

# Passive Reconstruction of Non-Target-Specific Discrete-Time LTI Systems

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**Abstract**—Much of the existing literature on the reconstruction of a system’s dynamical structure functions has focused on learning the structure of a system using experiments in which each measured state must be perturbed independently. This work develops a reconstruction procedure that does not require multiple targeted experiments, instead determining the structure of the network when inputs are drawn from a Gaussian distribution and are active simultaneously.

Although similar reconstruction procedures exist in the literature, this algorithm removes the restriction of target specificity, which states that each input must independently affect a measured state in the system. This allows for the reconstruction procedure to be applied to a larger number of networks that were previously not reconstructible because of their inherent structure. Furthermore, this is the first reconstruction procedure on the dynamical structure function to operate in the time-domain, rather than the frequency domain, in order to avoid the overhead and inaccuracies that could be introduced through transformations.

Dynamical structure functions, developed in [1], are a system representation that denote the structure and dynamics of a linear time-invariant system at a resolution consistent with the number of manifest variables. A system’s dynamical structure function details the *relationship among measured states* denoted by the transfer function matrix  $Q(z)$ , and the *relationship between inputs and measured states*, denoted  $P(z)$ , where  $z$  is a variable in the frequency domain. The dynamical structure function of a system contains more information about the structure of the system than the associated transfer function,  $G(z)$ , which details the input-output dynamics of the system and only contains structural information about the manner in which *inputs directly affect measured states*.

Rather than reconstruct the dynamical structure function, many existing algorithms attempt to determine the state space representation of a system,  $(A, B, C, D)$ , since it contains all the structural details of the system, i.e. it defines how *inputs affect internal states*, *internal states interact*, *inputs affect outputs*, and *states affect outputs*. However, determining a state space model of a system is an ill-posed problem that requires an extensive amount of a priori knowledge about the system, beyond its input-output dynamics, in order to reconstruct [2]. Note that determining the dynamical structure function from input-output data is also an ill-posed problem,

but requires less a priori information to reconstruct than the system’s state space realization [3], while having a stronger notion of structure than a system’s transfer function.

In [6], a robust network reconstruction algorithm that determines the dynamical structure function for systems with target specificity, i.e. systems in which each input independently affects a measured state, was developed. The algorithm was improved to run in polynomial time in [7], before being extended to all reconstructible systems in [8], based on identifiability conditions from [3]. These network reconstruction techniques for dynamical structure functions, however, all were set in the frequency domain and all assumed that experiments could be performed on the system. In particular, these works perturbed each input to *actively* probe the system and generate data informative enough to reconstruct its network structure.

Algorithms that use passive network reconstruction methods were presented in [9] and [10]; however, those were restricted to systems with target specificity, which requires each input to independently perturb a unique measured state. The novelty of the algorithm presented in this paper is that the target specificity restriction is removed which greatly increases the applicability of the reconstruction procedure. Additionally, the procedure is detailed in the time-domain in an attempt to circumvent potential inaccuracies that may be introduced through transformations on the system.

The paper begins with the derivation of the dynamical structure function and details the necessary and sufficient conditions required for network reconstruction of a system in Section I. Then in Section II, the dynamical structure function definition is extended from the frequency domain to the time domain. Section III details the main result, the passive reconstruction algorithm using the time domain representation of the dynamical structure function. Finally, in Section IV an illustrative example of the network reconstruction algorithm applied to a system with non-diagonal  $P(z)$ , i.e. a system *without* target specificity, is shown.

## I. BACKGROUND

In this section we derive the dynamical structure function representation of systems and detail the necessary and sufficient informativity conditions for network reconstruction of the dynamical structure functions, assuming no measurement or process noise in the system.

### A. Dynamical Structure Functions

This section gives an overview of the derivation of dynamical structure function. Consider the state space system given by:

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$$\begin{bmatrix} y[k+1] \\ \psi[k+1] \end{bmatrix} = \begin{bmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{bmatrix} \begin{bmatrix} y[k] \\ \psi[k] \end{bmatrix} + \begin{bmatrix} B_1 \\ B_2 \end{bmatrix} u[k]$$

$$y[k] = \begin{bmatrix} I & 0 \end{bmatrix} \begin{bmatrix} y[k] \\ \psi[k] \end{bmatrix}. \quad (1)$$

Note that  $D = 0$ , while  $C = [I \ 0]$  which allows the variables to be separated into the measured states,  $y$ , and the unmeasured states,  $\psi$ .

