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Dynamic speckle imaging based on dynamic mode decomposition

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technology through his unique vision and outstanding dedication

We present a data-driven method for capturing the evolution of spatially and temporally varying speckle patterns. Our method is based on the dynamic mode decomposition (DMD) technique, which is a powerful framework for analyzing the dynamics of nonlinear systems using dimensionality reduction. We describe the steps to be followed for applying the DMD framework to experimental as well as synthetic speckle image data and benchmark its performance against some well-established speckle analysis techniques. © Anita Publications. All rights reserved.

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1 Introduction

Speckle patterns are grainy, fluctuating intensity patterns that are observed when coherent radiation, such as a light beam from a laser, is incident on a target object. There are primarily two factors that contribute to this phenomenon; the first is the presence of inherent roughness associated with microscopic facets and irregularities that are present on the illuminated surface. Roughness features present on the illuminated object's surface cause the scattering of scalar field components that have either random phases or amplitudes or both, which then interfere at the detection plane creating a speckle pattern. The other factor is associated with samples that possess moving scatterers, perhaps best exemplified by biological samples such as live tissue or fruit, for instance, thereby yielding 'dynamic' speckle patterns. Speckle analysis is a robust, often frugal, non-destructive metrology tool for monitoring a wide range of physical and biological effects, especially those that demonstrate transient changes. A large suite of numerical and graphical analysis techniques for relating raw speckle images to the target object's topological and physiological signatures have been developed over the last few decades [1-3]. Dynamic speckle imaging (DSI) methods have been successfully employed for generating wide-area maps based on locally and globally defined correlation parameters, that identify different levels of scatterer activity with high spatiotemporal resolutions. DSI has been applied with great promise across diverse scenarios such as the visualization of blood flows in complex organ systems, degradation in agricultural produce, detection of corrosion, and the drying/curing of paints and functional coatings [4].

In this paper, we describe the application of the dynamic mode decomposition (DMD) technique to analyze dynamic speckle images captured sequentially over time. The DMD tool was originally developed for analysis in fluid mechanics [5] and applies to phenomena that exhibit both linear as well as nonlinear dynamics.

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Essentially, we compute the DMD modes of dynamic speckles and their corresponding eigenvalues, which together, capture the dynamic evolution of the sample under investigation. The dynamic modes extracted can be used to project large-dimensional data into a system with fewer degrees of freedom. Essentially, we compute the DMD of dynamic speckle data to derive the dominant spatial modes of the underlying physical phenomenon along with their dynamic evolution expressed in terms of damped sinusoids. Whereas a majority of established speckle contrast analyses techniques provide single contrast maps corresponding to the dynamic event under study, our proposed DMD framework provides more than one contrast map representing multiple dominant spatial modes that may be present in the dynamic phenomenon along with the proposed method retrieves more information from the dynamic speckle data in comparison to other conventional approaches for extracting insights from speckle images. However, it should be noted that the physical interpretation of the retrieved information is subject to the process under investigation.

2 Theory

The protocol for using speckle to analyze dynamic phenomena primarily involves recording a sequence of 'N' speckle images, each of size $P \times Q$ (say). We construct a column vector of size $PQ \times 1$ using each frame. Our next step is to stack these column vectors together to form a matrix D (which will be $PQ \times N$ in size). Each column in matrix D essentially encodes the extent of speckle variations ('activity') in the temporal domain. We subsequently apply the dynamic mode decomposition (DMD) framework to the matrix D [5]. DMD is a dimensionality reduction technique that is purely data-driven, i.e., it does not require any knowledge of underlying physics of the dynamics in terms of the governing equations [6]. Two matrices, X and X', are further derived from D; X is formed using the first to the second last columns of D whereas X' formed using the second column to the last column of D. Both X and X' are of size $PQ \times (N - 1)$. The objective of DMD approach is to find a best-fit linear operator A which satisfies the relation,

$$X' = AX. \tag{1}$$

$$A = X^{+} X^{+}, \qquad (2)$$

where symbol ⁺⁺ is the Moore-Penrose pseudoinverse. The sizes of X and X' are very large owing to the manner in which they have been constructed. For instance, if 1000 speckle images each of size 256×256 (pixels) are recorded, the matrix D becomes 65536×1000 in size (both X and X' are 65536×999 in size). One can readily appreciate the computational expense involved in determining the matrix A, as well as its eigenvalues and eigenvectors. The DMD framework overcomes this bottleneck by finding the eigenvectors and eigenvalues without explicitly computing the matrix A. This is achieved in the manner described below:

