Error Analysis in Dynamic Mode Decomposition

MEng. Project Poster Presentation

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Introduction

Dynamic Mode Decomposition (DMD) is an emerging dimensionality algorithm that obtains linear reduced-order models from high-dimensional, non-linear dynamical systems. It extracts the dominant spatio-temporal modes of the dynamical system that are associated with the oscillation frequency and decay/growth rate. These modes can then be used to construct an equation that allows us to observe the state of the system at a given point in time. DMD was first developed by Peter Schmid in 2008 to analyze the time evolution of fluid flows. Today, DMD and its variants have applications in diverse range of fields, including but not limited to, disease modelling, finance, robotics, neural data analysis and image processing. The rising popularity of DMD can be attributed to the fact that it is purely data-driven and does not require any knowledge of the underlying equations of the system.

The Standard DMD algorithm

- First data is split into two matrices:

$$\mathbf{X} = \begin{bmatrix} | & | & & | \\ \mathbf{x}(t_0) & \mathbf{x}(t_1) & \dots & \mathbf{x}(t_{m-2}) \\ | & | & & | \end{bmatrix} \qquad \mathbf{X}' = \begin{bmatrix} | & | & & | \\ \mathbf{x}(t_1) & \mathbf{x}(t_2) & \dots & \mathbf{x}(t_{m-1}) \\ | & | & & | \end{bmatrix}$$

- Assume there exists a best-fit linear matrix operator A such that

$$X' \approx AX$$

- Reduced SVD is performed on X where the truncation value *r* was chosen by the user:

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

  where U has dimensions *n* x *r*, Σ is a diagonal matrix with dimensions *r* x *r* and V has the dimensions *m* x *r*.

- Define the new dimensionally reduced operator matrix:

$$\tilde{A} = UX'V\Sigma^{-1}$$

- Spectral decomposition is done on the reduced operator matrix:

$$\tilde{A}W = W\Lambda$$

  where columns of W are the eigenvectors and Λ is a diagonal matrix of eigenvalues.
- Then, the eigenvectors of the original high-dimensional matrix can simply be obtained as

$$\Phi = UW$$

- Finally, each snapshot of the system can be reconstructed using the DMD modes and eigenvalues

$$x_k = \Phi\Lambda^k\mathbf{b}$$

  where $\mathbf{b} = \Phi^{-1} \cdot x_0$ represents the coefficients of the initial state x_0.

Methods

- To study DMD, first we need time-series data. One-dimensional Burger's equation was solved using Fast Fourier Transform (FFT) to give us a sequential set of spatio-temporal data points.

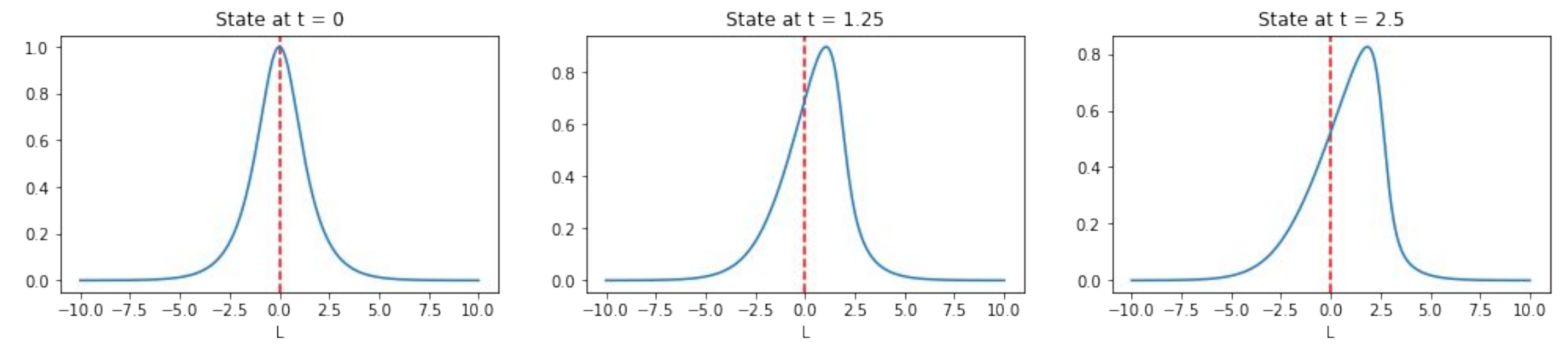

Figure 1. The solution to 1D Burger's equation, which is a travelling wave, at t = 0, 1.25 and 2.5 seconds.

