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Temporal Analysis Of COVID-19 Cases And Recovery Trends In Panvel City: A Spline Curve Approach

N. K. Patil[1], S.S. Jadhav[2], S.G. Pagare[3], M.A. Joshi[4], S.L. Khairnar[5*]

[1]*Department of Mathematics and Statistics, JVM'S Mehta Degree College, Airoli, Navi Mumbai*
[2]*Department of Mathematics, Sundarrao More College of Arts, Commerce & Science, Poladpur*
[3]*Department of Education, Brahma Valley Educational College of Anjaneri, Trimbakeshwar (Nashik)*
[4,5*]*Department of Mathematics, Changu Kana Thakur Arts, Commerce and Science College New Panvel*

***Corresponding Author:** S.L. Khairnar*
**Email Address: sagarkhairnar1604@gmail.com*

***Abstract**:*

The spline curve method in mathematical modeling, was assessed across degrees for its efficacy in fitting daily cured and COVID-19 positive patient data of Panvel City. This study highlights the critical role of selecting an appropriate degree in spline interpolation for reliable disease-related dataset modeling.

Keywords: Temporal, COVID-19, Recovery, Spline, Panvel.

Introduction:

The COVID-19 pandemic has unfolded as a global health crisis, prompting unprecedented challenges across diverse communities. Amidst this global landscape, understanding the local dynamics of the pandemic is essential for targeted and effective public health interventions. This study undertakes a focused investigation into the temporal trends of COVID-19 cases and recovery rates within Panvel City, employing a spline curve approach. Panvel City, with its unique demographic and geographic characteristics, serves as a microcosm for exploring localized patterns that may differ from broader regional or national trends.

The spline curve method is chosen for its ability to provide a flexible and smooth representation of temporal data, capturing non-linear variations and intricate patterns. By adopting this approach, the study seeks to unveil the temporal dynamics of COVID-19 within Panvel City, identifying critical points such as peaks and troughs in infection rates and recovery trends. This localized analysis aims to contribute valuable insights to the ongoing efforts of health authorities and policymakers in Panvel City, enabling them to tailor interventions and allocate resources effectively.

As the global community navigates through various phases of the pandemic, recognizing the specific challenges faced by individual cities and regions becomes paramount. The insights derived from this localized temporal analysis will not only contribute to the existing body of knowledge on COVID-19 but also offer practical guidance for mitigating the impact of the virus within Panvel City. Informed decision-making is pivotal for minimizing transmission, enhancing healthcare capacities, and fostering community resilience. This study serves as a dedicated effort to contribute to the understanding of the unique trajectory of COVID-19 in Panvel City, facilitating evidence-based strategies for public health management.

Literature Review:

In a comprehensive analysis of global SARS-CoV-2 genomes, Arevalo propose an innovative approach to identify major haplotypes based on the normalization of mutation frequencies by COVID-19 cases. Utilizing data from 48,776 genomes, the study identifies five major haplotypes associated with high-frequency mutations, emphasizing the significance of nucleocapsid mutations, particularly R203K and G204R, over the widely discussed D614G mutation in the spike protein. To facilitate ongoing monitoring and analysis, the authors introduce a web service for continuous updates and voluntary sharing of patient status information to enhance research efforts and improve the tracking of mutations and haplotypes globally [1]. In the context of the COVID-19 epidemic in India during Lockdown-1, Mahajan and Kaushal conduct a detailed evaluation of case fatality rate (CFR), case recovery rate (CRR), and mortality rate (MR). With a focus on 10,815 confirmed cases, the study reveals that many cases fall within the working-age group of 20–49 years, with 76% being male. Notably, the recovery rate exceeds the fatality rate, attributing the effective control of COVID-19 transmission in India to preventative measures and social distancing efforts implemented by state and central governments[2]. Examining the spatio-temporal dynamics of the COVID-19 pandemic in India, Ansumali et al. employ an SAIRD model on data from 186 districts, revealing a shift in the burden of infections from large metropolitan to sub-urban districts. The study observes a continuous improvement in epidemic parameters, including reproduction numbers, recovery rates, and death rates, with a noteworthy trend of the pandemic burden moving towards regions accessible by domestic airports and trains. The findings emphasize the importance of resource reorganization to address the evolving geographic distribution of the pandemic[3]. Conducting a meta-analysis across 36 European countries, KaradaÄŸ investigates COVID-19 case increase, case fatality, and case recovery rates. As of May 11, 2020, the study reports a standardized case increase rate of 5%, with a weekly decline of around 3%. Notably, the case fatality rate is estimated to be 4.5%, prompting the importance of monitoring specific countries for case fatality and recognizing treatment successes in others. The study provides crucial insights into the European pandemic landscape, emphasizing the need for ongoing vigilance and adaptive strategies [4]. In Shandong Province, China, Chang et al. conduct a detailed epidemiological analysis of COVID-19 cases from January 21 to March 1, 2020. Reporting 758 laboratory-confirmed cases, the study highlights a male-to-female ratio of 1.27:1, with high-risk clusters identified in central, eastern, and southern regions. The research reconstructs 54 transmission chains, elucidating the importance of avoiding household and community transmission. The findings underscore the significance of addressing geographical and temporal disparities to implement tailored public health measures [5]. In the wake of India becoming the third most affected country by the COVID-19 pandemic, Patil et al. address the urgent need for predicting the expected number of cases. With over 0.7 million confirmed cases, the study introduces a novel strategy employing the Multiple Aggregation Prediction Algorithm (MAPA) with Principal and Exponential Predictions. By validating the approach with data from different Indian states, the study demonstrates that Principal, Mean, and Exponential Predictions collectively provide a range within which the actual number of cases is likely to fall, offering a valuable tool for forecasting COVID-19 cases for the next 45 days[6]. Leclerc et al. explore the potential of the NHS Pathways triage system as an early warning system for monitoring COVID-19 transmission. Analyzing temporal trends in NHS Pathways reports until May 14, 2020, the study reveals that rates of growth/decline and effective reproduction numbers estimated from these data may be useful in tracking transmission, especially as lockdown restrictions are lifted. The study establishes a strong association between NHS Pathways reports and daily deaths reported 16 days later, suggesting the system's potential in serving as a crucial component of an early warning system for disease resurgence [7]. Bajaj et al. leverage regression, a supervised machine learning algorithm, to assess time-series datasets of COVID-19 in India and two Municipal Corporations of Maharashtra—Mira-Bhayander and Akola. The study's focus on localities such as Municipal Corporations reveals that the growth of COVID-19 cases exhibits different patterns, with exponential growth observed at the national level and cubic or multi-peak Gaussian patterns at a more localized scale. The findings underline the importance of regional-level strategies and decision-making policies in controlling the pandemic[8]. Saputra et al. investigate the correlation between solar radiation exposure and the pattern of COVID-19 cases in Jakarta, Indonesia. Using an ecological design integrating geographic information systems and statistical techniques, the study establishes a significant relationship between solar radiation exposure and COVID-19 cases. The spatial map overlaying solar radiation exposure and cases indicates that areas with high radiation tend to experience an earlier increase in cases. The findings suggest the importance of considering geographical and temporal conditions in strengthening region-specific prevention and control programs[9]. In exploring the successive waves of the COVID-19 outbreak in Italy, Vinceti et al. analyze the relation between mortality in the first and second waves within the same provinces. The study finds that provinces with the most severe initial outbreaks, as assessed through first-wave mortality, faced milder second waves. These findings, independent of vaccination or variant spread, highlight the potential utility of understanding the magnitude of successive waves in predicting the scope of new outbreaks[10]. Arévalo et al. highlight the global opportunity for analyzing the spreading and evolution of SARS-CoV-2 by sequencing a large number of genomes worldwide. They propose a normalization approach based on COVID-19 cases to track major haplotypes, identifying five major haplotypes across 171,461 genomes. The study emphasizes the current prevalence of haplotype OTU_3, characterized by mutations R203K and G204R, in four continents, and discusses temporal shifts in dominant haplotypes. Analysis of age, gender, and patient status does not reveal haplotype preferences. The study aims to contribute to ongoing monitoring and understanding of virus mutations and their implications[11]. Isniyati et al. focus on the spatiotemporal analysis of COVID-19 cases in Batang Regency, Indonesia. Using an observational spatiotemporal explanatory research design, the study identifies a change in the pattern of COVID-19 distribution from random to clustered. The analysis reveals significant spatial correlation and concentration in certain villages. The findings suggest the importance of spatiotemporal analysis in understanding the evolving distribution pattern of COVID-19 at the regional level, aiding in planning and response strategies[12]. Park et al. conduct a time series analysis of COVID-19 daily cases in the U.S., particularly focusing on Humboldt County. Utilizing autocorrelation, partial autocorrelation, and clustering analysis, the study identifies a 7-day seasonal pattern in Humboldt County and reveals a moderate positive correlation between daily cases and vaccination rates. The findings provide insights for future time-series forecasting and planning in the context of COVID-19 [Park et al.][13]. Sifriyani et al. introduce a Geographically Weighted Panel Regression model for spatial-temporal analysis of COVID-19 in Kalimantan Regency, Indonesia. The model incorporates geographic weighting functions and modified spatial interactions and time series. The study identifies health service factors as significant influencers on COVID-19 cases, providing recommendations for local governments to address challenges in their regions. The developed model contributes to spatial statistics and Geographic Information Systems (GIS) methodologies[14]. Annesser et al. compare statistical techniques estimating the association between SARS-CoV-2 RNA in wastewater and sludge and reported COVID-19 cases. Linear, generalized additive, and Poisson models outperform negative binomial models in relating SARS-CoV-2 RNA concentrations to reported cases. The study emphasizes the importance of selecting appropriate statistical models for accurate estimation in wastewater-based epidemiology [15]. Özen conducts a study analyzing the trends and predictions of COVID-19 in Turkey, emphasizing the uniqueness of the pandemic in terms of its duration, impact on public health, and socioeconomic consequences compared to previous pandemics. The research utilizes machine learning methods on daily data provided by the Turkish Ministry of Health, focusing on various time series data, including daily case numbers, severe patient numbers, daily death tolls, and daily recoveries. Polynomial regression, least squares polynomial fitting, and curve fitting are employed to predict future trends, with the curve fitting method yielding the best results for the four selected time series. The study emphasizes the importance of understanding the pandemic's progression for preparedness in facing potential future pandemics[16]. Haider et al. employ Geographic Information Science (GIS) to analyze the spatial distribution of COVID-19 cases in Afghanistan. Using an Inverse Distance Weighting (IDW) geospatial technique, the study investigates the total confirmed cases, deaths, and recoveries in different provinces. The Getis-Ord Gi* statistic method is applied to identify hotspots, revealing strong correlations between COVID-19 variables and population density. The findings highlight the potential of GIS in managing and controlling the pandemic, providing insights into disease trends, hotspots, and underserved populations during outbreaks[17]. Lawal et al. conduct trend analysis and GARCH modeling to predict the weekly confirmed cases of COVID-19 in the Federal Capital Territory (FCT) and Lagos, Nigeria. The study explores linear, quadratic, cubic, and quartic trends, identifying quadratic trends as the most suitable. GARCH(1,0) is established as the best model for predicting weekly confirmed cases. The study contributes to forecasting the pandemic's trajectory in specific regions, aiding in proactive measures and control efforts[18]. Mello-Sampayo focuses on the spatial analysis of positive COVID-19 cases among the elderly living in Residential Care Homes (RCH) in Portugal. The study employs Kernel density estimation, space-time statistics, and geographic weighted regression to identify clusters and analyze factors influencing infection risk. Results highlight priority geographic areas for intervention, emphasizing regions with high comorbidities and low income. The study provides insights for targeted actions to control COVID-19 in elderly care homes, suggesting improvements in income and health levels[19]. Yılmaz explores the socio-demographic and spatio-temporal distribution patterns of COVID-19 in Istanbul, Turkey. Using Ordinary Least Square (OLS) and Geographically Weighted Regression (GWR) methods, the study investigates relationships between COVID-19 intensity and factors such as gender, household size, population density, and education level. Findings indicate the significance of these factors in influencing exposure to COVID-19 and highlight the potential use of the study's outcomes for decision-making and control measures in densely populated urban areas[20].