The next step is to take the  $\mathcal{Z}$ -transform of the signals in (1). Assuming zero initial conditions, we get:

$$\begin{bmatrix} zY(z) \\ z\Psi(z) \end{bmatrix} = \begin{bmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{bmatrix} \begin{bmatrix} Y(z) \\ \Psi(z) \end{bmatrix} + \begin{bmatrix} B_1 \\ B_2 \end{bmatrix} U(z) \quad (2)$$

Solving for  $\Psi(z)$ , gives:

$$\Psi(z) = (zI - A_{22})^{-1} A_{21} Y(z) + (zI - A_{22})^{-1} B_2 U(z) \quad (3)$$

Substituting (3) into the first equation of (2) then yields

$$zY(z) = W(z)Y(z) + V(z)U(z)$$

where

$$W(z) = A_{11} + A_{12} (zI - A_{22})^{-1} A_{21}$$

and

$$V(z) = A_{12} (zI - A_{22})^{-1} B_2 + B_1.$$

Let  $D(z)$  be a matrix with the diagonal terms of  $W(z)$ , i.e.  $D(z) = \text{diag}(W_{11}(z), W_{22}(z), \dots, W_{pp}(z))$ . Then,

$$(zI - D(z))Y(z) = (W(z) - D(z))Y(z) + V(z)U(z)$$

Note that  $zI - D(z)$  is always invertible since  $D(z)$  is always proper. We then have:

$$Y(z) = Q(z)Y(z) + P(z)U(z) \quad (4)$$

where

$$Q(z) = (zI - D(z))^{-1} (W(z) - D(z)) \quad (5)$$

and

$$P(z) = (zI - D(z))^{-1} V(z) \quad (6)$$

Note that since  $W(z) - D(z)$  is a hollow matrix (a matrix with zeros along the diagonal), then  $Q(z)$  is also a hollow matrix.

The matrix  $Q(z)$  is a matrix of strictly proper transfer function from  $Y_i(z)$  to  $Y_j(z)$ ,  $i \neq j$  relating each measured signal to all other measured signals. Likewise,  $P(z)$  is a matrix of strictly proper transfer function from each input to each output without depending on any additional measured state  $Y_i(z)$ . Together, the pair  $(Q(z), P(z))$  is known as the dynamical structure function of the system.

## B. Necessary and Sufficient Informativity Conditions for Network Reconstruction [3]

In order to detail the necessary and sufficient conditions for network reconstruction of the dynamical structure function, we introduce the following notation. Let  $A \in \mathbb{C}^{n \times m}$  and  $B \in \mathbb{C}^{k \times l}$ . Then:

- $\text{blkdiag}(A, B) = \begin{bmatrix} A & 0 \\ 0 & B \end{bmatrix}$ ,
- $A_{-i}$  is the matrix  $A$  without its  $i^{\text{th}}$  column,
- $A^T$  is the transpose of matrix  $A$ ,
- $\mathcal{R}(A)$  is the range of  $A$ ,
- $\vec{a}$  is the vector stack of the columns of  $A$
- and  $\overleftarrow{a}$  is the vector stack of the columns of  $A^T$ .

In order to determine the conditions that are necessary and sufficient for the reconstruction of the dynamical structure function from data, we construct a map of the elements of the dynamical structure function to the associated transfer function, which can be determined using system identification on input-output data. We begin by noting that the transfer function,  $G(z)$ , of the system in (1) is related to its dynamical structure,  $(Q(z), P(z))$ , by the following equation

$$G(z) = (I - Q(z))^{-1} P(z) \quad (7)$$

which can be rearranged to get:

$$\begin{bmatrix} I & G(z)^T \end{bmatrix} \begin{bmatrix} P(z)^T \\ Q(z)^T \end{bmatrix} = G(z)^T \quad (8)$$

Now, note that

$$\bar{A}\bar{X} = \bar{B} \iff \text{blkdiag}(\bar{A}, \dots, \bar{A})\vec{x} = \vec{b}$$

and defining  $X(z) = [P(z)^T \ Q(z)^T]$  we can then rewrite (8) as

$$\begin{bmatrix} I & \text{blkdiag}(G(z)^T, \dots, G(z)^T) \end{bmatrix} \vec{x}(z) = \overleftarrow{g}(z). \quad (9)$$

