Disease Progression prediction based using X-rays

Introduction

The idea of longitudinal analysis is to prioritize the patients based on the prognostic and severity predictions given by the model.To be able to recommend care by monitoring disease progression and evaluate the effect of interventions in clinical care.

 In the context of covid treatment ,the other approaches being used for   were a deep learning–based CT segmentation of pulmonary opacities (3) for improving quantification of the disease. A convolutional neural network based on U-Net architecture was developed to predict the 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 linear dynamics of the form

$$d/dtx = Ax.$$

The solution of above equation is given by $x(t0 + t) = e At x(t0)$

The dynamics are entirely characterized by the eigenvalues and eigenvectors of the matrix A, given by the eigen-decomposition of A: $AT = T\Lambda$

 When A has n distinct eigenvalues, then Λ is a diagonal matrix containing the eigenvalues λj and T is a matrix whose columns are the linearly independent eigenvectors ξj associated with eigenvalues λj . In this case, it is possible to write A = TΛT−1 , and the solution becomes

$$x(t0 + t) = T e \Lambda t T - 1 x(t0)$$

 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 Schmid in fluid dynamics.We can extract from this data , the spatio 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

$$\hat{\varphi} \triangleq Uw. \tag{6}$$

6. If desired, the DMD modes can be scaled in a number of ways, as described in Appendix A.

Fig 1 - Standard DMD mode reference - [1]

When we feed the data as it evolves in time into DMD .We are 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 which are present in this data so therefore we get spatial temporal modes and a linear dynamical system.

So that means we get a best fit linear operator A (Ref Fig 1) that fits and best maps X to Y (refer Fig 1)DMD approximates the leading eigen decomposition of the A matrix. The dominant eigenvalues and eigenvectors of A and then we can reshape it into eigen flow fields and use them 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 seen in fig 1 row 1 are the x rays taken on admission and following two consecutive days.Using this longitudinal data, the tall X matrix was constructed with time difference between each being 1 day.
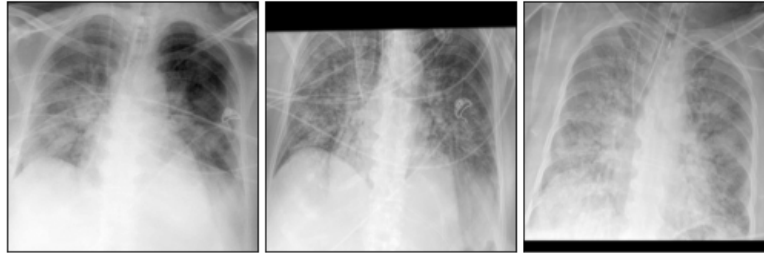
Fig 1 : Original X Rays

After building the eigen decomposition each eigenvalue in mu tells us something about the dynamic behavior of its corresponding DMD mode. If the eigenvalue has a non-zero imaginary part, then there is 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.
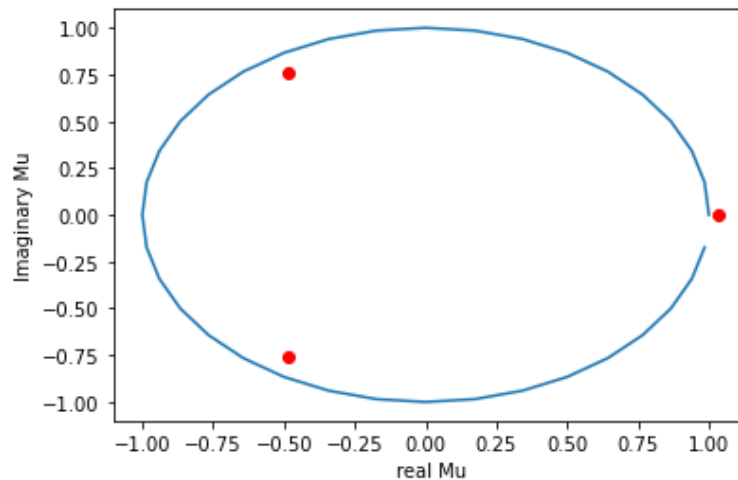

Figure 3 : Eigen plot

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 fig 4. The fourth xray in Fig 4 was reconstructed from the initial condition and it is our prediction one step in time for this patient
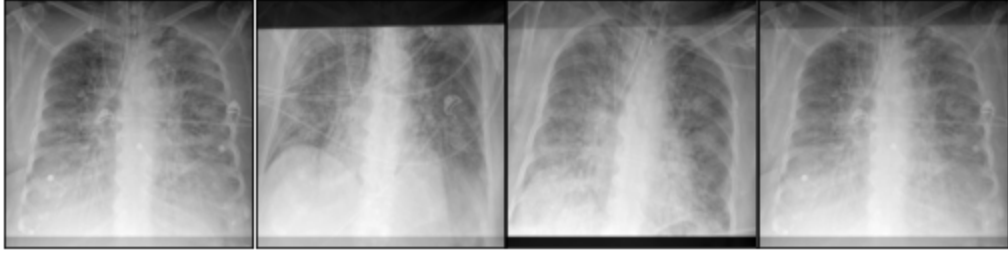
Figure 4- Reconstructed Modes

Future Work

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/