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Dynamic Mode Decomposition with Control: A Case Study of Covid-19 and Vaccination

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ABSTRACT

Epidemic diseases have posed great threats to human societies throughout history and have seriously affected public health. Epidemic diseases can spread rapidly and cause major deaths and economic losses. Therefore, the control and management of epidemic diseases requires new approaches developed with scientific and technological developments. The method of Dynamic Mode Decomposition with Control (DMDc) is a machine learning technique that predicts the state of systems, that affect the dynamic system from the outside and change the nature of the system. This technique is used to examine how the variables, factors, and effects in the data are related to each other and how they change over time. In this article, the DMDc method used the weekly cumulative number of COVID-19 cases per 100 thousand of Turkey's 81 provinces between February 8 and September 11, 2021, as the situation matrix, and the total number of vaccines per 100 thousand in the same time interval as the control matrix and then calculated error values of the DMD and DMDc are compared with under the different error metrics. In this paper, the number of cases and vaccines in the Turkish Ministry of Health TURCOVID-19 open data set was used.

Keywords: Dynamic mode decomposition, control, data-driven dynamic systems, singular value decomposition, machine learning

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DMDk ile Kovid-19 ve Aşılamaya İlişkin Bir Örnek Olay İncelemesi

ÖZ

Epidemik hastalıklar tarih boyunca insan toplumlarına büyük tehditler oluşturmuş ve kamu sağlığını ciddi şekilde etkilemiştir. Epidemik hastalıklar hızla yayılabilir, büyük ölümlere ve ekonomik kayıplara yol açabilir. Bu nedenle, salgın hastalıkların kontrolü ve yönetimi, bilimsel ve teknolojik gelişmelerle birlikte geliştirilen yeni yaklaşımlar gerektirir. Dinamik Mod Ayrıştırmasında Kontrol (DMAk), dinamik sistemi dışardan etkileyen değişkenin, sistemi kontrol etmek amacıyla dahil edilmesiyle sistemin durumunun incelendiği bir makine öğrenmesi tekniğidir. Bu teknik, verilerdeki değişkenlerin, faktörlerin ve etkilerin birbirleriyle nasıl ilişkilendiklerini ve zamanla nasıl değiştiklerini incelemek için kullanılır. Bu çalışmada DMAk yönteminde, 8 Şubat ile 11 Eylül 2021 tarihleri arasında Türkiye'nin 81 ilinin 100 bin kişideki haftalık kümülatif COVID-19 vaka sayısı durum matrisi, aynı tarih aralığında 100 bin kişideki toplam aşı sayısı kontrol matrisi olarak kullanıldı. Daha sonra Dinamik Mod Ayrıştırması (DMA) algoritması ile DMAk algoritmasının hata değerleri farklı hata metrikleri altında karşılaştırıldı. Bu çalışmada, Türkiye Sağlık Bakanlığı'nın COVID-19 vaka ve aşı sayısını içeren TURCOVID-19 açık veri kullanıldı.

Anahtar Kelimeler: Dinamik mod ayrıştırması, kontrol, veriye dayalı dinamik sistemlAcknowledgment ayrıştırması, makine öğrenmesi

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1. Introduction

The rapid spread and development of epidemic diseases is a major challenge to modern medicine and epidemiology. However, dynamic mode separation with mathematical models and machine learning techniques is emerging as an important strategic tool in combating epidemics. This approach helps us overcome the limitations of traditional epidemiological methods and better understand the control of epidemics while providing the ability to predict future situations.

Basic mathematical models of epidemics are important tools used to analyze the dynamics of disease spread and interactions between individuals. These models help us better understand the control and prediction of epidemics in the fields of epidemiology and public health. SIR Model (Susceptibility-Infected-Resistance Model) [1], SEIR Model (Susceptibility-Infected-Exposure-Resistance Model) [2], SIS Model (Susceptibility-Infected-Susceptibility Model) [3], Stochastic Models, and Agent-Based Models [4] are the most basic mathematical modeling types in the literature for epidemic diseases. However, with the development of technology and the increasing number of data sets, mathematical modeling is being replaced by machine learning techniques that provide maximum efficiency in both time and computational cost. These techniques, combined with big data analytics, data mining, and artificial intelligence applications, help us better analyze the spread patterns of epidemics, develop control strategies, and predict future epidemics.