- The standard DMD was fitted on the resulting dataset.
- For the first analysis, the truncation value *r*, of the SVD step in the DMD algorithm, was varied to see the effect of rank truncation on the DMD error in the interpolation mode. In addition, this gives us the optimum *r* value to perform further analyses with the DMD algorithm.
- Second, to study error growth in the extrapolation mode, DMD was fitted on only the first portion of our original time series data. The remaining portion was used to compare to the future state prediction by the DMD algorithm.
- Next, an analysis was done to see how fitting DMD on a larger dataset (i.e. more snapshots taken from a wider range of the time domain) affects the prediction accuracy of DMD. The results were compared with those of a separate analysis where the sampling rate of data is increased but the range of the time domain is kept the same.
- Lastly, a theoretical estimator for DMD prediction error from literature was implemented and compared with the actual error growth in the extrapolation mode.

DMD modes and eigenvalues

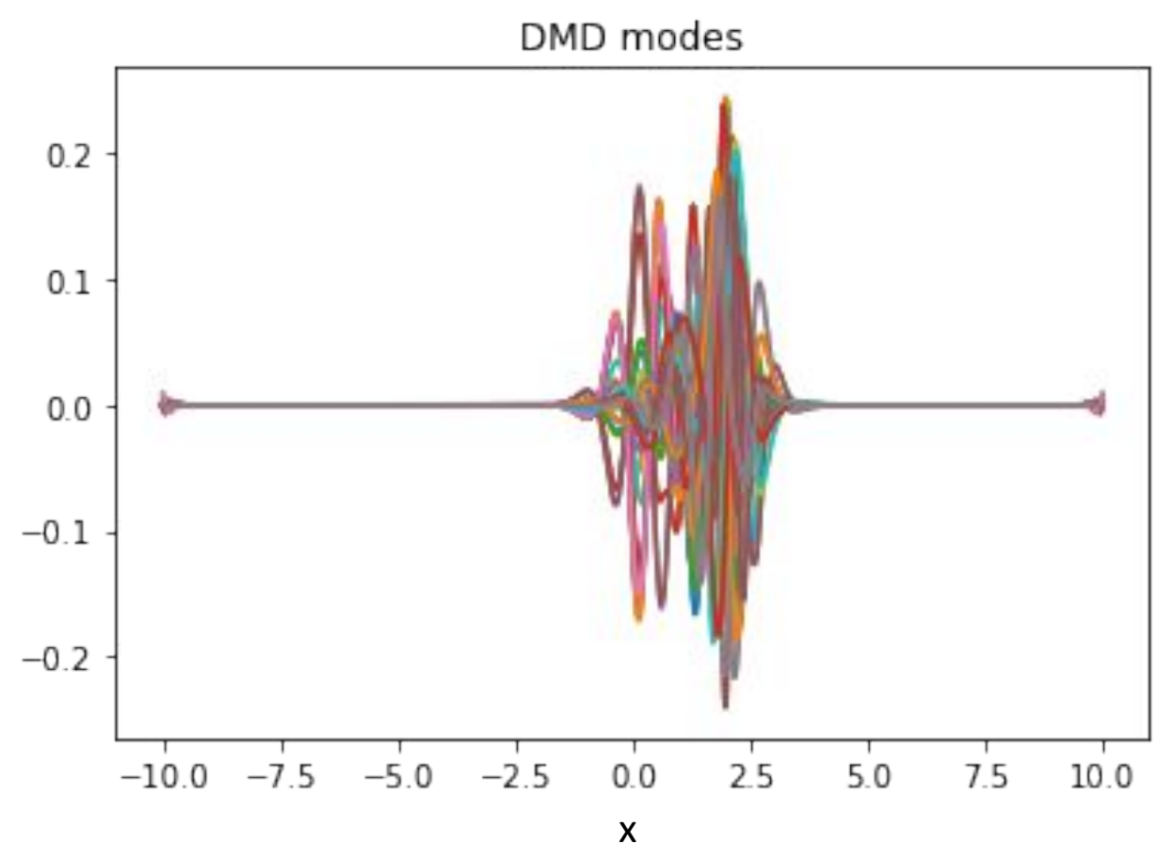

Figure 2. The plot shows the DMD modes or the eigenvectors which represent the separate patterns that the data is decomposed into.

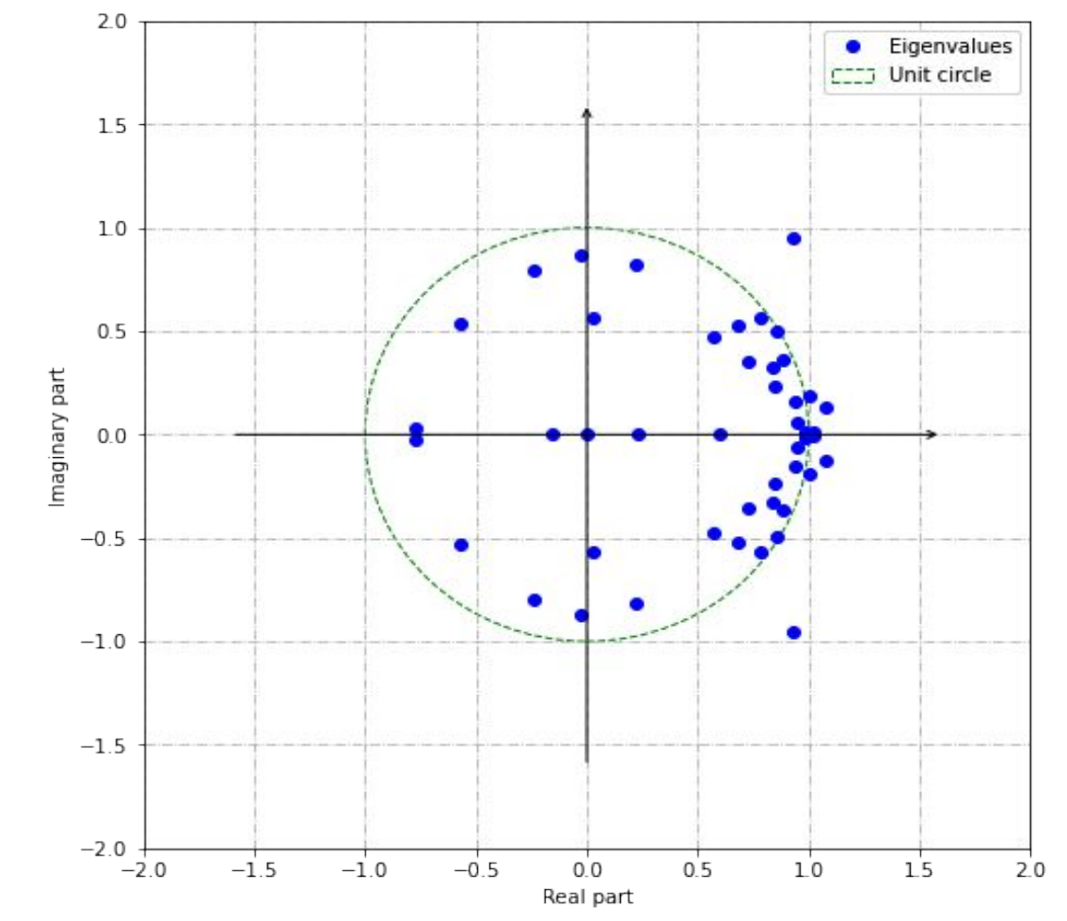

Figure 3. The plot shows the eigenvalues of the system, each of which corresponds to a DMD mode. The relative position each eigenvalue to the unit circle tells us the temporal behavior of the corresponding DMD mode.

