Physica A 404 (2014) 118–125

Contents lists available at ScienceDirect

Physica A

journal homepage: www.elsevier.com/locate/physa

Network reconstruction by linear dynamics

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HIGHLIGHTS

- Applying linear dynamics to network reconstruction.
- Highly computational efficiency.
- Novel network reconstruction method.

ARTICLE INFO

Article history:
Received 13 November 2013
Received in revised form 12 February 2014
Available online 2 March 2014

Keywords:
Phase synchronization
Coupled oscillators
Network reconstruction
Linear dynamics

ABSTRACT

Inferring connectivity of complex network from its node dynamics is of great significance in many cross-disciplinary fields. In this paper, we extend the previous network reconstruction method based on phase synchronization with nonlinearly coupled system to a linearly coupled one. *We test these two methods and prove that both of them are feasible* for the reconstruction of any unknown network structure. Compared to the nonlinear method, however, we find that *from* the computational efficiency point of view the linear reconstruction method is always superb, showing its own unique merits, such as simpler in the algorithm realization, faster in the computational time, and more efficient in the final reconstruction result. On the other hand, *we also briefly discuss* the limitation of the linear reconstruction method.

1. Introduction

We all live in a dynamical world! The cooperative dynamics of highly inter-wined elements is not only rich, but also complex which is determined by the connection topology, node dynamical diversity, and the forms of interaction [1–12]. Since the dynamics is always closely connected with certain systems function, predicting and determining the complicated dynamics of coupled systems on complex networks have attracted a lot of interest. See, for example, Refs. [1–4] and references therein.

On the other hand, however, the reverse question from dynamics to structure, namely, how to infer (or reconstruct) the network topology from dynamical observations, is also a key fundamental problem in network science. It is closely related to a variety of applications in many realistic systems, such as in genetic engineering, physiological network, and many other biological systems. In order to uncover the inner structure information from the dynamical information of individual units of the network, so far several methods have been proposed, including the methods relying on identical synchronization [13], phase synchronization [14–16], Lyapunov function or Lyapunov exponent [17–20], feedback control [21,22], and

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http://dx.doi.org/10.1016/j.physa.2014.02.067
0378-4371/

compressive-sensing [23,24]. For instance, Yu et al. [13] introduced an identical synchronization method to identify networks of chaotic oscillators; by having full knowledge of all model parameters, the network topology of a cloned system is varied progressively via error minimization until it becomes coincident with the original system. Timme et al. [14–16] presented a method mainly based on the phase synchronization, which showed a successful reconstruction for different dynamics and exhibited the method's robustness in the presence of external driving and substantial noise. Wang and coworkers [23,24] suggested a method of compressive sensing for reconstructing network. The main idea is to expand the vector field or map of the underlying system into a suitable function series, or use the power series expansions to expand to arbitrary order for a sparse vector, and then apply the l_1-norm technique to realize compressive sensing.

In this paper, we generalize the classical network reconstruction method based on the phase synchronization [14–16]. We still consider the generalized *Kuramoto* phase oscillators [25] as a paradigmatic model but change the nonlinear coupling term to a linear one. Interestingly, with the profit of linear systems, the linear reconstruction becomes much simpler. Meanwhile, we find that the reconstruction time gets much shorter (e.g., it is only approximately one twentieth of that for the usual nonlinear reconstruction under the same parameters) and the reconstruction result becomes much better. Finally, to show the great merit of linear systems for network reconstruction, we even propose a faster algorithm, which simply relies on the coupled map lattices (*CML*).

