \) represents known signals or control inputs that can influence the \( i \)-th state variable. The interaction matrix \( A = (a_{ij}) \in \mathbb{R}^{n \times n} \) captures the direct interactions between nodes, naturally defining the interconnection network of the system by associating \( a_{ij} \) to the link \( j \rightarrow i \) between node \( i \) and node \( j \). By appropriately choosing the coupling functions, Eq. (1) can model a broad class of networked systems [14]. Given some function \( \mathcal{P} \) of the interaction matrix—which we call a property—NR aims to recover the value of \( \mathcal{P}(A) \) from given temporal data \( \{x_i(t), u_i(t)\}_{i=1}^{n} \), \( \forall t \in [t_0, t_1] \), and given uncertainty of the coupling functions.

Note that the classical parameter identification (PI) problem for (1) aims to recover the interaction matrix itself (i.e. reconstructing the identity property) [15–17]. But in many cases, instead of reconstructing \( A \) itself, we may want to reconstruct properties like its sign pattern \( S = [s_{ij}] = [\text{sign}(a_{ij})] \in \{-1, 0, 1\}^{n \times n} \), connectivity pattern \( C = [c_{ij}] = ||s_{ij}|| \in \{0, 1\}^{n \times n} \), adjacency pattern \( K = [k_{ij}] = [c_{ij}(1 - \delta_{ij})] \in \{0, 1\}^{n \times n} \) (\( \delta_{ij} \) is the Kronecker delta) or in-degree sequence \( d = [d_i] = [\sum_j c_{ij}] \in \mathbb{Z}^n \). Indeed, a key insight of network science is that important properties of networked systems—such as sign-stability, structural
controllability/observability and epidemic thresholds—can be determined from \( S, C, K \) or \( d \) without knowing \( A \) \cite{4, 8, 10, 18, 20}. Note that these properties cannot be easily reconstructed by computing correlations in the data, simply because correlations capture both direct and indirect interactions.

NR helps us understand, diagnose and control the dynamics of diverse complex networked systems, deepening our understanding of human diseases and ecological networks, and letting us build more resilient power grids and sensor networks \cite{21–27}. Yet, despite a decade of extensive studies, NR remains an outstanding challenge \cite{11, 12, 28}. Many existing algorithms do not perform significantly better than random guesses \cite{12, 13}, and even well-established methods can provide contradictory results for relatively simple networks \cite{29}. It has been realized that these problems originate from our ignorance of the fundamental limitations of network reconstruction, governing which properties of the interaction matrix can be recovered from given temporal data and knowledge of the coupling functions \cite{11, 12}. Indeed, it is still unclear if an NR algorithm fails to recover the correct value for \( P(A) \) due to some design flaws, or due to limitations intrinsic to the available temporal data and/or our uncertainty about the coupling functions. Furthermore, it is also unclear if NR can be solved with less informative data that that is necessary to solve the classical PI problem. Our intuition suggests that NR is easier (in the sense of requiring less informative temporal data) than PI simply because we are recovering less information (e.g. \( K \) instead of \( A \)). But, is this true?

Here we characterize the fundamental limitations of NR for the first time, by deriving necessary (and in some cases sufficient) conditions to reconstruct any desired property of the interaction matrix. We find that fundamental limitations arise from our uncertainty about the coupling functions, or uninformative temporal data, or both. The first class of fundamental limitations is due to our uncertainty about the coupling functions, rendering a natural trade-off: the more information we want to reconstruct about the interaction matrix the more certain we need to be about the coupling functions. To show this, we characterize necessary conditions that our uncertainty about the coupling functions needs to satisfy in order to reconstruct some desired property of the interaction matrix. For example, we show that it is possible to reconstruct the adjacency pattern \( K \) without knowing exactly the coupling functions. But, in order to reconstruct the interaction matrix \( A \) itself, it is necessary to know these functions exactly. Hence, if we are uncertain about the coupling
functions, NR is easier than PI.

The second class of fundamental limitations originates from uninformative data only, leading to a rather counterintuitive result: regardless of how much information we aim to reconstruct (e.g. edge-weights, sign pattern, adjacency pattern or in-degree sequence), the measured data needs to be equally informative. This happens even if we know the coupling functions exactly. We prove that the same condition on the measured data is generically necessary regardless of the property to be reconstructed. Hence, in the sense of informativeness of the measured data, reconstructing any property of the interaction matrix is as difficult as reconstructing the interaction matrix itself, i.e. NR is as difficult as PI. In order to circumvent this limitation without acquiring more temporal data (i.e. performing more experiments), we show that prior knowledge of the interaction matrix is extremely useful.