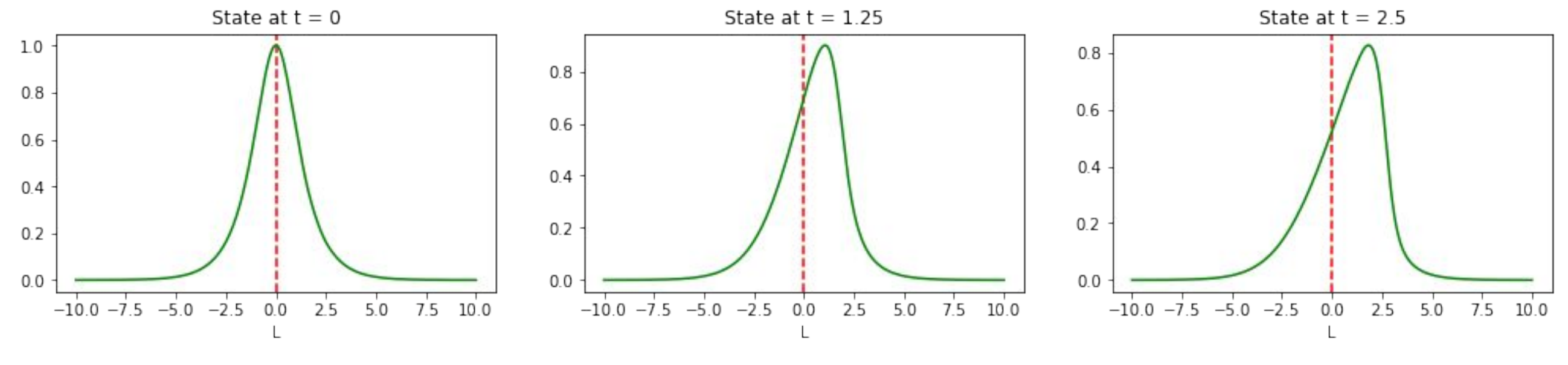

Figure 4. Reconstructed system using the DMD modes and the eigenvalues.