Since  $Q(z)$  is hollow, as noted in Section I-A, we can abuse notation to redefine  $\vec{x}(z)$  to remove the columns that correspond to the zero elements, reducing Equation (9) to the following:

$$L(z)\vec{x}(z) = \overleftarrow{g}(z). \quad (10)$$

where  $L(z) \in \mathbb{R}^{pm \times p^2 - p + pm}$  and

$$L(z) = \begin{bmatrix} I & \text{blkdiag}(G_{-1}(z)^T, G_{-2}(z)^T, \dots, G_{-p}(z)^T) \end{bmatrix}.$$

Identifiability conditions can then be established by determining which elements of  $\vec{x}(z)$  must be known a priori in order to reduce the relationship to an injective map. To accomplish this, consider the matrix  $\bar{T} \in \mathbb{R}^{p^2 - p + pm \times k}$  such that

$$\vec{x}(z) = \bar{T}h(z) \quad (11)$$

where  $h(z)$  is an arbitrary vector of transfer functions.

**Lemma 1.** *Given a system characterized by the transfer function  $G(z)$ , its dynamical structure function  $(Q(z), P(z))$  can be identified if and only if*

- 1)  $M(z) = L(z)\bar{T}$  is injective, i.e.  $\text{rank}(M(z)) = k$ , and
- 2)  $\overleftarrow{g}(z) \in \mathcal{R}(M(z))$ .

*Proof.* The proof for Lemma 1 is given in [3].  $\square$

## II. TIME-DOMAIN REPRESENTATIONS OF THE DYNAMICAL STRUCTURE FUNCTION

The dynamical structure function up to this point has only been defined in the frequency domain in the literature. We now extend the system representation to the time-domain, which is preferable for the development of the passive reconstruction algorithm. Previous network reconstruction techniques in the literature required system identification procedures to occur before the reconstructive step. While this is not difficult, the added layer of complexity could lead to worse performance in the reconstruction algorithm, which is avoided by performing the reconstruction procedure directly on the data.

### A. Representations

Given the dynamical structure function of the form (4), taking the inverse  $\mathcal{Z}$ -transform yields

$$y_t = Q_t * y_t + P_t * u_t \quad (12)$$

which we call the convolution representation of the dynamical structure function and where  $*$  is the convolution operator and  $y_t$  is the output and  $u_t$  is the output at time  $t$ .

Note that (12) can be written in the form of matrix multiplication:

$$\bar{y}_r = \bar{Q}_r \bar{y}_r + \bar{P}_r \bar{u}_r \quad (13)$$

where  $\bar{y}_r = [y_1^T \ y_2^T \ \dots \ y_r^T]^T$ ,  $\bar{u}_r = [u_1^T \ u_2^T \ \dots \ u_r^T]^T$ ,

$$\bar{Q}_r = \begin{bmatrix} 0 & \dots & \dots & \dots \\ Q_1 & \ddots & & \\ Q_2 & Q_1 & \ddots & \\ \vdots & \ddots & \ddots & \ddots \\ Q_r & & & \ddots \end{bmatrix}, \bar{P}_r = \begin{bmatrix} 0 & \dots & \dots & \dots \\ P_1 & \ddots & & \\ P_2 & P_1 & \ddots & \\ \vdots & \ddots & \ddots & \ddots \\ P_r & & & \ddots \end{bmatrix} \quad (14)$$

which we call the Toeplitz representation of the dynamical structure function.

As we will see in Section III-B stable systems result in matrices  $(\bar{Q}_r, \bar{P}_r)$  with entries  $Q_i$  and  $P_i$  that tend to zero as  $r \rightarrow \infty$ . This fact allows us to approximate  $(\bar{Q}_\infty, \bar{P}_\infty)$  arbitrarily well with matrices of finite dimensions.

### III. MAIN RESULT

Some previous reconstruction algorithms actively probe the system by constructing a sequence of experiments that independently inject an appropriate signal (e.g. a step) at each input (while holding all other inputs at zero) and measuring the entire system response [1], [6]. In situations where we have controlled access to the system inputs and can conduct such experiments, this process may be a convenient way to generate data that is very informative about the system's network structure.