These two classes of fundamental limitations indicate that when we are uncertain about the coupling functions (true for many complex systems) PI is impossible, but we can still reconstruct some properties of the interaction matrix provided the measured temporal data is informative enough and interactions are pairwise. In this sense, NR is easier than PI. Yet, ironically, even if we are completely certain about the coupling functions, with less informative data NR does not allow us to do more —it is as difficult as PI.

I. RESULTS

A property $P(A)$ can be reconstructed if and only if (iff) any two interaction matrices $A_1, A_2 \in \mathbb{R}^{n \times n}$ with different properties $P(A_1) \neq P(A_2)$ produce different node trajectories \( \{x_i(t)\}_{i=1}^n, t \in [t_0, t_1], \) a notion of identifiability or distinguishability [15].

We study the distinguishability of the interaction matrix by defining the interconnection vector of node $i$ as $a_i = (a_{i1}, \cdots, a_{in})^T \in \mathbb{R}^n$, which is just the transpose of $A$’s $i$-th row. We also define the regressor vector $f_i(x) = (f_{i1}(x_i, x_1), \cdots, f_{in}(x_i, x_n))^T$ of node $i$, characterizing the coupling functions associated to node $i$. Then (1) can be rewritten as

\[
\dot{x}_i(t) = f_i^T(x(t))a_i + u_i(t), \quad i = 1, \cdots, n.
\]  

(2)

with $x = (x_1, \cdots, x_n)^T \in \mathbb{R}^n$ the state vector. Using this notation, the distinguishability of $P(A)$ is equivalent to the distinguishability of $P(a_i)$ for $i = 1, \cdots, n$. 
FIG. 1. Two sources of indistinguishability.  

a. Indistinguishability due to unknown coupling functions

The same dynamics can be characterized by two regressors with different coupling functions (purple and green), yielding indistinguishable networks that differ in their edge-weights, sign patterns, connectivity patterns and degree sequences.

b. Indistinguishability due to uninformative data

With the classical population dynamics described by the generalized Lotka-Volterra (GLV) model \( \dot{x}_i = r_i x_i + \sum_j a_{ij} x_i x_j \), the two different networks shown in the top panel —representing two different inter-species interaction matrices— produce identical node trajectories \( x(t) \) (bottom panel). Here the growth rate vector is \( r = (0, -0.5, 0.5, -0.5, 0)^T \) and initial abundance \( x(0) = (0.895349, 0.72093, 0.255814, 1.82558, 1.82558)^T \). In these two examples, it is impossible to reconstruct the edge-weights, sign-pattern, connectivity-pattern or degree sequence of the network simply because we cannot decide which one of the two networks produced the measured node trajectories.

In many cases, due to our lack of knowledge of the exact coupling functions, we may not know the true regressor \( f_i \) but only a family of regressors \( \{\bar{f}_i\} \) to which it belongs. Members of the family can be considered as deformations \( \bar{f}_i(x) = g_i(f_i(x)) \) of the true regressor \( f_i(x) \) obtained by applying some transformation \( g_i : \mathbb{R}^n \rightarrow \mathbb{R}^n \). This family can be characterized by a set \( G_i^* \) of admissible transformations, specified as follows: (i) this set is a group [30], and (ii) any \( g_i \in G_i^* \) is a continuous function that preserves pairwise interactions. Consider also the group \( G_{i,\text{lin}}^* \) of linear transformations that preserve pairwise interactions. These linear transformations can be associated with nonsingular matrices \( G_i^{\text{lin}} \in \mathbb{R}^{n \times n} \) with nonzero entries only in its diagonal and \( i \)-th column (see Fig.1a and SI-2). Let \( G_{i,\text{lin}} \) denote
the transpose of $G_{i,\text{lin}}^*$, i.e. $G_i \in G_{i,\text{lin}}$ if and only if $G_i^T \in G_{i,\text{lin}}^*$. Hereafter we use the following observation: since $G_{i,\text{lin}}^* \subset G_i^*$, a necessary condition to reconstruct a property when $g_i \in G_i^*$ is that it can be reconstructed when $g_i \in G_{i,\text{lin}}^*$. Consequently, in order to characterize the fundamental limitations of network reconstruction, we can focus on linear transformations only. We will show that linear transformations are enough to produce severe limitations in the properties that can be reconstructed. Using the notion of structural stability, we later discuss the effects of deformations that do not belong to $G_i^*$.