Step 1: The singular value decomposition (SVD) of the matrix X is defined as,

$$X = U \Sigma V^T$$

(3)

where U and V are unitary matrices containing the left singular vector and the right singular vector, respectively; the superscript 'T' denotes the transpose operation. Σ represents the diagonal matrix consisting of the singular values arranged in the descending order. Both matrices (U and V) are truncated to include the first 'r' columns only. Simultaneously, only the first 'r' rows and 'r' columns of the Σ matrix are considered. **Step 2**: Using Eq (3), Eq (1) can be rewritten as,

$$U^{T}X' = U^{T}AU \Sigma V^{T}$$
(4)

Step 3: Equation (4) can be rearranged as,

$$U^{T}AU = U^{T}X'V\Sigma^{-1} = \tilde{A}$$

Step 4: The matrix \tilde{A} is computed by utilitizing the first 'r' dominant singular vectors. That is, first 'r' columns of matrices U, V, and the first $r \times r$ block of the diagonal matrix Σ are used to generate \tilde{A} . This is

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more efficient than calculating A directly. The value of 'r' is the deciding factor in determining the dynamic modes under investigation.

Step 5: Utilizing the fact that A and \tilde{A} both have the same eigenvalues, we derive the eigenvalues and eigenvectors (also the DMD modes) of A by performing the eigen decomposition of \tilde{A} . The eigenvectors of A can be calculated using the formula

$$\Phi = X' V \Sigma^{-1} W$$

(6)

where *W* is the eigenvector of the matrix \tilde{A} . Verification of the assumption that Φ represents the exact eigenvectors of the matrix A can be found in Tu *et al* [7]. The columns of the matrix Φ represent the dynamic modes of associated with dominant spatial behavior of the dynamic process under observation. An eigenvalue corresponding to each mode quantifies the frequency of temporal variation. Each of these modes oscillates at a distinct temporal frequency [4]. Figure 1 depicts how we apply the DMD framework for analyzing dynamic speckle images. A pseudocode is also provided in Table 1.



Fig 1. Steps involved in computing DMD on a given speckle sequence.

Table 1. Algorithm to compute DMD on given speckle sequence

Algorithm to compute DMD (Pseudocode)

Initialise a data matrix D

For i = 1: total number of frames

Create a column vector of each frame

D(:, i) =frame in the form of column vector

End

Construct matrix X from D by selecting the first to penultimate columns

Construct matrix X' from D by selecting the second to last columns

% pseudocode for the steps computed in the "DMD engine"

 $[U, \Sigma, V] = svd(X)$

Select the first 'r' columns of matrix U and V

Select the first 'r' rows and 'r' columns of the matrix Σ

Project A on to the 'r' dimensions to get the matrix \tilde{A} using Eq (5) Compute the eigen-decomposition of \tilde{A} to get the eigen-values "E" and eigen-vectors "W" Reconstruct the eigen-vectors of the matrix \tilde{A} " Φ " using Eq (6)