However, in some situations, we may not have the ability to actively perturb each input. In these cases, the data obtained from observations of the system will not, in general,

be informative enough to reconstruct network structure. Nevertheless, there has been some work where researchers have been willing to assume that the system is intrinsically perturbed by independent stochastic processes acting on each input [9], [10], although these results assume target specificity. Here, we drop the target specificity assumption, but do assume that the inputs, though not controlled, are measured and provide a persistency of excitation on the system to ensure the input-output data is rich enough for reconstruction.

### A. Learning the Toeplitz Representation

The process of learning the Toeplitz representation in (13) is similar to learning the frequency-domain dynamical structure function using the necessary and sufficient conditions developed in [3]. First, we will extend those conditions from the frequency-domain to the time-domain, then we will discuss how the amount of data we collect will affect our estimate of  $r$  in (13) and thus, our current understanding of the system's structure and dynamics.

1) *Necessary and Sufficient Conditions for Time-Domain Network Reconstruction:* Given (14), each  $Q_i$  has  $p^2 - p$  unknowns and each  $P_i$  has  $pm$  unknowns, which means in  $\bar{Q}_r$  and  $\bar{P}_r$  there are a total of  $(p^2 - p + pm)r$  unknowns. Now, take (13) to be rewritten as

$$\bar{y}_r = [\bar{Q}_r \ \bar{P}_r] \begin{bmatrix} \bar{y}_r \\ \bar{u}_r \end{bmatrix}$$

Taking the transpose of both sides yields

$$\bar{y}_r^T = [\bar{y}_r^T \ \bar{u}_r^T] \begin{bmatrix} \bar{Q}_r^T \\ \bar{P}_r^T \end{bmatrix}$$

Next, we can write:

$$[y_1^T \ \dots \ y_r^T] = [y_1^T \ \dots \ y_r^T \ u_1^T \ \dots \ u_r^T] \begin{bmatrix} 0 & Q_1^T & \dots & Q_r^T \\ \vdots & \ddots & \ddots & \vdots \\ 0 & \dots & 0 & Q_1^T \\ 0 & P_1^T & \dots & P_r^T \\ \vdots & \ddots & \ddots & \vdots \\ 0 & \dots & 0 & P_1^T \end{bmatrix}$$

which is equivalent to the series of equations

$$\begin{aligned} y_1^T &= 0, \\ y_2^T &= [y_1^T \ u_1^T] \begin{bmatrix} Q_1^T \\ P_1^T \end{bmatrix}, \\ y_3^T &= [y_1^T \ y_2^T \ u_1^T \ u_2^T] \begin{bmatrix} Q_2^T \\ Q_1^T \\ P_2^T \\ P_1^T \end{bmatrix}, \text{ etc.} \end{aligned}$$

Finally, defining

$$\hat{x} = [Q_1^T \ \dots \ Q_r^T \ P_1^T \ \dots \ P_r^T]$$

allows us to write (13) as

$$\hat{y} = \hat{L} \hat{x}$$

where  $\hat{L} \in \mathbb{R}^{fp \times (p^2 - p + pm)r}$ ,  $f$  is the number of data points collected,  $\hat{y} = [y_1^T \ \dots \ y_1^T \ \dots \ y_f^T \ \dots \ y_f^T]^T$ , and

$$\hat{L} = \begin{bmatrix} y_1^T & 0 & 0 & \dots & 0 & 0 & 0 & u_1^T & 0 & 0 & \dots & 0 & 0 & 0 \\ 0 & \ddots & 0 & \dots & 0 & \ddots & 0 & 0 & \ddots & 0 & \dots & 0 & \ddots & 0 \\ 0 & 0 & y_1^T & \dots & 0 & 0 & 0 & 0 & 0 & u_1^T & \dots & 0 & 0 & 0 \\ \vdots & & \vdots & & \vdots & & \vdots & & \vdots & & & \vdots & & \vdots \\ y_f^T & 0 & 0 & \dots & y_1^T & 0 & 0 & u_f^T & 0 & 0 & \dots & u_1^T & 0 & 0 \\ 0 & \ddots & 0 & \dots & 0 & \ddots & 0 & 0 & \ddots & 0 & \dots & 0 & \ddots & 0 \\ 0 & 0 & y_f^T & \dots & 0 & 0 & y_1^T & 0 & 0 & u_f^T & \dots & 0 & 0 & u_1^T \end{bmatrix}$$

Now, given a static matrix

$$\bar{T} = \begin{bmatrix} T_1 & T_2 \\ T_3 & T_4 \end{bmatrix},$$

representing the a priori information in the frequency domain, where  $T_1$  is the a priori information about the system that indicates how the reduced elements of  $Q(z)$  map to the original elements of  $Q(z)$ , with  $T_2$  performing a similar function from the reduced elements of  $Q(z)$  to the original elements of  $P(z)$ , and so on.