A. Indistinguishable interconnection vectors

Two candidate interconnection vectors $v_1, v_2 \in \mathbb{R}^n$ will be indistinguishable if they produce the same right-hand side in Eq. (2) for some regressor in the family $\{\bar{f}_i\}$. This is equivalent to the condition

$$f_i^T(x(t))v_1 = f_i^T(x(t))G_i v_2, \quad \forall t \in [t_0, t_1],$$

for some matrix $G_i \in G_{i,\text{lin}}$, where $x(t)$ is the measured node trajectories. Multiplying this equation by $f_i(x(t))$ from the left and integrating over the time interval $[t_0, t_1]$ we obtain

$$M_i(t_0, t_1)(v_1 - G_i v_2) = 0,$$

where $M_i(t_0, t_1) = \int_{t_0}^{t_1} f_i(x(t))f_i^T(x(t)) \, dt$ is a constant $n \times n$ matrix. It is obvious that (3) implies (4), but the converse implication is not so obvious (Proposition 1 of SI-3). Indeed, it constitutes the main obstacle to extend our analysis to more general uncertainty of the coupling functions. Hereafter we write $M_i$ instead of $M_i(t_0, t_1)$, unless the specific time interval is important for the discussion. From (4), the set of all pairs of indistinguishable interconnection vectors for node $i$ is given by

$$\Omega_i = \left\{(v_1, v_2) \in \mathbb{R}^n \times \mathbb{R}^n \mid \exists G_i \in G_{i,\text{lin}} \text{ such that } (v_1 - G_i v_2) \in \ker M_i \right\}. \quad (5)$$

The above equation shows two sources of indistinguishability, rendering two classes of fundamental limitations of NR. First, unknown coupling functions causes two vectors to be indistinguishable if they can be transformed to each other via some $G_i \in G_{i,\text{lin}}$. This set of indistinguishable vectors $\{(v_1, v_2) \mid v_1 = G_i v_2, G_i \in G_{i,\text{lin}}\}$ is then the partition $\mathcal{O}_i$ of $\mathbb{R}^n$ by the orbits of the group $G_{i,\text{lin}}$ [30], Fig. 2a and SI-2. An orbit is called low-dimensional if its
dimension is < n (purple, blue, green and brown orbits in Fig. 2a). The orbits in Fig. 2a show that unknown coupling functions allow us to distinguish only if \( \dot{x}_i \) depends on \( x_j \) for \( j \neq i \) (i.e. the adjacency pattern of the interconnection vector), see Proposition 2a and Example 1 in SI-5. This is a consequence of the invariance of the adjacency pattern to the transformations in \( G_i^* \) (i.e. prior knowledge of the coupling functions). Other properties like edge-weights, connectivity patterns or degree sequence are indistinguishable and cannot be reconstructed (Proposition 2b in SI-5). Second, even if \( f_i(x) \) is exactly known, indistinguishability can still emerge due to uninformative data (Fig. 1b), making \( v_1 \) indistinguishable from \( v_2 \) if \( v_1 - v_2 \in \ker M_i \) and \( \ker M_i \) is nontrivial (i.e. contains a linear subspace different from \( 0 \)). In other words, the endpoints of \( v_1 \) and \( v_2 \) can be connected by an hyperplane parallel to \( \ker M_i \), Fig. 2b. Note that hyperplanes parallel to \( \ker M_i \) are often called fibers of the quotient space \( \mathbb{R}^n / \ker M_i \).

Combining these two sources of indistinguishability, \( v_1 \) is indistinguishable from \( v_2 \) iff it is possible to transform \( v_2 \) using an element of \( G_{i,\text{lin}} \) in a way that the line (or more generally, hyperplane) passing trough \( v_1 \) and \( G_{i,\text{lin}} v_2 \) is a fiber. Consequently, orbits of \( G_{i,\text{lin}} \) intersected by a fiber of \( \mathbb{R}^n / \ker M_i \) become indistinguishable and we can ‘glue’ them together to form a partition \( \mathcal{O}_{\ker M_i}^i \) of \( \mathbb{R}^n \) into sets of indistinguishable interconnection vectors, Fig. 2c. If \( \ker M_i \) is not contained in low-dimensional orbits, then \( \mathcal{O}_{\ker M_i}^i = \mathbb{R}^n \) and all vectors are indistinguishable. If, however, \( \ker M_i \) is contained in low-dimensional orbits then we can reconstruct the adjacency pattern of the interaction matrix (right panel of Fig. 2c). Note that the partition of indistinguishable interconnection vectors due to the nonlinear deformations cannot be finer than \( \mathcal{O}_{\ker M_i}^i \) obtained via linear deformations.