Time series analysis, artificial neural networks (ANN), classification models, clustering, and dimension reduction techniques are the main machine learning techniques used in epidemiology and epidemic diseases [5], [6].

In this study, dynamic mode decomposition (DMD) and dynamic mode decomposition with control (DMDc) machine learning techniques are used; these methods are based on the singular value decomposition (SVD) dimension reduction technique. Both DMD and DMDc are applied to the real Turkey COVID-19 data set, and then the error values are compared by calculating the state estimation of the number of cases.

2. Related Works

The earliest demonstration of the DMD algorithm in analyzing both numerical and experimental data was published by Schmid [7]. In this study, he used the Arnoldi method and various other decomposition techniques to investigate and break down the underlying mechanisms of fluid flow. Unlike previous approaches that relied on models, this work focused on a data-driven DMD procedure that extracts dynamic information. The study successfully applied the DMD algorithm to three different examples.

The foundations and applications of DMD are described in depth in [8] by Tu et.al. This study also covers subjects such as how DMD is handled, how the data set is evaluated, and how the basic modes are derived. Besides that, complex how DMD can be employed in nonlinear systems and the approaches that should be used are covered. The mathematical relationships between DMD and Koopman operator theory are demonstrated. The Koopman operator is a one-dimensional linear operator that describes the development of observables whose modes and eigenvalues describe any (even nonlinear) dynamical system. Also included in this study are system identification approaches such as the Eigensystem realization algorithm (ERA) and linear inverse modeling (LIM). Connections between DMD, ERA, and LIM were also examined.

Brunton et. al., in their work, investigated the governing equations of dynamic systems [9]. Methods from sparse representation and symbolic regression were used in this work. The topic of determining governing equations from data for dynamical systems was covered. A machine learning method that induces sparsity has been devised to extract governing equations from noisy measurement data. This study offered recommendations for the DMD and DMDc methodologies' data arrangement, library construction, and observable selection.

Kutz et. al., take over in their book one of the most fundamental studies covering the theory and applications of dynamic systems, the DMD algorithm [10]. This book is the most comprehensive resource covering the basic theoretical and mathematical foundations of DMD and its types, such as multiresolution DMD and DMDc. The chapters of the book include topics such as Koopman analysis, fluid dynamics, video processing, time delays, and nonlinear observables. These topics include examining numerical examples for DMD and

DMDc, such as theory and Matlab application codes.

Basic examples demonstrating how to use DMDc to solve problems are included in [11]. The dynamic system cannot be correctly modeled by the DMD approach when an external coercive force is applied. Proctor et al. developed the DMDc method, which includes the external force parameter in the system, to fill in the missing information in the DMD method. All of DMD's benefits are taken advantage of by the DMDc approach. It was shown in the study that the DMDc method can be used to make an inconsistent system consistent with its control parameter. Furthermore, a DMDc model for data analysis on infectious diseases is examined, where a control variable is the addition of mass vaccination to the system.

Dekhici et al. generated biogas simulation data using the Anaerobic Model 2 (AM2) in [12]. The DMDc algorithm which uses the dilution rate as the control input—was run using this data. This study also found that adding the control parameter to anaerobic digestion boosted the biogas production's efficiency.

Onstenk, in this study, used the DMDc algorithm to optimize the production process of three-dimensional printers used for the production of large-sized objects [13]. In this study, the data of the dynamic system were obtained by simulating the differential equations of the mass-spring system in Matlab. Then the pressure applied during the inflation of balloons produced from hyperelastic material with a 3D printer was included in the system as a control parameter, and the error values of the DMD and DMDc algorithms were compared.

Mustavee et al. discussed the example of human mobility restriction, which is one of the control types in epidemic diseases [14]. In this study, the COVID-19 epidemic in the US state of Florida was estimated by parameterizing with the control matrix according to the percentage of people using areas such as shopping malls, parks, and public transportation. In addition, the DMDc algorithm was applied to the Hankel matrix based on different h time delay parameters for the state matrix, and mobility data from the Google Community Movement Report was used as the control matrix.