Note that  $\hat{T}$  is the a priori information that maps the reduced element of each  $Q_i$  and  $P_i$  for  $i = 1, \dots, r$  to the unreduced elements of the appropriate matrices, and that the a priori information applies to each  $Q_i$  and  $P_i$  in the same manner, yielding

$$\hat{T} = \begin{bmatrix} T_1 & \dots & 0 & T_2 & \dots & 0 \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ 0 & \dots & T_1 & 0 & \dots & T_2 \\ T_3 & \dots & 0 & T_4 & \dots & 0 \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ 0 & \dots & T_3 & 0 & \dots & T_4 \end{bmatrix} \quad (15)$$

Note if  $\bar{T}$  is not static,  $\hat{T}$  is determined from the inverse  $\mathcal{Z}$ -transform of  $\bar{T}$ .

This leads us to the necessary and sufficient conditions for passive reconstruction:

**Theorem 1.** *Given a system characterized by the transfer function  $G$ , its dynamical structure function  $(Q, P)$  can be identified in the time domain if and only if*

- 1)  $\hat{M} = \hat{L}\hat{T}$  is injective, i.e.  $\text{rank}(\hat{M}) = kr$ ,
- 2)  $\hat{y} \in \mathcal{R}(\hat{M})$ , and
- 3)  $r$  chosen sufficiently large.

*Proof.* This follows directly from the results of Lemma 1, where  $\hat{T}$  is constructed by iteratively applying  $\bar{T}$  to the entries  $Q_i$  and  $P_i$  for  $i = 1, \dots, r$  as shown in (15) if  $\bar{T}$  is static. If  $\bar{T}$  is dynamic,  $\hat{T}$  is constructed by taking the inverse  $\mathcal{Z}$ -transform to get  $T_i$  and then applying each  $T_i$  to  $Q_i$  and  $P_i$  for  $i = 1, \dots, r$ .  $\square$

2) *Incremental System Understanding:* Here we discuss the notion of choosing  $r$  sufficiently large, specifically looking at the Boolean structure in terms of  $\sum_{i=0}^r Q_i$  from reconstructed Toeplitz representation for small values of  $r$ . This will help us inform our understanding of why part 3 of Theorem 1 is a necessary condition in the time domain.

**Example 1.** *Consider a system  $\mathcal{S}$  where the a priori information required for reconstruction is the Boolean structure*

of  $P(z)$ . In this scenario, the Boolean structure of

$$Q(z) = \begin{bmatrix} 0 & 0 & 1 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{bmatrix},$$

but this information is unknown a priori.

Using the necessary and sufficient conditions for reconstruction without  $r$  chosen sufficiently large yields the following Boolean structures

$r$	2	5	28	120
$Q_{\text{bool}}$	$\begin{bmatrix} 0 & 1 & 1 \\ 1 & 0 & 1 \\ 1 & 1 & 0 \end{bmatrix}$	$\begin{bmatrix} 0 & 1 & 1 \\ 1 & 0 & 0 \\ 1 & 1 & 0 \end{bmatrix}$	$\begin{bmatrix} 0 & 0 & 1 \\ 1 & 0 & 0 \\ 1 & 1 & 0 \end{bmatrix}$	$\begin{bmatrix} 0 & 0 & 1 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{bmatrix}$

(16)

Note that although  $r = 120$  yields the smallest  $r$  required to determine correct Boolean structure, a larger  $r$  value may be necessary in order to learn the correct dynamics of the system.

This example illustrates that the reconstruction procedure improves gradually as more data is collected from the system.

### B. Learning the Convolution Representation

Given the Toeplitz representation of the dynamical structure function, the convolution representation can then be determined. First, it is necessary to determine the delays on each link. Assuming zero initial conditions, the number of time steps it takes for a link in  $Q(z)$  or  $P(z)$  to become non-zero is the definition of the delay on the link. This means that the first non-zero element of the  $(\hat{i}, \hat{j})^{\text{th}}$  entry in  $Q_{\hat{k}}$  or  $(\bar{i}, \bar{j})^{\text{th}}$  in  $P_{\bar{k}}$ , for some  $\hat{k}, \bar{k} \in (1, \dots, r)$ , the delays on the links are given by  $w_{(\hat{i}, \hat{j})} = \hat{k}$  or  $w_{(\bar{i}, \bar{j})} = \bar{k}$ , respectively. If there are no non-zero elements, then no link exists. Given the links, we then attempt to learn the functions of the respective links in the time-domain, the form of which is derived in Theorem 2.