Aggarwal et al. undertake a study to calculate COVID-19 cases in Punjab, India, using a modified B-spline function and the differential quadrature method. Real data and Google Community Mobility Reports for Punjab districts are utilized, with Google mobility data providing insights into social behavior changes for analyzing COVID-19 spread. The study aims to demonstrate the predictive ability of the model and contributes to understanding the pandemic's dynamics in the region[21]. Susanna et al. investigate the relationship between wind speed and COVID-19 cases in Jakarta, Indonesia. Conducting an ecological study integrating geographic information systems, the study finds a strong positive correlation between average wind speed and COVID-19 cases in Jakarta. Areas with high wind speeds, particularly coastal regions, show an increased number of cases, emphasizing the role of wind speed in SARS-CoV-2 spread when health protocols are not properly implemented [22]. Hembram et al. analyze the spatial and temporal distribution of COVID-19 cases in West Bengal, India, from May 31, 2020, to December 31, 2021. Using ArcGIS software and demographic data, the study identifies high-incidence districts and emphasizes the importance of evaluating disease severity and developing effective policies for control and prevention[23]. Hastari et al. focus on Sukoharjo Regency in Indonesia, conducting a spatial and temporal analysis of COVID-19 cases. The study identifies spatial autocorrelation, clustering, and a peak in cases in July 2021. The findings contribute to understanding the transmission mechanism and can aid in developing targeted interventions[24]. Shan et al. propose a graph-learning technique to infer the graph structure of COVID-19 data, identifying influential countries for pandemic response analysis. The method accurately estimates the graph Laplacian, providing improved results compared to existing techniques. The identified influential countries contribute to the study of COVID-19 spread[25]. Putri et al. investigate influencing factors and the spatial and temporal distribution of COVID-19 in West Java, Indonesia. Using PIKOBAR data, the study employs regression analysis and temporal charts to analyze the impact of policies and events on transmission. The study aids in understanding distribution patterns for effective control and assessment programs[26]. Rahardiantoro develops a generalized lasso model for spatio-temporal clustering of COVID-19 data, demonstrating its accuracy through simulations. The method outperforms existing approaches in detecting temporal and spatial effects, providing valuable insights into dynamic behavior and clustering patterns[27]. Li develops a compartmentalized model to analyze the competitive spread of Omicron and Delta strains of COVID-19. Adedire et al. conduct a statistical analysis of COVID-19 data in Rivers State, Nigeria, covering infected population, discharged cases, and deaths. Using one-way ANOVA and correlation analysis, the study identifies significant differences in means and relationships among the variables, highlighting the relatively low mortality rate in the region[28].