Results

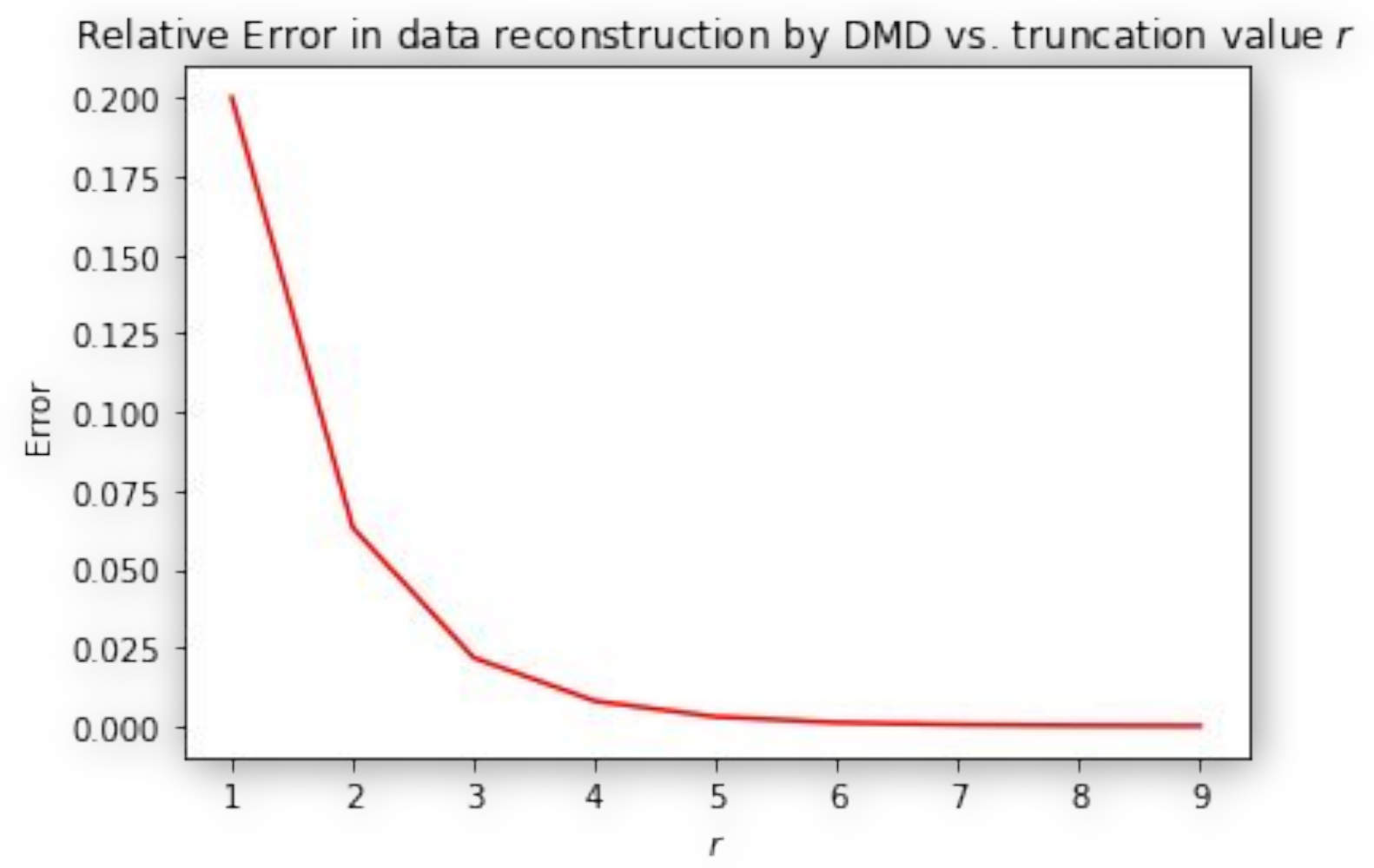

Figure 5. The plot shows how the truncation value (or rank) *r* used in SVD part of the DMD algorithm affects the interpolation error (i.e. data reconstruction error). At r=7, the truncation value used in subsequent analyses, the interpolation error is in the order of 10^{-18}.