Note also that the matrix \( M_i \) in (4) is typically unknown because the true regressor \( f_i \) is unknown. Certainly, choosing any regressor \( \tilde{f}_i = G_i^\dagger f_i, G_i \in G_{i,\text{lin}} \), we can only compute

\[
\tilde{M}_i(t_0, t_1) = \int_{t_0}^{t_1} \tilde{f}_i(x(t)) \tilde{f}_i^\dagger(x(t)) \, dt = G_i^\dagger M_i(t_0, t_1) G_i.
\]

Therefore, we have only access to properties of \( M_i \) that remain invariant under \( G_i^\dagger M_i G_i \) for any \( G_i \in G_{i,\text{lin}} \). To find those invariant properties, note that if \( \tilde{v} \in \ker \tilde{M}_i \) then \( v = G_i \tilde{v} \in \ker M_i \), since \( 0 = \tilde{M}_i \tilde{v} = G_i^\dagger M_i G_i \tilde{v} \) and \( G_i^\dagger \) has full rank. Thus, \( G_{i,\text{lin}} \) transforms \( \ker \tilde{M}_i \) into \( \ker M_i \) (and vice-versa, because it is a group), and we can only know the orbit \( G_{i,\text{lin}}(\ker M_i) \) corresponding to this subspace. For example, the condition \( \ker \tilde{M}_i = \{0\} \) for some \( G_i \in G_{i,\text{lin}} \)
implies that

\[ \ker M_i = \{0\}, \]  

(6)
because \( G_{i, \text{lin}}(0) = 0 \) (i.e., \( 0 = G_i0 \) for any \( G_i \)). This shows that we can tell if \( M_i \) is nonsingular using any \( \bar{M}_i \). Equation (6) is an important condition in system identification literature known as *Persistent Excitation* (PE) and it is necessary and sufficient to solve the classical PI problem [31]. With (6) the data is informative enough in the sense it does not produce indistinguishability. In general, we can build the partition of indistinguishable vectors using any \( \bar{M}_i \), i.e., \( \mathcal{O}_i^{\ker \bar{M}_i} = \mathcal{O}_i^{\ker M_i} \) (see Lemma 1 of SI-6 for the proof).

**B. Necessary condition to distinguish a property**

Let \( \mathcal{P} : \mathbb{R}^n \to \mathcal{Y} \) be the property of the interconnection vector we want to reconstruct, where \( \mathcal{Y} \) is its image. For example, \( \mathcal{Y} = \{-1, 0, 1\}^n \) if \( \mathcal{P} \) is the sign pattern, or \( \mathcal{Y} = \{0, 1\}^n \) if \( \mathcal{P} \) is the adjacency or connectivity pattern. The property \( \mathcal{P} \) can be reconstructed only if any two interconnection vectors \( v_1, v_2 \in \mathbb{R}^n \) that have different properties \( y_1 = \mathcal{P}(v_1) \neq \mathcal{P}(v_2) = y_2 \) are distinguishable, i.e., belong to different orbits of \( \mathcal{O}_i^{\ker M_i} \). Let \( \mathcal{P}(a) = \mathcal{P}^{-1}(y) = \{v \in \mathbb{R}^n | \mathcal{P}(v) = y\} \). Then \( \mathcal{P}(a_i) \) can be reconstructed only if all two sets in the collection \( C_P = \{P_y \subseteq \mathbb{R}^n | y \in \mathcal{Y}\} \) belong to different orbits \( \mathcal{O}_i^{\ker M_i} \). When the deformations are a-priori known to be linear, this condition is also sufficient.

**C. The role of our knowledge of the coupling functions**

We could shrink or enlarge the group of transformations \( \mathcal{G}_{i, \text{lin}} \) according to our uncertainty of the coupling functions. For example, it will collapse to the single element \( \mathcal{G}_{i, \text{lin}} = \{I_{n \times n}\} \) if we know the coupling functions exactly, or will increase to \( \mathcal{G}_{i, \text{lin}} = \{\text{nonsingular } \mathbb{R}^{n \times n} \text{ matrices}\} \) if we do not have any knowledge of them. We emphasize that if \( \mathcal{G}_{i, \text{lin}} \) is enlarged (e.g., by including nonlinear transformations or more general interactions between nodes), existing orbits may merge but new orbits cannot appear because the original linear transformations preserving pairwise interaction remain in the group.

