Cigniti

Understanding Disease (COVID) Progression using Chest X-Rays

A Tech Brief

Introduction

COVID-19 is now a global pandemic, with close to 5 million infections globally. As patients get admitted to hospitals, it becomes important for clinicians to understand which of these patients have the potential to turn critical, so that hospitals can plan and prepare accordingly. Longitudinal Chest X-Ray analysis will enable hospitals to prioritize patient care based on the prognostic and severity predictions given by the model. We attempt to provide this insight by generating X-Rays for future time-periods for a patient by studying the previous X-Rays of that patient. This helps the clinician better understand the spread of the disease in a patient, thereby planning better interventions.

In the context of COVID treatment, a deep learning-based CT segmentation of pulmonary opacities is in use. It helps improve the quantification of the disease. Based on U-Net architecture, a convolution neural network is developed to predict expert segmentation.

Our Approach

When there is a multiscale system, we cannot always define the function that governs the system. Whenever possible, it is desirable to work with the linear dynamics of the form.

$$dx/dt = Ax$$

The solution of the above equation is given by:

$$x(t_0 + t) = e^{At} x(t_0)$$

The dynamics are entirely characterized by the eigenvalues and eigenvectors of the matrix A, given by the eigen-decomposition of A:

When A has n distinct eigenvalues, then Λ is a diagonal matrix containing the eigenvalues λ_j and T is a matrix whose columns are the linearly independent eigenvectors ξ_j associated with eigenvalues λ_j . In this case, it is possible to write $A = T\Lambda T^{-1}$, and the solution becomes

$$x(t_0 + t) = T e^{\Lambda t} T^{-1} x(t_0)$$

DMD is a technique to obtain reduced order models for high dimensional systems. It's a purely data-driven method and does not require any knowledge of the underlying equations, originally introduced by Peter Schmidt in fluid dynamics.

As far as we know, this is the first time DMD (Dynamic Mode Decomposition) is being used to study and predict Chest X-Rays in the COVID-19 scenario.

We can extract, from this data, the spatial-temporal coherent structures or patterns that dominate the mentioned data from the dynamical system. DMD is defined to be the eigen decomposition of an approximating best fit linear operator.

Refer to Fig 1 to understand the steps followed in computing standard DMD.

Algorithm 1 (Standard DMD).

1. Arrange the data $\{z_0, \ldots, z_m\}$ into matrices
$$X \triangleq \begin{bmatrix} z_0 & \cdots & z_{m-1} \end{bmatrix}, \qquad Y \triangleq \begin{bmatrix} z_1 & \cdots & z_m \end{bmatrix}. \tag{2}$$
2. Compute the (reduced) SVD of X (see [32]), writing
$$X = U\Sigma V^*, \tag{3}$$
where U is $n \times r$, Σ is diagonal and $r \times r$, V is $m \times r$, and r is the rank of X.
3. Define the matrix
$$\tilde{A} \triangleq U^* Y V \Sigma^{-1}. \tag{4}$$
4. Compute eigenvalues and eigenvectors of $\tilde{A}$, writing
$$\tilde{A}w = \lambda w. \tag{5}$$
5. The DMD mode corresponding to the DMD eigenvalue λ is then given by
$$\varphi \triangleq Uw. \tag{6}$$
6. If desired, the DMD modes can be scaled in a number of ways, as described in Appendix A.

Figure 1: Standard DMD mode reference – [1]

When we feed the data, as it evolves in time, into DMD, we are actually stacking the data into tall vectors evolving in time into vectors; one is shifted delta t in time X and Y. X is any system that exists in high dimensional space n. All the measurements of the vector in n dimensions have n-1 degrees of freedom. There are dominant patterns that are present in this data, so therefore we get spatial-temporal modes and a linear dynamical system.

This means that we get a best fit linear operator A (please refer Fig. 1) that fits and best maps X to Y (please refer Fig. 1). DMD approximates the leading eigen decomposition of the A matrix. The dominant eigenvalues and eigenvectors of A can be reshaped into Eigen flow fields and used to see how this structure evolves in time. It's very much like PCA, where we try to find a low-rank structure and approximate it with a linear dynamical system.