To summarize the relevant studies from a general perspective, the fundamentals and applications of the DMD method are included in the studies in [7,8,9,10], and the fundamentals and applications of the DMDc method are included in the studies conducted in [11,12,13,14].

In this study, TC Ministry of Health TURCOVID19 Open Data was used as a data set [16], [17].

3. Method and Material

The main purpose of using the DMDc method in this study is that DMD cannot predict the system correctly when there is an external force, such as vaccination, acting on the dynamic system. If the external force (in this study it is vaccination) is added to the system as a control parameter then the prediction can be more accurate. One of the important points to consider when applying the DMDc method: In the DMDc algorithm, the singular value decomposition cut-off value p in equation (7) must be greater than the value decomposition cut-off value r in equation (8) [10]. In this study, p=30 and r=29 are selected to obtain a minimum error value.

Dynamic Mode Decomposition with Control (DMDc) [7] is a data-driven method that does not require knowledge of the underlying governing equations but only snapshots in time of observables and actuation (external forces) data obtained from experimental, historical, simulations. Controlling high-dimensional systems requires challenging tasks since they do not scale well with the dimensions of the system. In dealing with this challenging task, high-dimensional observational dimensionality reduction techniques are used. DMDc contains the Singular Value Decomposition (SVD) reduction technique.

DMDc aims to analyze the relationship between a future measurement, the current measurement, and the current control measurement given by the following:

$$x_{k+1} = Ax_k + Bu_k$$

where $x_j \in R^n, u_j \in R^l, A \in R^{n\times n}$ and $B \in R^{n\times l}$. We can store state measurements X, X', and control measurements Y as i Fig1.

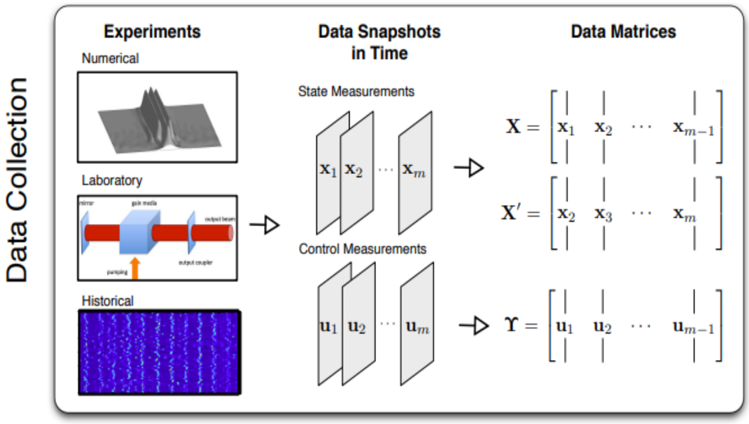

Fig. 1. Data collection from experimental, historical, simulations [11]

3.1. Dynamic Mode Decomposition (DMD) algorithm

In general, dynamic systems are represented by equation (1)

$$\frac{dx}{dt} = f(x, t; \mu) \tag{1}$$

Even if the function $f(x, t; \mu)$ in the system of equations (1) is not known. DMD finds the approximation solution by converting it to a local dynamical system (2).

$$\frac{dx}{dt} = Ax \tag{2}$$

The continuous-time dynamical system (2) turns into a discrete-time step dynamical system $x_{k+1} = Ax_k$ at time step Δt, $x \in R^n$, $A \in R^{n\times n}$, $x_k = x(k\Delta t)$ and m is the total number of cases, X' is a one-step shifted in time X matrices given below

$$X = \begin{bmatrix} \uparrow \uparrow & & \uparrow \\ x_1 x_2 & \dots \dots & x_{m-1} \\ \downarrow \downarrow & & \downarrow \end{bmatrix} \qquad X' = \begin{bmatrix} \uparrow \uparrow & & \uparrow \\ x_2 x_3 & \dots \dots & x_m \\ \downarrow \downarrow & & \downarrow \end{bmatrix}$$

Moore-Penrose pseudoinverse [8] is used to find the dynamic modes and eigenvalues of matrix A.

$$A = X' X^{\dagger} \tag{3}$$

Singular Value Decomposition (SVD) is used to find the pseudoinverse X' of the matrix X.