**Theorem 2.** *Given that*

$$Q(z) = (zI - D(z))^{-1}(A_{12}(zI - A_{22})^{-1})A_{21} + A_{11}$$

and

$$P(z) = (zI - D(z))^{-1}(A_{12}(zI - A_{22})^{-1})B_2 + B_1$$

the entries of the corresponding inverse  $\mathcal{Z}$ -transform will have the form

$$a_k \delta_{t,0} + \sum_{i=0}^{w_k} b_i (c_i)^t \quad (17)$$

where  $w_k$  is the number of delays in the corresponding link.

*Proof.* Consider the definition of the inverse  $\mathcal{Z}$ -transform which states

$$\begin{aligned} x[t] &= \mathcal{Z}^{-1}\{X(z)\} \\ &= \frac{1}{2\pi i} \oint_C X(z) z^{t-1} dz \\ &= \sum [\text{Residues of } X(z) z^{t-1} \text{ at the poles of } X(z)]. \end{aligned}$$

The residue of  $X(z)$  at the pole  $z_0$  is denoted

$$\text{Res}(X(z), z_0) = X(z)(z - z_0)|_{z_0}.$$

Since they are strictly proper transfer function matrices, the entries of  $Q(z)$  and  $P(z)$  can be written as the sum of partial fractions of the form  $\frac{\alpha_i}{z-\beta_i}$ . Then, defining

$$H_{j,k}(z) = Q_{j,k}(z)z^{t-1}$$

implies

$$H_{j,k}(z) = \sum_{i=0}^w \frac{\alpha_i z^{t-1}}{z - \beta_i}$$

The sum of the residues is then evaluated as

$$\begin{aligned} \sum_{i=0}^w \text{Res}_{(j,k)(z), \beta_i} &= \alpha_i z^{t-1} \Big|_{\beta_i} \\ &= \alpha_i \beta_i^{t-1} \\ &= \frac{\alpha_i}{\beta_i} \beta_i^t \end{aligned}$$

This gives us  $b_i = \frac{\alpha_i}{\beta_i}$  and  $c_i = \beta_i$ ,  $\forall i \in (0, w)$ . Assuming zero initial conditions then yields  $a = -\sum_{i=0}^w b_i$ .  $\square$

Given the form in Equation (17) which represents the entries in  $Q_t$  and  $P_t$ , we can then determine each entry by fitting together the  $Q_i$ 's or  $P_j$ 's using a nonlinear least squares algorithm. This process can be done in MATLAB using a custom curve fit. In order to tune the fitting process, we used the following heuristic:

- 1) Step 1: Change the default maximum function evaluations of the model and maximum amount of iterations to  $2r$  and attempt to fit the parameters.
- 2) Step 2: If a solution is not found, iterate through all possible maximum function evaluations and maximum amount of iterations from  $v = 1, \dots, 3r$ .
- 3) Step 3: If a solution is still not found, then randomly change the start point of the fitting algorithm and repeat Steps 1 and 2 until a solution is found or a stopping condition is met, using the best solution so far.

### C. Finding the Dynamical Structure Function

Once the convolution representation has been determined, take the  $\mathcal{Z}$ -transform of  $Q(t)$  and  $P(t)$  to get the dynamical structure function  $Q(z)$  and  $P(z)$ , which is the output of the algorithm.

## IV. NUMERICAL EXAMPLE

The following example reconstructs a dynamical structure function,  $(Q, P)$ , with non-diagonal  $P$ , to illustrate that this method can reconstruct systems without target specificity in the time-domain that were not previously reconstructed in this manner.