Data

The COVID-19 images and longitudinal information were collected from Dr Cohen's site [5] using the metadata file.

Results

The data in Figure 2 depicts the X-Rays taken on admission and the following two consecutive days. Using this longitudinal data, the tall X matrix is constructed with a time difference of each passing day.

Figure 2: Original X Rays

After building the Eigen decomposition, each eigenvalue in mu tells us something about the dynamic behaviour of its corresponding DMD mode. If the eigenvalue has a non-zero imaginary part, then there is an oscillation in the corresponding DMD mode. If the eigenvalue is inside the unit circle, then the mode is decaying. If the eigenvalue is outside, then the mode is growing. If the eigenvalue falls exactly on the unit circle, then the mode either grows or decays. From Figure 3, we can observe that one of the modes is growing while the other two are decaying.

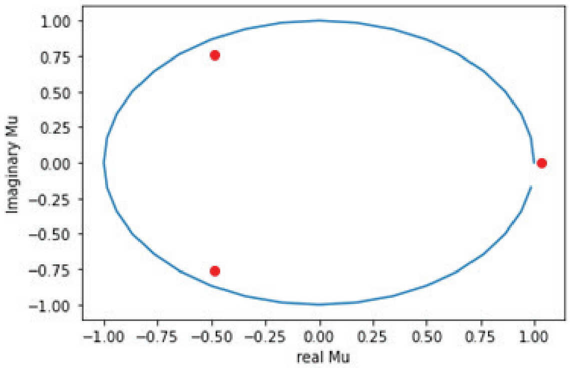

Figure 3: Eigen plot

Equipped with the Eigendecomposition of A and a basic understanding of the nature of the system Y=AX, it is possible to construct a matrix Ψ. This corresponds to the system's time evolution in time T. We have used this data to calculate the DMD and were able to predict the data one time-step ahead in time (Figure 4). The fourth X-ray in Fig. 4 was reconstructed from the initial condition and it is our prediction, one step in time for this patient.

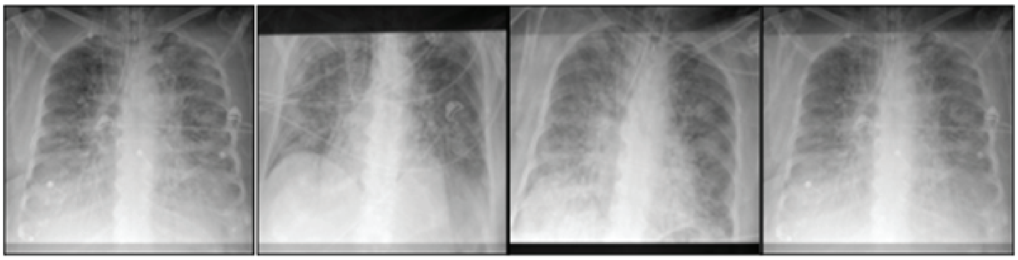

Figure 4: Reconstructed Modes

Future Work

We are planning to use the Koopman operator to better understand & estimate the non-linear modes too. We hope to publish this subsequent work in the next couple of weeks.

References

[1]Kutz, J. Nathan. Data-driven modeling& scientific computation: methods for complex systems & big data. OUP Oxford, 2013.

[2]Tu, Jonathan H., et al. “On dynamic mode decomposition: theory and applications.” arXiv preprint arXiv:1312.0041 (2013). http://cwrowley.princeton.edu/papers/Tu-DMD.pdf

[3] https://pubs.rsna.org/doi/full/10.1148/ryct.2020200082

[4] https://en.wikipedia.org/wiki/Dynamic_mode_decomposition

[5] https://github.com/ieee8023/covid-chestxray-dataset

[6] http://www.pyrunner.com/weblog/2016/07/25/

[7] http://dmdbook.com/

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