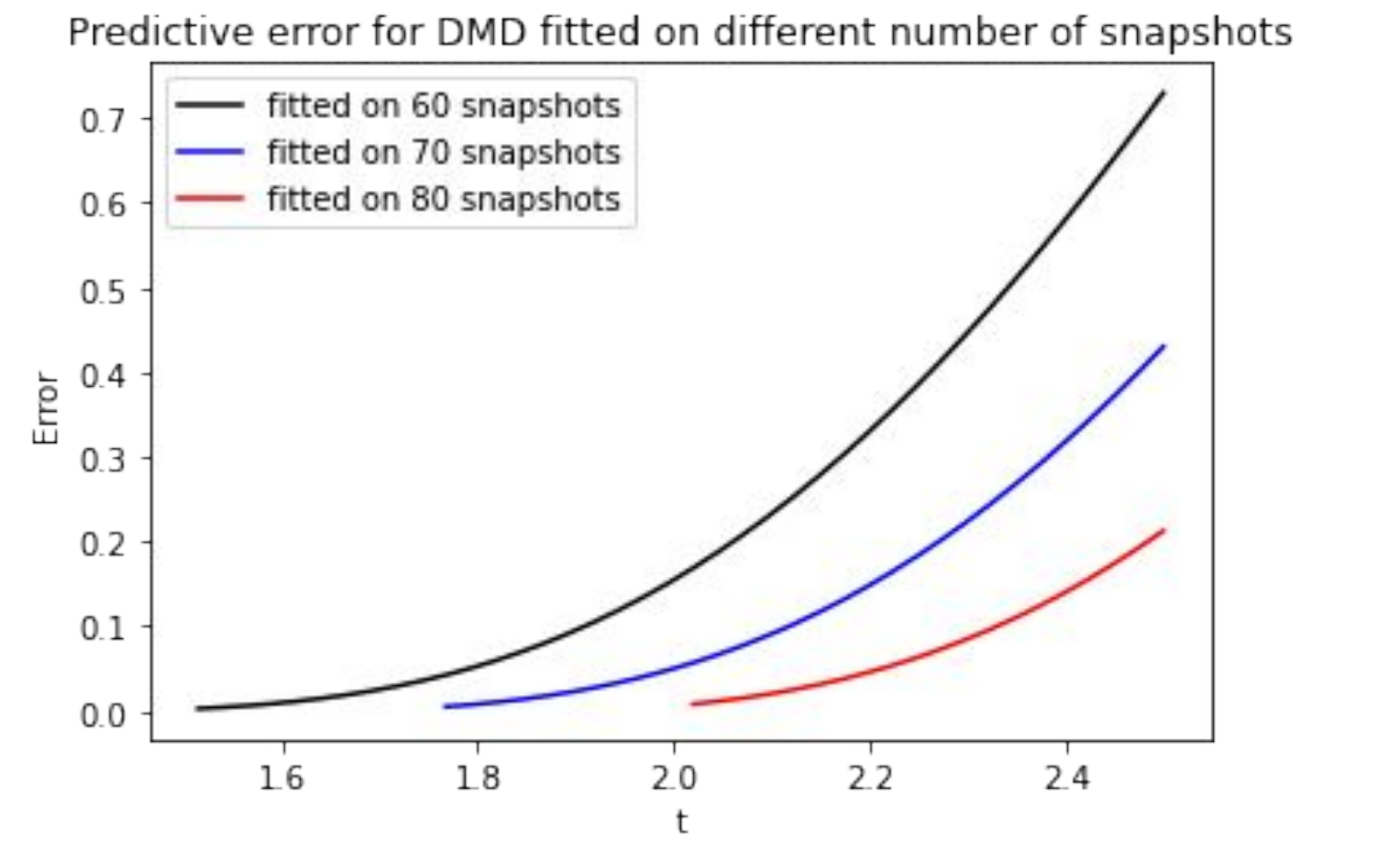

Figure 6. The plot shows that the future state prediction error for the standard DMD algorithm grows exponentially in time. Additionally, it shows that the more snapshots of data (i.e. data spanning longer length of time domain) that DMD is fitted on, the more accurate the DMD prediction is.