Since our previous analysis only depends on the group property of the transformations, it can be straightforwardly extended to any linear group \( \mathcal{G}_i \). It is just necessary to find its orbits \( \mathcal{O}_i \) and build the corresponding \( \mathcal{O}_i^{\ker M_i} \). From this observation, in order to reconstruct
some property of the interaction matrix, it is necessary that (i) our uncertainty about the
coupling functions is small enough (i.e., any two sets in $C_P$ belong to different orbits of
$G_i$), and (ii) the measured temporal data is informative enough (i.e., hyperplanes parallel
to $G_i(\ker M_i)$ do not glue orbits together). For example, in order to reconstruct the edge-
weights it is necessary to know the coupling functions exactly ($G_i = \{I\}$), because only then
any two vectors belong to different orbits.

D. Specifying the coupling functions

It is possible to reduce $G_i$ to $\{I\}$ when the system we aim to model indicates the appro-
priate coupling functions to use. For example, the generalized Lotka-Volterra (GLV) model
can provide a good starting point for ecological systems [14]. Linear coupling functions are
appropriate if the system remains close to an operating point (e.g., a steady-state). Candidate coupling functions for the model can also be computationally searched or improved
using symbolic regression [32]. In these cases indistinguishability emerges only from uninfor-
mative data: $v_1$ is indistinguishable from $v_2$ iff $v_1 - v_2 \in \ker M_i$. Consequently, a property
$P(a_i)$ can be reconstructed iff all two sets in the collection $C_P = \{P_y \subseteq \mathbb{R}^n | y \in \mathbb{Y}\}$ can be
separated by a fiber, Fig. S1. A fiber is an hyperplane and thus partitions $\mathbb{R}^n$ in two regions;
we say it separates $P_{y_1}$ from $P_{y_2}$ if $P_{y_1}$ belong to one region and $P_{y_2}$ belongs to the other
region or the fiber, Fig. 2b.

By specifying the coupling functions we can reconstruct more information such as the
interaction matrix itself (i.e., edge-weights). Setting $P = \text{Identity}$ we obtain $C_P = \mathbb{R}^n$,
showing that the necessary and sufficient condition to reconstruct $A$ is to distinguish between
any two different interconnection vectors in $\mathbb{R}^n$. This is possible iff the PE condition (6)
holds, a classical result from system identification theory [31]. Without PE it is still possible
to distinguish, for example, the adjacency-pattern of the interconnection vector when $\ker M_i$
is exactly ‘horizontally’ oriented. In fact, from the right panel of Fig. 2c, we can separate
the sets $P_y$ of vectors with different adjacency-patterns (orange and red regions) using the
same red region as separating fiber. However, this situation is pathological in the sense
that an infinitesimal change in the fiber’s orientation will eliminate the distinguishability.
Note also that other properties like sign-pattern, connectivity pattern or degree sequence
are indistinguishable.
E. Persistent excitation is generically necessary

Any mathematical model only approximates the dynamic behavior of a real system. Therefore, we can only expect that the “true” coupling functions are sufficiently close (but not exactly equal) to some deformation \( \hat{f}_i(x) = G_i^T f_i(x) \), \( G_i \in G_{i,\text{lin}} \). Considering this, it is important to understand if the distinguishability conditions derived earlier remain true under arbitrary but sufficiently small deformations of the coupling functions, a notion known as structural stability [33, 34]. Otherwise, these conditions represent non-generic cases that cannot appear in practice because they vanish under infinitesimal deformations.

We proved that the PE condition (6) is structurally stable (Theorem 1, SI-7). However, when \( \ker M_i \) is non-trivial, the condition that it belongs to low-dimensional orbits is structurally unstable (Theorem 2, SI-7). To understand the implications of these results, let’s consider an arbitrary deformation \( \hat{f}_i(x) \) with ‘size’ \( \delta > 0 \), i.e., \( \| \hat{f}_i(x(t)) - \bar{f}_i(x(t)) \| \leq \delta, \forall t \in [t_0, t_1] \). The PE condition is structurally stable because there exists \( \delta > 0 \) sufficiently small such that if \( \bar{f}_i(x(t)) \) has PE then any \( \hat{f}_i(x(t)) \) also has PE, Fig.3a. Indeed, regardless of the size of the deformation, almost any analytic deformation of the regressor will also have PE (Theorem 3, SI-8). In practice, these two results imply that we can check if given temporal data satisfies the PE condition without knowing the coupling functions exactly.