The Singular Value Decomposition of matrix X is as follows.

$$X' \approx U\Sigma V^* = [\tilde{U} \quad \tilde{U}_{rem}] \begin{bmatrix} \tilde{\Sigma} & 0 \\ 0 & \tilde{\Sigma}_{rem} \end{bmatrix} \begin{bmatrix} \widetilde{V^*} \\ \widetilde{V^*}_{rem} \end{bmatrix} \tag{4}$$

$U \in R^{n\times n}, \Sigma \in R^{n\times m-1}$, $\widetilde{V^*} \in R^{m-1\times m-1}, \tilde{U} \in R^{n\times r}, \tilde{\Sigma} \in R^{r\times r}$, $\widetilde{V^*} \in R^{r\times m-1}$, where rem represents the remainder, and * indicates the conjugated transpose, $m-1-r$ represents the singular value.

When Equation (4) is reduced with appropriate r selection, the approach to the matrix A is as follows.

$$\tilde{A} = \tilde{U}^* \tilde{V} \tilde{\Sigma}^{-1}$$

Eigen-decomposition of $\tilde{A}$ is obtained in $\tilde{A}W = W\Lambda$.

The columns of W are eigenvectors of A and λ_k are eigenvalues of A, (λ_k are diagonal elements of Λ).

DMD method computes the following relationship between the eigenvectors of $\tilde{A}$ and the dynamic modes of A and the columns of Φ;

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

The approximation solution $x(t)$ is found in all time steps as follows.

$$x(t) \approx \sum_{k=1}^{r} \Phi_k \exp(\omega_k t)\, b_k = \Phi \exp(\Omega \mathrm{t})\ \mathrm{b}.$$

$\omega_k = \ln(\lambda_k)/\Delta \mathrm{t}$, $\Omega = diag(\omega)$ is a diagonal matrix with diagonal elements ω_k, b_k is the initial condition for each dynamic mode.

3.2. Dynamic Mode Decomposition with Control (DMDc) algorithm

In the Dynamic Mode Decomposition with Control (DMDc) algorithm, data is stored as a state and control matrix [11]. Here, X, X′ are state matrices and ϒ is the control matrix given below.

$$X = \begin{bmatrix} \uparrow \uparrow & & \uparrow \\ x_1 x_2 & \ldots\ldots & x_{m-1} \\ \downarrow \downarrow & & \downarrow \end{bmatrix} \quad X' = \begin{bmatrix} \uparrow \uparrow & & \uparrow \\ x_2 x_3 & \ldots\ldots & x_m \\ \downarrow \downarrow & & \downarrow \end{bmatrix} \quad \Upsilon = \begin{bmatrix} \uparrow \uparrow & & \uparrow \\ u_1 u_2 & \ldots\ldots & u_{m-1} \\ \downarrow \downarrow & & \downarrow \end{bmatrix}$$

The aim of DMDc is to analyze the relationship between a future system measurement with the current measurement and the current control measurement given by the following:

$$x_{k+1} = Ax_k + Bu_k \tag{5}$$

where $x_j \in R^n$, $u_j \in R^l$, $A \in R^{n\times n}$ and $B \in R^{n\times l}$.

To find best-fit operators A and B for the dynamical system in Eq. (5) can be manipulated by giving the following representation.

$$X' = [A \quad B]\begin{bmatrix} X \\ \Upsilon \end{bmatrix} = G\Omega \tag{6}$$

And then performed the given below steps to find DMDc modes.

1) Compute the singular value decomposition of Ω with truncation value p

$$\Omega \approx \tilde{U}\tilde{\Sigma}\tilde{V}^* \tag{7}$$

(* is a conjugate transpose)

2) Compute the singular value decomposition of X' with truncation value r

$$X' \approx \hat{U}\hat{\Sigma}\hat{V}^* \tag{8}$$

3) Compute the approximation of the operators $G = [A \quad B]$ compute the following:

$$\tilde{A} = \hat{U}^* X'\, \tilde{V}\tilde{\Sigma}^{-1}\tilde{U}^*{}_1\hat{U} \tag{9}$$

$$\tilde{B} = \hat{U}^* X'\, \tilde{V}\tilde{\Sigma}^{-1} \tag{10}$$

4) Perform the eigenvalue decomposition given by the following:

$$\tilde{A}W = W\Lambda \tag{11}$$

5) Compute the dynamic modes of the operator A by the same way DMD

$$\Phi = X' \, \tilde{V}\tilde{\Sigma}^{-1}\tilde{U}^{*}{}_{1}\hat{U}W \tag{12}$$