3 Results

The most robust way to evaluate the performance of the DMD algorithm is to apply it to images that have been generated synthetically using known parameters. All simulations were performed using MATLAB (MATLAB 2020b, The MathWorks Inc.) on a computer with a 3GHz processor and 8 GB RAM. Several methods for simulating dynamic speckle sequences have been reported in literature [8-10]. We have selected the method as described in [9] to generate speckles with pre-defined temporal and spatial correlations and the reader is directed to the same for further details. Accordingly, the speckle intensity at the image plane can be computed as

$$I(p, q, t) = |F^{-1}(H(p, q) * F(e^{j\varphi(p, q, t)}))|^2$$

where I(p, q, t) represents the intensity of a pixel (p, q) in the t^{th} frame; F and F^{-1} represent the Fourier and inverse Fourier transform operations, respectively; H(p, q) represents the transfer function of the imaging system; $\varphi(p, q, t)$ represents the random phase of object scattered light recorded at time t. We consider $p \in [0, P-1], q \in [0, Q-1]$, and $t \le N$. The random phase values are considered to be uniformly distributed between $[-\pi, \pi]$. The evaluation of phase over time in the generation of dynamic speckles is given by:

$$\varphi(p, q, t) = \varphi(p, q, t-1) + G(p, q, t) \sqrt{(ln(c(p, q, t-1) - ln(c(p, q, t))))}$$
(10)

where G(p, q, t) is a randomly generated matrix at ^tth instance with a mean of 0 and variance of 1. Fifty speckle images (N = 50), each of size 512×512 were generated. The size of each speckle was set to be equal to the pixel size. The stack of speckle images were generated using pre-defined spatial and temporal correlation values that were spatially assigned as depicted in Fig 2. The first frame of the generated dataset is shown in Fig 3 for illustration.



Fig 2. (a) Spatial correlation map for N = 50. (b) Temporal intensity correlation for each of the regions marked with different colors.

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The DMD of simulated dynamic speckle data was computed to obtain a contrast map denoting speckle activity. In order to benchmark the efficacy of the DMD approach against other standard qualitative speckle contrast descriptor algorithms, we analyzed our simulated speckle dataset with the Fujii and Generalized Differences (GD) methods. The contrast maps evaluated using DMD, Fujii, and GD are shown in Fig 3. It is evident from the contrast between regions of distinct speckle activity is higher in DMD in comparison with those obtained using Fujii and GD. Additionally, the boundaries separating these distinct regions are more clearly defined in the output obtained using DMD. The Fujii and GD algorithms produce a single image to depict speckle activity whereas the DMD method produces a set of images (corresponding to each spatial mode) as shown in Fig 4; as mentioned earlier, each mode denotes the dominant features of the spatial constituents of the phenomenon under consideration. The value of 'r' is used to select the spatial modes of interest. Since DMD is essentially a data-driven technique, the choice of 'r' depends on the extent of observed activity/phenomenon being studied. For the present simulation r = 5 is considered. It can be observed that DMD decomposes the spatial activity of speckles into the background signal (as shown in Fig 4(a)) and the remaining spatial modes representing foreground activities.



Fig 3. (a) Representative simulated speckle image. Speckle contrast maps obtained using (b) DMD (c) Fujii and (d) Generalized Differences.



Fig 4. (a) First (b) second and (c) third spatial modes evaluated for the simulated example.

Figure 5 depicts a comparison of the computation times taken by all three algorithms as a function of the number of frames. We observe that the DMD method not only produces superior contrast maps, but does so within smaller time durations. Although the DMD approach is marginally slower than the Fujii method for a larger number of frames, the spatial contrast is found to be higher than the latter. Next, we compared the performance of DMD with the Fujii and GD methods using experimentally acquired speckle images. Figures 6 and 8 show the comparison between the DMD, Fujii, and GD algorithms applied to dynamic speckle images of a hydrated maize seed (available in public domain at [11]) and an excised rodent brain (shared with us by the authors of [12]). Figures 7 and 9 show the spatial modes corresponding to maize seed and rodent's brain, respectively.

The quantitative performance comparison among the speckle contrast imaging algorithms was performed using the synthetically generated dataset. The speckle contrast value is evaluated for the contrast map images obtained using DMD, Fujii, and GD for all the regions mentioned in Fig 2 (a). The ratio (σ/μ) quantifies the noise level in the speckle image and is generically refered to as the contrast. Here σ is the standard deviation, and μ is the mean of the speckle intensities. The values are obtained by processing the images shown in Figs 3(b), 3(c), and 3(d). The results demonstrate quantitatively that the DMD algorithm provides superior contrast in comparison to the GD and Fujii algorithms.