In contrast, when \( \ker M_i \) is non-trivial (i.e., contains a linear subspace of \( \mathbb{R}^n \) different from \( 0 \)) and belongs to low-dimensional orbits, then for any \( \delta > 0 \) there is a deformation \( \hat{f}_i(x) \) —a rotation, indeed— such that \( \ker \hat{M}_i \) belongs to the \( n \)-dimensional orbit, Fig.3b. Here \( \hat{M}_i = \int_{t_0}^{t_1} \hat{f}_i(x(t)) \hat{f}_i^T(x(t)) dt. \)

The analysis above shows that only two generic cases exist: (i) \( \ker M_i = \{0\} \) and indistinguishable vectors emerge only due to uncertain coupling functions \( O_i^{ker M_i} = O_i \); and (ii) \( \ker M_i \) is not trivial and is contained in the \( n \)-dimensional orbit, so all interconnection vectors become indistinguishable \( O_i^{ker M_i} = \mathbb{R}^n \).

Consequently, in a generic case, the PE condition (6) is necessary in order to reconstruct any property. Even if the coupling functions are exactly known, without PE we cannot generically reconstruct the sign/connectivity/adjacency patterns or degree sequence. The reason is simple: for all these properties there is no gap between the sets \( C_P \). For example, for \( \varepsilon \approx 0 \), the vectors \( v_1 = (\varepsilon, 0, \cdots, 0)^T \) and \( v_2 = 0 \) are infinitesimally close in \( \mathbb{R}^n \) but have different connectivity or degree sequence. Therefore, even when the sets \( P_u \) can be separated
by a fiber with a particular orientation (e.g., $P_{y_1}$ and $P_{y_2}$ shown in Fig.2b), an infinitesimal deformation in the coupling functions changes this orientation producing indistinguishable interconnection vectors with different properties. The question is how to create these gaps and solve NR problems without PE.

In the following, we show that knowing prior information about the interaction matrix $A$ shrinks the domain of a property $P$, create gaps between the sets $P_y$ in $C_P$ and hence relax the PE condition.

**F. Prior knowledge of the interaction matrix relaxes the PE condition**

For clarity, in this section we assume that the coupling functions are exactly known. The simplest prior information of $A$ is that the interconnection vectors satisfy:

$$a_i \in \mathbb{V}, \quad i = 1, \ldots, n,$$

where $\mathbb{V} \subseteq \mathbb{R}^n$ is a known set. Prior information shrinks the domain of the property $P$ from $\mathbb{R}^n$ to $\mathbb{V}$, i.e., $P : \mathbb{V} \subseteq \mathbb{R}^n \rightarrow \mathbb{Y}$. Two typical cases are: (i) $a_{ij}$ takes a finite number of values (e.g., binary signed interactions) and $\mathbb{V} = \cup_y P_y$ is a discrete set since each $P_y$ is a point, Fig.4a; and (ii) $a_{ij}$ are bounded as

$$a_{ij} \in [-a_{\text{max}}, -a_{\text{min}}] \cup [-\epsilon, \epsilon] \cup [a_{\text{min}}, a_{\text{max}}]$$

for some known constants $0 \leq \epsilon < a_{\text{min}} < a_{\text{max}}$. In this case $\mathbb{V} = \cup_y P_y$, where $P_0$ is an $\epsilon$ neighborhood of zero (which can be associated to ‘zero’ sign-pattern), and each of the $3^n - 1$ remaining sets lies in a different orthant $\mathbb{R}^n$ (and thus be associated to distinct sign patterns), see Fig.4b. A similar analysis can be applied in the case when ‘network sparsity’ is the prior information, SI-9.

In case (i), $A$ itself can be reconstructed without PE if we can separate each point composing $\mathbb{V}$ with a fiber. If $\dim(\ker M_i) < n$, this is generically possible because an infinitesimal deformation will change any ‘pathological’ orientation that contains two points. In case (ii), the sign or connectivity pattern can be reconstructed without PE if there is a gap between the sets $P_y$ such that a fiber can separate them, Fig.4b. The condition that a fiber fits in a gap is structurally stable. If this gap increases ($a_{\text{min}} - \epsilon$ increases and $a_{\text{max}} - a_{\text{min}}$ decreases), it becomes even easier for the fibers to fit. However, the interaction matrix $A$ itself cannot be reconstructed because it is impossible to separate two points inside one $P_y$. 