3.3. Error metrics

In this section, the error values are calculated by taking the differences between the real state matrix X and each cell of the X_{DMD} and X_{DMDc} created by the DMD and DMDc algorithms, respectively. Here, X_{DMD} and X_{DMDc} are matrices has 81×30 dimensions. Used error metrics in this study; RMSE, MAE and MAPE, which are used for time series applications.

Root Mean Square Error (RMSE)

It is an error metric calculated by taking the square root of the mean of the sum of the squares of the differences between the estimated model and the actual value. Its formula is as follows [15].

$$RMSE = \sqrt{\frac{1}{n}\sum\nolimits_{i=1}^{n}(y_i - y_i')^2}$$

Mean Absolute Error (MAE)

It is the error metric calculated by taking the average of the sum of the absolute values of the differences between the estimated model and the actual value [15].

$$MAE = \frac{1}{n}\sum\nolimits_{i=1}^{n}|y_i - y_i'|$$

Mean Absolute Percentage Error (MAPE)

It is the percentage of the sum of the absolute values of the difference between the predicted values and the real values [15].

$$MAPE = \frac{100}{n}\sum\nolimits_{i=1}^{n}\left|\frac{y_i - y_i^{!}}{y_i}\right|$$

y_i = real value
y_i' = predicted value
n = number of observations

4. Results and Discussion

There are two types of control mechanisms to prevent the spread of epidemic diseases. The first is the restriction of human mobility and the second is the direct control technique vaccine. The first example of control-type human mobility restriction was discussed in the study [14]. The COVID-19 epidemic in the US state of Florida was estimated by parameterizing the control matrix according to the percentage of people using areas such as shopping malls, parks, and public transportation. In this study, the second type, direct vaccination control, was examined. The control diagram of epidemic diseases is given in Fig2.

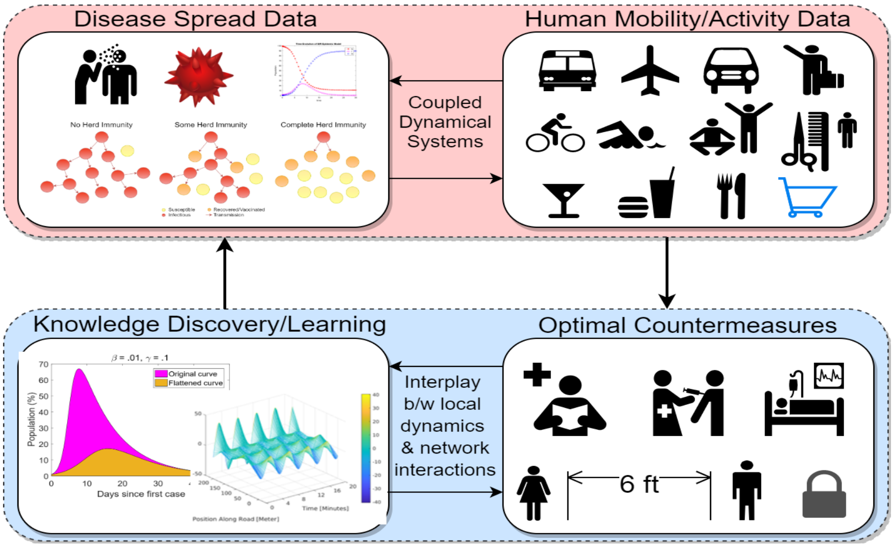

Fig. 2. The control diagram of epidemic diseases [14]