**Example 2. (Non-Diagonal  $P$ )** Consider the following stable state space system:

$$\begin{aligned} x[k+1] &= \begin{bmatrix} .75 & 0 & 0 & 0 & 0 & 1.2 \\ -1 & -.35 & 0 & 0 & 0 & 0 \\ 0 & 0 & .85 & -1 & 0 & 0 \\ 0 & -.73 & 0 & .95 & 0 & 0 \\ 0 & 0 & .43 & 0 & -.6 & 0 \\ 0 & 0 & 0 & 0 & 0 & .55 \end{bmatrix} x[k] + \begin{bmatrix} 1.4 & 0 & -1.4 \\ 0 & -.25 & 0 \\ 0 & 0 & .75 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} u[k] \\ y[k] &= \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \end{bmatrix} x[k] \end{aligned} \quad (18)$$

the corresponding dynamical structure function is

$$\begin{aligned} Q(z) &= \begin{bmatrix} 0 & 0 & \frac{41.28}{(4z-3)(5z+3)(20z-11)} \\ \frac{-2}{20z+7} & 0 & 0 \\ 0 & \frac{292}{(20z-17)(20z-19)} & 0 \end{bmatrix} \\ P(z) &= \begin{bmatrix} \frac{5.6}{4z-3} & 0 & \frac{-5.6}{4z-3} \\ 0 & \frac{-5}{20z+7} & 0 \\ 0 & 0 & \frac{15}{20z-17} \end{bmatrix} \end{aligned} \quad (19)$$

The corresponding transfer function is full, so it does not detail any internal structure, only that all the inputs affect all the outputs, even though the system has a clear ring structure, as seen in Figure 1.

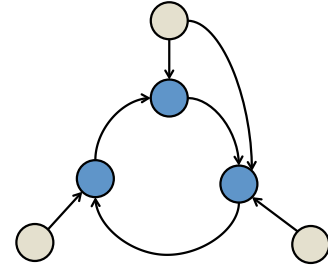


Fig. 1: The structure of the dynamical structure function of the system in (18). Light nodes represent inputs and dark nodes represent measured states, with links representing causal dependencies among the manifest variables.

The convolution representation of the dynamical structure function, rounded to three decimal places, is then given by

$$\begin{aligned} Q(t)[1, 3] &= .51(.75)^t - .11(-.6)^t - .816(.55)^t + .416\delta \\ Q(t)[2, 1] &= .286(-.35)^t - .286\delta \\ Q(t)[3, 2] &= 7.684(.95)^t - 8.588(.85)^t + .904\delta \\ P(t)[1, 1] &= 1.867(.75)^t - 1.867\delta \\ P(t)[1, 3] &= -P(t)[1, 1] = -1.867(.75)^t + 1.867\delta \\ P(t)[2, 2] &= .714(-.35)^t - .714\delta \\ P(t)[3, 3] &= .882(.85)^t - .882\delta \end{aligned} \quad (20)$$

where  $\delta$  represents the Kronecker delta  $\delta_{(t,0)}$ . This example uses the passive reconstruction method to reconstruct the dynamical structure function of the system in Equation 18 using simulated data and no noise. Note that  $P(t)[1, 3] = -P(t)[1, 1]$  is part of the a priori information used to ensure that the system is reconstructible.

For this example we chose  $r = 600$ , noting that the longest decay (slowest dynamics) is only around 150 time steps. Typically  $r$  should be chosen so as to overestimate the actual decay of the system, as in this case. 2000 data points were collected, and the reconstruction fits are shown in Figure 2. The number of data points was chosen because, after being reduced for a priori information, the system has 9 unknowns in  $Q(z)$  and  $P(z)$ , which means there are 9 unknowns in each of the  $(Q_i, P_i)$  pairs. This means that the matrix  $\hat{M}$ , Theorem 1, will have 5400 columns, which comes from  $k = 9$  and  $r = 600$ . In order to achieve full column rank for  $\hat{M}$  we

need at least that many rows, which is why at least  $f = 1800$  data points are required to reconstruct the system given that  $p = 3$ .

Using the described fitting process, we can determine the entries of the convolution representation of the dynamical structure function to be:

$$\begin{aligned}
 Q(t)[1, 3] &= .5096(.75)^t - .1108(-.6)^t - .8158(.55)^t \\
 &\quad + .417\delta \\
 Q(t)[2, 1] &= .2839(-.3556)^t - .2839\delta \\
 Q(t)[3, 2] &= 7.684(.95)^t - 8.588(.85)^t + .904\delta \\
 P(t)[1, 1] &= 1.867(.75)^t - 1.867\delta \\
 P(t)[1, 3] &= -P(t)[1, 1] = -1.867(.75)^t + 1.867\delta \\
 P(t)[2, 2] &= .7143(-.35)^t - .7143\delta \\
 P(t)[3, 3] &= .8824(.85)^t - .8824\delta
 \end{aligned} \tag{21}$$

which is almost exactly the same as the actual convolution representation in Equation 20. This example shows it is possible to reconstruct a system without target specificity in the time-domain without active experiments.