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G. Example

We illustrate our results in a basic problem of network reconstruction using steady-state data. Consider two species \((x_1, x_2)\) interacting in a food web and suppose we measure their steady-state abundances \(x(t) = \text{const}, \forall t \in [t_0, t_1]\). The goal is to reconstruct the sign-pattern of the interaction matrix characterizing who eats whom. Since the data is constant, any regressor \(\bar{f}_i(x(t))\) is also constant and all \(\bar{M}_i\)'s have rank 1 at most. Thus, the PE condition \((\ref{eq:PE})\) cannot be satisfied. Consequently, our analysis shows that without better specifying the coupling functions of the model, all interconnection vectors are generically indistinguishable and it is impossible to reconstruct any property of the interaction matrix.

To circumvent this problem we specify the coupling functions using the GLV model \(\dot{x}_i = r_i x_i + \sum_{j=1}^{2} a_{ij} x_i x_j\). We assume that the growth rates \(r_i\) are known. This uncontrolled model can be rewritten as in \((\ref{eq:GLV})\) using \(f_{ij}(x_i, x_j) = x_i x_j\) and \(u_i(t) = r_i x_i(t)\). Note that \(M_i(t_0, t_1) = x_i^2 \cdot (t_1 - t_0) \cdot x x^T\) has rank 1 at most, and it is still generically impossible to reconstruct exactly the interaction matrix \(A = (a_{ij})\) or any other property of it. This coincides with the fact that one steady-state experiment is generically not enough for parameter identification \((\ref{ref:parameter_identification})\). Yet, assuming known bounds of the interactions \((\ref{eq:interaction_bounds})\), we can reconstruct exactly the sign-pattern. For this, it is necessary and sufficient to separate the \(3^2\) sets in \(C_P\) by lines parallel to \(\ker M_i\). SI-10 presents a numerical example when this is possible, and SI-4 shows an NR method based on our analysis.

II. DISCUSSION

We now discuss the implications of our results. Regardless of the property of the interaction matrix \(A\) we aim to reconstruct and even if we know the coupling functions exactly, we proved that PE \((\ref{eq:PE})\) is generically necessary. This fundamental limitation implies that reconstructing less information of the interaction matrix generically does not mean we can solve an NR problem with less informative data. In particular, when only steady-state data from a single experiment is available, our result implies that generically no property of the interaction matrix can be reconstructed, not even mentioning the interaction matrix itself \((\ref{ref:parameter_identification})\). From a different angle, the PE condition also serves as guideline to design experiments \((\ref{ref:experiments})\) that can provide sufficiently informative data. For instance, simply changing the initial
conditions of the two-species ecological network of our previous example can produce PE using the GLV model. Available control inputs and intrinsic noise on the dynamics are also useful for this [37, 38]. Notice that in system identification literature PI is often performed in real time, so the PE condition should hold uniformly in the initial time [16, 17, 31].

The advantage of using NR to reconstruct less information of the interaction matrix is that we can have more uncertainty about the system dynamics. For example, if we aim to reconstruct the adjacency-pattern $K$ and the PE condition holds, we can consider the set of all dynamic systems with pairwise coupling functions and we need little knowledge of the true system dynamics. We can check the PE condition even when the coupling functions are not exactly known (SI-7 and SI-8). Indeed, for linear deformations, we characterized an optimal tradeoff: given a property of $A$ to reconstruct, the uncertainty on the coupling functions should be small enough (orbits distinguish the property) and the measured data should be informative enough (to ensure PE in the family of regressors). It remains open to understand how much indistinguishability is created by considering general nonlinear deformations.

Experimentally measured data usually has poor information content, in the sense that it typically cannot satisfy the PE condition. For example, current gene sequencing is frequently constrained to measure steady-state data only, which cannot satisfy the PE condition for any regressor. In order to circumvent this fundamental limitation of NR, we have shown that prior knowledge of the interaction matrix can relax the PE condition allowing us to solve the NR problem.

We notice that a different class of fundamental limitation in NR has been discussed in literature: solving an NR problem is impossible without measuring all time-varying nodes in the network [39]. If the state variables of unmeasured nodes are constant, then NR is actually possible (SI-11). Previous works considered the distinguishability of the parameters themselves only (i.e., the identity property) and were restricted to known coupling functions [11, 12]. Our analysis characterizes necessary conditions to distinguish any property of the interaction matrix under uncertain coupling functions, and it can be straightforwardly extended to include arbitrary-order interactions (e.g., $x_ix_jx_k$) and some nonlinear parametrizations (e.g., $x_i/(a_{ij} + x_j))$, SI-12. The analysis of uncertain coupling functions is motivated by existing NR algorithms that completely ignore our knowledge about the system dynamics, [40] and references therein. It is also possible to analyze the effect of
noise and more general uncertainty of the coupling functions at the cost of less constructive results [41].