Dynamic Mode Decomposition with Control (DMDc) can be applied to the field of computational epidemiology focusing on the eradication and reduction of diseases [9]. In this study, we applied the DMDc method to the weekly number of COVID-19 cases per 100 thousand people in 81 provinces of Turkey between February 8 and September 11, 2021, as a state matrix and the total number of vaccinations per 100 thousand people in the same time interval was used as control matrix. The data set used is TC Retrieved from the Ministry of Health TURCOVID19 Open Data site [16], [17]. Its website is shown in Fig.3. Dynamic Mode Decomposition (DMD) and DMDc methods were applied to this data set in Matlab; computed singular value decomposition of Ω with truncation value p in (3), computed the singular value decomposition of X' with truncation value r in (4), computed the approximation of the operators A and B in (5), (6) performed the eigenvalue decomposition in (7), computed the dynamic modes of the operator A in (8). The results were compared for both methods and error metrics such as Root Mean Square Error (RMSE), Mean Absolute Error (MAE), and Mean Absolute Percentage Error (MAPE) were calculated.

Açık Veri

Türkiye COVID19 pandemisiyle ilgili verileri analize hazır şekilde XLS ve CSV dosya formatlarıyla sizlere arz ediyoruz. Böylece konuyla ilgili akademik çalışmalara hız kazandırmayı ve konuyla ilgili herkese vakit kazandırmayı umuyoruz.

Veri yayınlandıkça güncellenen veri setlerine erişmek için indirmek istediğiniz veri setine ait aşağıdaki butonlara tıklamanız yeterli. Ayrıca veri bilimi ile ilgilenen ve COVID-19 mücadelesine katkı sunan geliştiricilerin ihtiyaç duyduğu otomatik veri akışı için sürekli güncellenen sabit csv linkleri de aşağıda mevcuttur.

Tespit ettiğiniz hata veya eksikleri buradan bildirebilirsiniz.

Kaynaklar:
Sağlık Bakanlığı Günlük Tablo
Sağlık Bakanlığı Durum Raporları
İBB Vefat Sorgulama | turkiye.gov.tr
Sağlık Bakanlığı COVID19 Aşısı Bilgilendirme Platformu

Fig.3. The website of TURCOVID19 [16], [17].

The matrix X represents the weekly cumulative number of cases per 100 thousand people in 81 provinces between February 8 and September 11, 2021. The control matrix Υ represents the weekly cumulative number of vaccinations per 100 thousand people in the same date range. The DMD and DMDc algorithms were applied to each case, respectively. The state estimate error values calculated by selecting the r and p dimension parameters that give the smallest error value in the error metric are given in the table below.

Table 1. Comparison of DMD and DMDc Error

Error Metrics	**DMD**	**DMDc**
RMSE	90,0868	0,7907
MAE	63,3380	0,4136
MAPE	52,3908	0,9953

As shown in Table 1, it was seen that the performance of DMDc smaller than DMD errors under the RMSE, MAE, MAPE error metrics. The comparison of the number of COVID-19 cases in Turkey with the outputs of the DMD and DMDc algorithms is illustrated in three-dimensional plots in Matlab, as shown below in Fig. 4, Fig. 5, Fig. 6.