Methodology:

We have systematically gathered data pertaining to the number of positive and cured patients within the municipal boundaries of Panvel City from April 16, 2020, to May 20, 2021. It is essential to note that data for certain days within this period were unavailable. The dataset, comprising 252 days, commenced on Day 1, corresponding to April 16, 2020, and concluded on the 252nd day, corresponding to May 20, 2021. Days with missing data were excluded from consideration. Subsequently, we employed the spline method to interpolate and align the dataset accurately. This interpolation was executed using polynomials to ensure a comprehensive and robust fit to the actual data, thereby facilitating a detailed analysis of trends and patterns in the context of positive and cured COVID-19 cases in Panvel City. This methodology aims to provide an in-depth understanding of the temporal dynamics of COVID-19 cases and recovery trends within Panvel City, utilizing the flexibility and adaptability of the spline curve method. The results will contribute valuable insights for local health authorities and policymakers in Panvel, aiding in the formulation of targeted and evidence-based interventions.

A polynomial with degree n means a linear combination of the terms X^j , $j = 0,1,2, \dots, n$. For every set of data points, there is a unique interpolation polynomial with degree n being the number of points minus one. From a complicated mathematical model or a function $G(X)$, we can obtain the data points. If we acquire an interpolation polynomial, we can easily replace the original model, i.e., the function, with the interpolation polynomial for the purpose of analysis and design.

We can represent the n $points$ $\{(Z_1, Q(Z_1)), (Z_2, Q(Z_2)), \dots, (Z_n, Q(Z_n))\}$ in the form of a polynomial of degree (n-1) :

$$Q(x) = \gamma_{n-1} Z^{n-1} + \cdots + \gamma_2 Z^2 + \gamma_1 Z + \gamma_0$$

Further, this polynomial can be expressed as $PZ = R$. P is the n \times n matrix known as the Vandermonde matrix, Z and R are $n \times 1$ matrices given as:

$$P = \begin{bmatrix} Z_1^{n-1} & \cdots & Z_1 & 1 \\ Z_2^{n-1} & \cdots & Z_2 & 1 \\ \vdots & \ddots & \vdots & \vdots \\ Z_n^{n-1} & \cdots & Z_n & 1 \end{bmatrix}, Z = \begin{bmatrix} \gamma_{n-1} \\ \gamma_{n-2} \\ \vdots \\ \gamma_1 \\ \gamma_0 \end{bmatrix}, R = \begin{bmatrix} Q(Z_1) \\ Q(Z_2) \\ \vdots \\ Q(Z_n) \end{bmatrix}$$

The solution for accurate interpolation in systems with round-off errors involves understanding the trade-offs between high-order interpolating polynomials and their potential pitfalls.