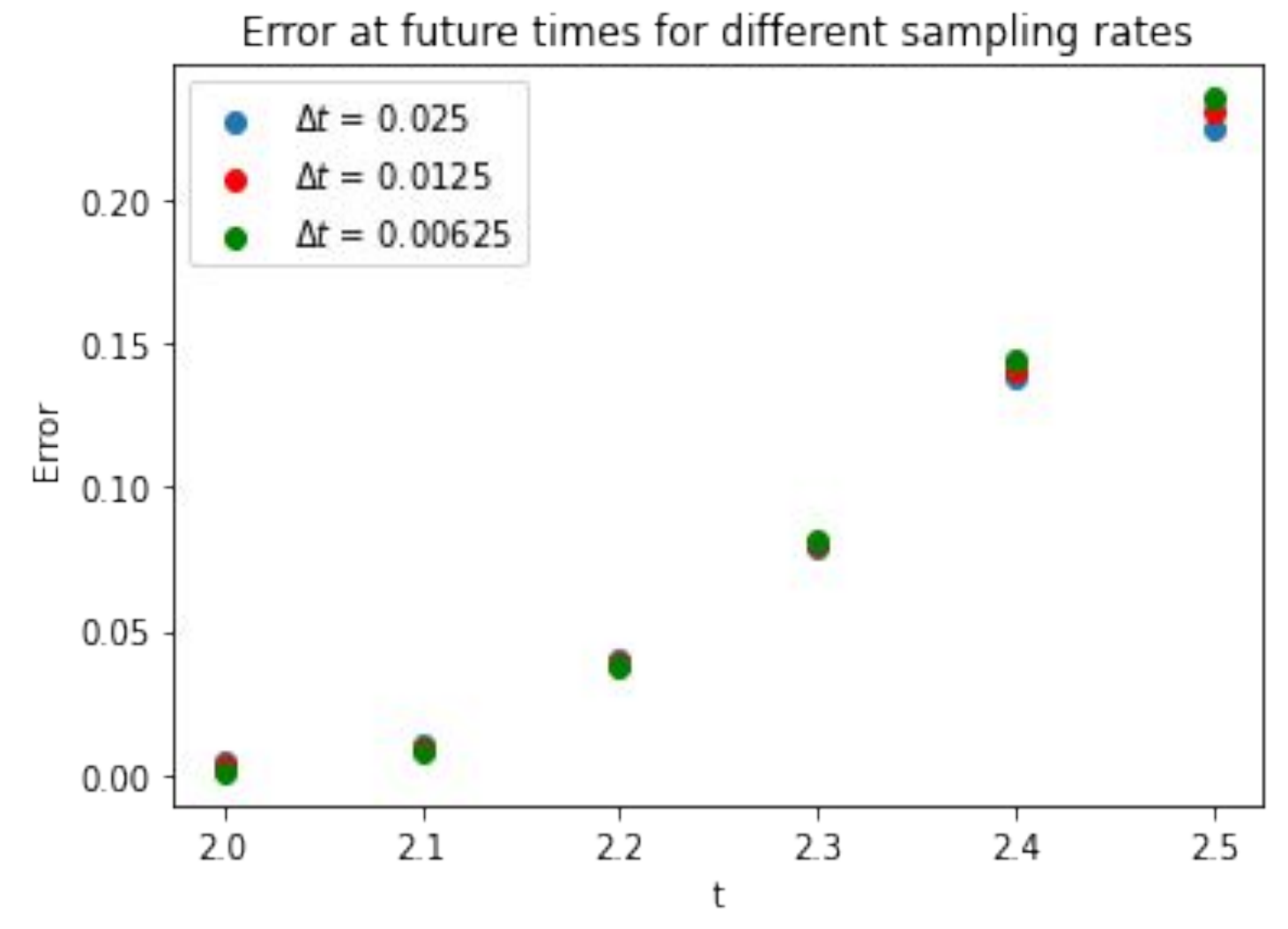

Figure 7. The plot shows the prediction error at different times in the future for three sampling rates. It shows that oversampling can increase the error growth at later times in the extrapolation mode.