Fig 5. Computation time of different algorithms evaluated as a function of the total number of frames.



Fig 6. (a) Randomly selected maize seed speckle image (from [8]). Spatial contrast map obtained using (b) DMD (c) Fujii and (d) GD.



Fig 7. (a) First (b) second and (c) third spatial modes of the maizse seed dataset.

		Table 2. (a) Speckle contrast values of 3(b) computed using DMD						
		Region-1 (R1)	Region-2 (R2)	Region-3 (R3)	Region-4 (R4)	Region-5 (R5)		
Mean (μ) Standard Dev (σ)		6.00E-03	4.39E-02	7.62E-02	1.16E-01	1.70E-01		
		0	0.0011	0.0032	0.0072	0.0147		
Contra	st (σ/μ)	0.00E+00	2.57E-02	4.19E-02	6.25E-02	8.64E-02		
Table 2. (b) Speckle contrast values of 3(c) computed using Fujii.								
		Region-1 (R1)	Region-2 (R2)	Region-3 (R3)	Region-4 (R4)	Region-5 (R5)		
Mean	(μ)	1.05E-01	3.09E-01	4.01E-01	4.84E-01	5.61E-01		
Standard Dev (σ)		0.004	0.0088	0.0108	0.0119	0.0119		
Contrast (σ/μ)		3.84E-02	2.86E-02	2.70E-02	2.47E-02	2.12E-02		

	Table 2. (c) Speckle contrast values of 3(d) computed using GD.							
	Region-1 (R1)	Region-2 (R2)	Region-3 (R3)	Region-4 (R4)	Region-5 (R5)			
Mean (µ)	1.36E-01	2.97E-01	3.82E-01	4.56E-01	5.25E-01			
Standard Dev (σ)	0.0022	0.0058	0.0087	0.0111	0.0129			
Contrast (σ/μ)	1.61E-02	1.95E-02	2.29E-02	2.44E-02	2.45E-02			



Fig 8. (a) Randomly selected speckle image from [9]. Spatial contrast map obtained using (b) DMD (c) Fujii (d) GD

4 Conclusion

In this paper, we demonstrate the application of the dynamic mode decomposition (DMD) algorithm for generating speckle contrast 'activity' maps from dynamic speckle image datasets. The primary advantage of this method is that it does not require any knowledge of the equations governing the physical processes that result in transient changes of the speckle patterns, i. e, it can be referred to as an 'equation-free' modeling technique. We do not have to model the dynamics of the system under study every time we change the specimen. The measurements obtained are sufficient to compute the matrix A that captures the dynamics in the system. The choice of 'r' is crucial for identifying the valid spatial modes describing the speckle image



Fig 9. (a) First (b) second and (c) third spatial modes of speckle images of rodent brain [12].

dataset. The performance of the DMD algorithm was evaluated by benchmarking it against other popular methods like Fujii and Generalised Differences (GD). As seen in Fig 5, the computation time taken by DMD is significantly lesser (by a factor of ~6) than that of the GD approach, and does not increase non-linearly with increasing input frame size. As such, the DMD algorithm's performance appears similar to Fujii but becomes slightly slower for larger frame sizes. The speckle contrast values obtained for the different regions of the simulated data (Fig 2) using DMD, Fujii, and GD as mentioned in Table 2 show that the graininess of the speckle is higher as compared to both Fujii and GD. Further, algorithms like Fujii, GD discard the temporal information and produce only a single contrast map but DMD preserves both the temporal and spatial dynamics. DMD decomposes the given data into a set of spatio-temporal dominant coherent features or 'modes' that can be used to fully describe the target under study and we anticipate that this technique will contribute towards deriving deeper insights from dynamic speckle data for monitoring and assessing time-varying phenomena.

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