## V. CONCLUSION

This paper presents a passive network reconstruction algorithm, allowing for the structure and dynamics of a system to be determined directly from input-output data without the need for multiple experiments and removing the restriction of target specificity that plagues many similar reconstruction methods. Furthermore, an illustrative example showed the effectiveness of this procedure on a system without target specificity. Future work will focus on ensuring the algorithm is robust to measurement and process noise.

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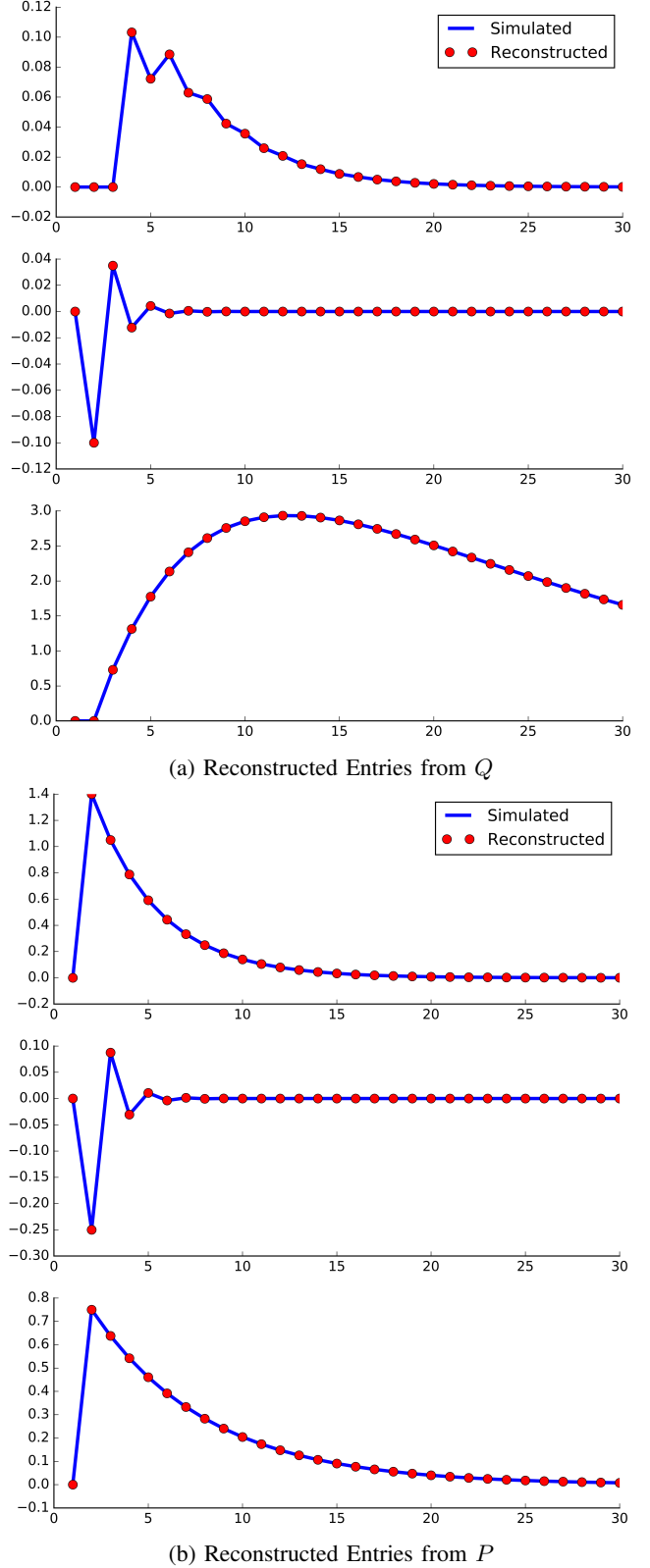


Fig. 2: Each figure corresponds to an unknown entry in  $Q$  and  $P$ , with order as in (20). The line in each represents the simulated results of the corresponding equation. The dots represent the reconstructed values of each unknown entry.