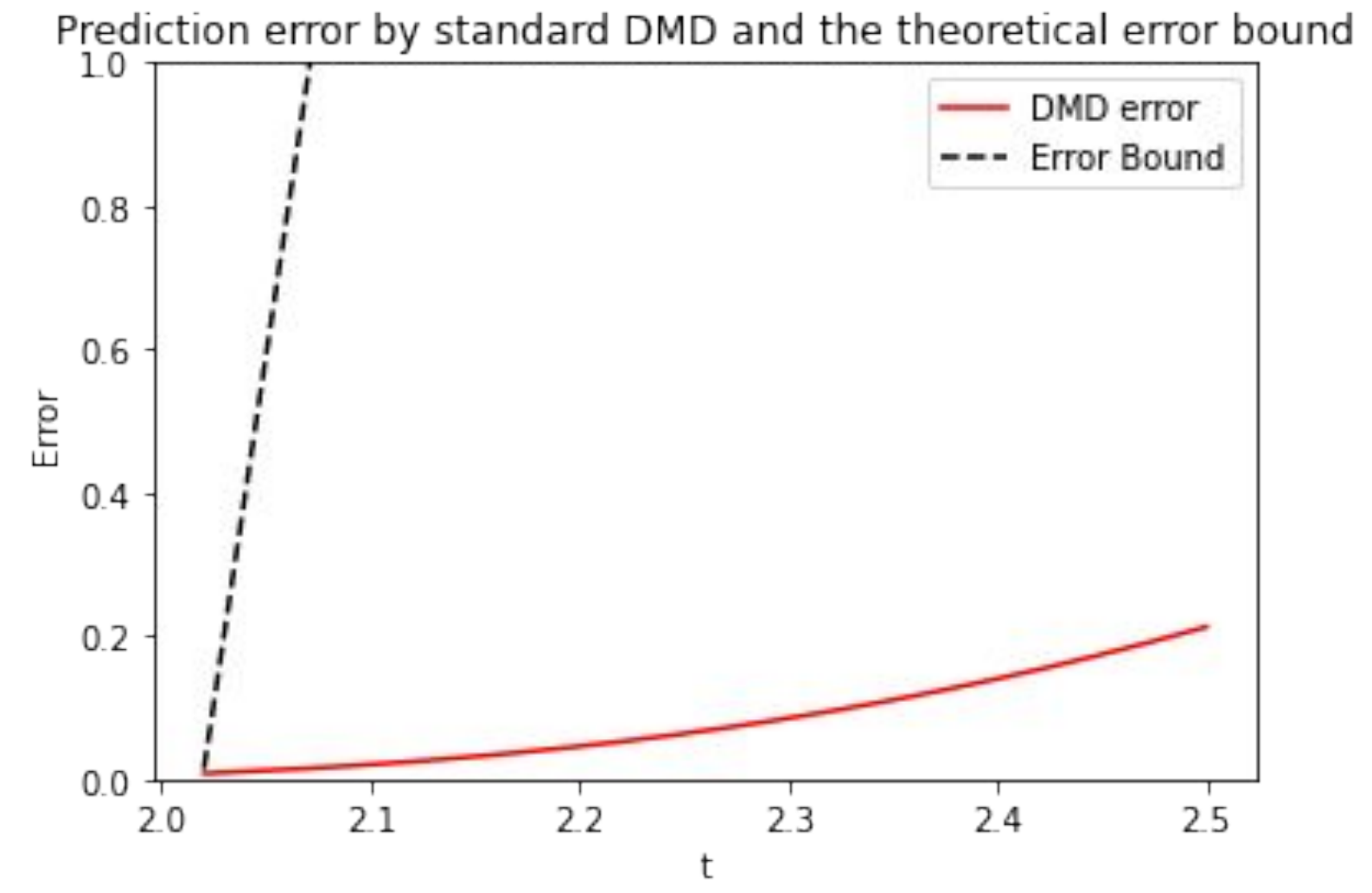

Figure 8. A theoretical error bound from literature was implemented, which turns to be linear and hence fails to effectively bound the actual error which grows in a non-linear fashion.

Conclusions and Future Work

- We observed how DMD can be used to extract the spatio-temporal patterns from a time-series dataset, in the form of modes and eigenvalues, which can be used to reconstruct the system with relatively small value of *r* or predict the state of the system in the near future (with limited accuracy).
- The predictive error by the standard DMD algorithm is shown to have an exponential-like growth. However, when DMD is fitted on data that is collected from a wider span of the time domain, the prediction accuracy improves as this allows DMD to capture the dynamics of the system better.
- Oversampling the data can increase the predictive error at later times in the extrapolation mode.
- A further in-depth analysis of the theoretical error bound is necessary in order to implement it correctly and use it for further analysis with DMD.

References & Acknowledgements

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