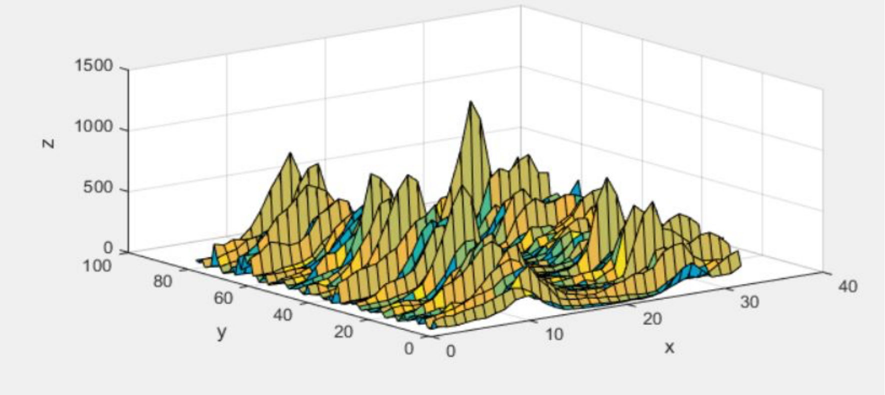

Fig. 4. Original Turkey COVID-19 Data Case Number

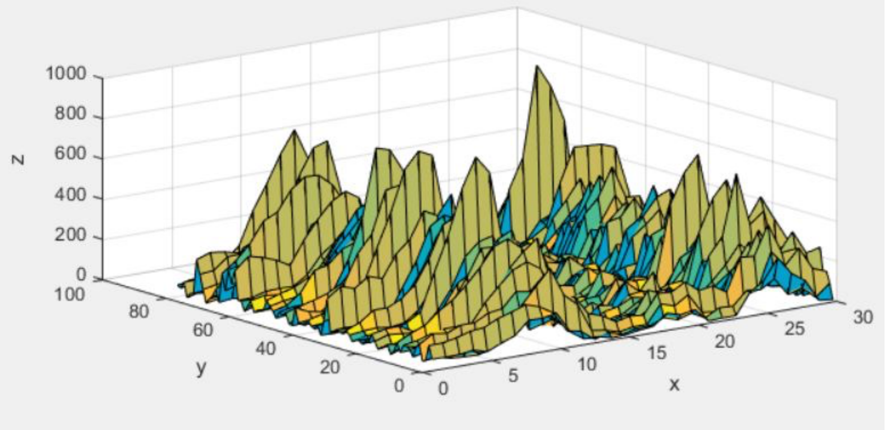

Fig. 5. Prediction of DMD Turkey COVID-19 Case Number

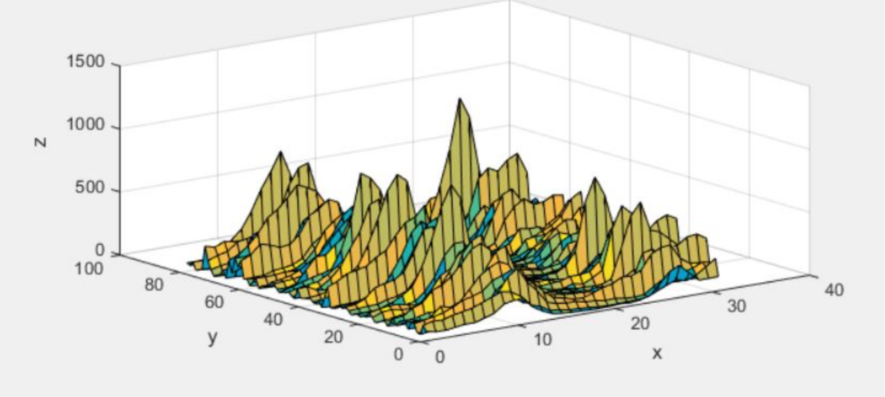

Fig. 6. Prediction of DMDc Turkey COVID-19 Case Number

In these figures, the x-axis represents the number of weeks (time), the y-axis represents the 81 provinces of Turkey, and the z-axis represents the total number of COVID-19 cases in Turkey.

5. Conclusions and Future Work

As a result, in this study, the situation matrix for the Turkey COVID-19 data set is taken as the weekly cumulative number of cases per 100 thousand people in Turkey's 81 provinces between February 8 and September 11, 2021. The control matrix is taken as the weekly cumulative number of vaccinations per 100 thousand people in the same time interval. Then DMD and DMDc algorithm errors are calculated. The error of the Dynamic Mode Decomposition with Control (DMDc) algorithm, in which the state estimation of the system is made by including the parameter (vaccination) that negatively affects the nature of the dynamic system, is smaller than the Dynamic Mode Decomposition (DMD) algorithm in all error metrics (RMSE, MAE, and MAPE).

The difference between this study and others in the literature is that for Dynamic Mode Decomposition with Control (DMDc) applications, data sets obtained from numerical solutions or simulations are not used, but rather real data is used directly. There are few studies in the literature where the DMDc method has been applied to real data sets [16], [17].

Notably, the DMDc approach demonstrates reduced state prediction errors across various error metrics when compared to the standard DMD method, particularly in the context of limited data a noteworthy outcome of this research.

However, the DMDc method cannot predict the future state due to the small amount of data set. As a future work, we aim to make a future state estimation of Turkey's COVID-19 case number using the DMDc algorithm and data augmentation techniques.

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Conflict of Interest Statement

The authors declare that there is no conflict of interest.

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