2. Nonlinear reconstruction algorithm

Here we briefly summarize the nonlinear reconstruction algorithm used in Refs. [14,15]. The generalized *Kuramoto* model can be described by

$$\dot{\theta}_i(t) = \omega_i + \varepsilon \sum_{j=1}^{N} a_{ij} f_{ij}(t), \quad i = 1, \ldots, N \tag{1}$$

where $i, j \in 1, \ldots, N$ with N indicating the total number of oscillators, $\theta_i(t)$ is the phase of oscillator i at time t, ω_i represents the natural frequency of node i, ε denotes the couple strength for all units, and a_{ij} is the element of the adjacency matrix A of the network ($a_{ij} = 1$ if i and j are connected, and $a_{ij} = 0$ otherwise). Here the nonlinear function f_{ij} is usually chosen as a sinusoidal function:

$$f_{ij}(t) = \sin(\theta_j(t) - \theta_i(t)). \tag{2}$$

Under the assumption that the coupling strength should be sufficiently large, namely, $\varepsilon > \varepsilon_c$ with ε_c being the critical couple strength for the global phase synchronization, an identical average frequency Ω exists for all i's. Immediately we have

$$\omega_i + \varepsilon \sum_{j=1}^{N} a_{ij} f_{ij}(t) = \Omega, \tag{3}$$

which can be rewritten as

$$\begin{pmatrix} a_{i1} & a_{i2} & \cdots & a_{iN} \end{pmatrix} \begin{pmatrix} f_{1i} \\ f_{2i} \\ \cdots \\ f_{Ni} \end{pmatrix} = (\Omega - \omega_i)/\varepsilon, \quad i = 1, \ldots, N. \tag{4}$$

To solve the above N unknowns $(a_{i1}, a_{i2}, \ldots, a_{iN})$, we have to set N constraints, similar to Eq. (4). The strategy is we should repeat N-times experiments for different sets of natural frequencies ω_{ik}. Here we use the subscript k to denote the k-th experiment and keep it for all other symbols afterwards. After computing and recording all these Ω_k and f_{ijk} for N independent realizations, we obtain

$$\begin{pmatrix} a_{i1} & a_{i2} & \cdots & a_{iN} \end{pmatrix} \begin{pmatrix} f_{1i1} & f_{1i2} & \cdots & f_{1iN} \\ f_{2i1} & f_{2i2} & \cdots & f_{2iN} \\ \cdots & \cdots & \cdots & \cdots \\ f_{Ni1} & f_{Ni2} & \cdots & f_{NiN} \end{pmatrix} = \begin{pmatrix} (\Omega_1 - \omega_{i1})/\varepsilon & (\Omega_2 - \omega_{i2})/\varepsilon & \cdots & (\Omega_N - \omega_{iN})/\varepsilon \end{pmatrix}, \tag{5}$$

and further

$$\begin{pmatrix} a_{i1} & a_{i2} & \cdots & a_{iN} \end{pmatrix} = \begin{pmatrix} (\Omega_1 - \omega_{i1})/\varepsilon & (\Omega_2 - \omega_{i2})/\varepsilon & \cdots & (\Omega_N - \omega_{iN})/\varepsilon \end{pmatrix} \begin{pmatrix} f_{1i1} & f_{1i2} & \cdots & f_{1iN} \\ f_{2i1} & f_{2i2} & \cdots & f_{2iN} \\ \cdots & \cdots & \cdots & \cdots \\ f_{Ni1} & f_{Ni2} & \cdots & f_{NiN} \end{pmatrix}^{-1}. \tag{6}$$

Therefore, the first N unknowns $(a_{i1}, a_{i2}, \ldots, a_{iN})$ (i.e., the first row of the adjacency matrix A) can be solved. Similarly for other rows and the whole matrix A, we have to reconstruct them row by row by applying Eq. (6) N times, as the matrix f on the right side of Eq. (6) depends on i. Clearly it is quite inconvenient and time-consuming for such mass data saving and function calculations for all f_{ijk}. Afterwards, we will see if the nonlinear function f_{ij} is substituted by a linear one, this troublesomeness is gone. Here it is notable that to avoid the ill-condition of Eq. (6) owing to $f_{iik} = 0$, f_{iik} should be set as a nonzero value; $f_{iik} = 1$ is chosen in the work [14].