Our results indicate that a better characterization of the uncertainty in the system’s coupling functions and prior information of the interaction matrix are extremely useful to make practical improvements in network reconstructions. This, in turn, calls for the design of better algorithms (SI-4) that incorporate such information, and that provide a guarantee of correct network reconstruction.

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FIG. 2. Indistinguishability of interconnection vectors. a. Indistinguishable vectors due to unknown coupling functions can be transformed into each other using some transformation \( G_i \in G_{i,\text{lin}} \). Sets of those indistinguishable vectors are the partition of \( \mathbb{R}^n \) by the orbits \( O_i \) of \( G_{i,\text{lin}} \), here shown in different colors for \( n = 2 \) and \( n = 3 \). Purple regions should be interpreted as points, and blue regions as lines. The grey region is another orbit. We can distinguish an interconnection vector in the blue orbit (e.g., \( v_2 \) with component \( a_{ij} = 0 \)) from an interconnection vector in the orange orbit (e.g., \( v_1 \) or \( v_3 \) with component \( a_{ij} \neq 0 \)), illustrating that we can distinguish the adjacency of the interconnection vector (i.e., whether \( a_{ij} \) is zero or not for \( j \neq i \)). Nevertheless, since \( v_1 \) and \( v_3 \) belong to the same orbit and hence are indistinguishable, but they have different degree sequences and sign or connectivity patterns, these properties cannot be reconstructed.

b. Due to uninformative measured temporal data, the interconnection vector \( v_1 \) is indistinguishable from \( v_2 \) because \( v_1 - v_2 \in \ker M_i \), that is, both vectors are joined by a fiber (shown in red).

Note also that we can separate the sets \( P_{y_1} \) and \( P_{y_2} \) with the particular orientation of the fibers. However, since there is no gap between these sets, any change in the orientation of the fibers (regardless of how small it is) will produce indistinguishable interconnection vectors that belong to different sets. This illustrates that the PE condition remains generically necessary if there is no gap between the sets in \( C_P = \{ P^{-1}(y) \subseteq \mathbb{V} | y \in \mathbb{Y} \} \).

c. Indistinguishable vectors in network reconstruction appear by combining both kinds of indistinguishable vectors, gluing together orbits of \( G_{i,\text{lin}} \) when they are intersected by a fiber of \( \mathbb{R}^n / \ker M_i \). In the left panel, since \( \ker M_i \) is not contained in low-dimensional orbits, all orbits are are glued \( O_i^{\ker M_i} = \mathbb{R}^2 \) and all vectors become indistinguishable (e.g., \( v_1 \) is indistinguishable from \( v_3 \)). In the right panel, \( \ker M_i \) is horizontally oriented and hence contained in low-dimensional orbits. We can then distinguish between \( v_2 \) and \( v_3 \) and hence reconstruct the adjacency pattern of the interaction matrix.
**FIG. 3. Schematic illustration of structural stability.**

**a.** The Persistent Excitation condition (6) is structurally stable because once some regressor \( \tilde{f}_i \) has PE, any small enough deformation \( \hat{f}_i \) of it also has PE. **b.** When \( \text{ker} M_i \) is nontrivial, the condition that it belongs to low-dimensional orbits is structurally unstable because there always exists a infinitesimal deformation \( \hat{f}_i \) such that \( \text{ker} \hat{M}_i \) belongs to the \( n \)-dimensional orbit.

**FIG. 4. Prior information of the interaction matrix relaxes the PE condition.**

**a.** When the edge-weights \( a_{ij} \)'s take a finite-number of values, the set \( \mathcal{V} \) is discrete (shown in grey). Then distinguishability of the edge-weights is generic, because an infinitesimal deformation will change any fiber that contains two elements of \( \mathcal{V} \) (grey points). **b.** Example for the sets \( P_y \) (shown in grey) in the case of known bounds of the edge-weight (8). Though the edge-weights cannot be distinguished, the sign-pattern (and connectivity) can still be distinguished since there exist hyperplanes parallel to \( \text{ker} M_i \) (shown in blue) separating every \( P_y \). This condition is structurally stable.