When dealing with large datasets, using high-order interpolating polynomials might lead to overfitting. Using a single high-degree polynomial to interpolate between points can pass exactly through these points but may not generalize well between them, especially if the number of points is limited. To mitigate this, employing multiple low-order polynomials for piecewise interpolation—known as spline interpolation—can yield better results. Each polynomial within this approach is valid within an interval between two or more points and maintains the same degree but with different coefficients. In spline interpolation, the points where adjacent splines meet are called knots. At these knots, the derivative may not be continuous, leading to abrupt changes in slope. To ensure a smoother interpolation function, higher-order polynomials can be used to enforce continuity of the second derivative at each knot point. This helps improve the smoothness of the underlying function being interpolated. The key elements of the spline method revolve around determining the lowest-order polynomial spline T_i that passes through two adjacent interpolating points $\left(Z_j, G(Z_j)\right)$ and $\left(Z_{j+1}, G(Z_{j+1})\right)$. This spline should satisfy specific conditions:

1. Interpolation: The spline T_j must interpolate the given points $\left(Z_j, G(Z_j)\right)$ and $\left(Z_{j+1}, G(Z_{j+1})\right)$.
2. Continuity of First Derivative: The slope (first derivative) of T_j at Z_j should be equal to the slope of the previous spline T_{j-1} at Z_j .
3. Continuity of Second Derivative: The concavity (second derivative) of T_j at Z_j must be the same as that of the previous spline T_{j-1} at Z_j.

These conditions result in four constraints that need to be satisfied to determine the characteristics of the spline T_j accurately. These constraints ensure a smooth and continuous transition between adjacent splines while maintaining the desired properties at the interpolation points and providing a coherent overall interpolation function:

$$T_j(Z_j) = G(Z_j),\ T_j(Z_{j+1}) = G(Z_{j+1}),\ T_j'(Z_j) = T_{j-1}'(Z_j),\ T_j''(Z_j) = T_{j-1}''(Z_j)$$

Where T', T'' and ''denotes the first and second derivative w.r.t. Z respectively.
The polynomial that fulfils these four constraints necessitates a minimum of four degrees of freedom, typically corresponding to a 3rd-order polynomial, commonly referred to as a cubic polynomial. Therefore, T_j has the form:

$$T_j(Z) = \gamma_{j,3}Z^3 + \gamma_{j,2}Z^2 + \gamma_{j,1}Z + \gamma_{j,0} \quad \forall j = 0,1,2, \dots n-1$$

We need n-1 splines to accommodate and interpolate n data points.
To calculate all 4(n-1) spline coefficients, solving 4(n-1) equations is necessary. Specifically, when dealing with cubic splines involving three data points (Z_1, Z_2, Z_3) , we determine that 2 cubic splines are required for these three points.

After solving, we get the following system:

$$\begin{bmatrix} Z_1^3 & Z_1^2 & Z_1 & 1 & 0 & 0 & 0 & 0 \\ Z_2^3 & Z_2^2 & Z_2 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & Z_2^3 & Z_2^2 & Z_2 & 1 \\ 0 & 0 & 0 & 0 & Z_3^3 & Z_3^2 & Z_3 & 1 \\ 3Z_2^2 & 2Z_2 & 1 & 0 & -3Z_2^2 & -2Z_2 & -1 & 0 \\ 3Z_2 & 1 & 0 & 0 & -3Z_2 & -1 & 0 & 0 \\ 3Z_1^2 & 2Z_1 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 3Z_3^2 & 2Z_3 & 1 & 0 \end{bmatrix} \begin{bmatrix} \gamma_{1,3} \\ \gamma_{1,2} \\ \gamma_{1,1} \\ \gamma_{1,0} \\ \gamma_{2,3} \\ \gamma_{2,2} \\ \gamma_{2,1} \\ \gamma_{2,0} \end{bmatrix} = \begin{bmatrix} Q(Z_1) \\ Q(Z_2) \\ Q(Z_2) \\ Q(Z_3) \\ 0 \\ 0 \\ Q'(Z_1) \\ Q'(Z_3) \end{bmatrix}$$

Results and Discussion:

In this study, two datasets were employed for data analysis, focusing on the daily progression of actual cured patient numbers. The spline method was applied across degrees 1 to 8 to examine its efficacy in fitting the data. Figures 1, 2, 3, 4, 9, and 10 revealed that degrees 1, 2, 3, and 4 exhibited inadequate fitting with the actual data. Conversely, Figures 5, 6, 7, and 8 demonstrated that degrees 5, 6, 7, and 8 provided a more suitable fit to the actual data, with degrees 7 and 8 yielding the most accurate fitting for cured patient data. Similarly, the daily progression of COVID-19 positive patients was plotted in Figures 11 to 20. While Figures 11, 12, 13, 14, 19, and 20 indicated that the spline method did not offer accurate fitting, Figures 15, 16, 17, and 18 showed that degrees 5, 6, 7, and 8 exhibited a close fit to the actual data. Notably, degrees 7 and 8 provided the most precise fitting.

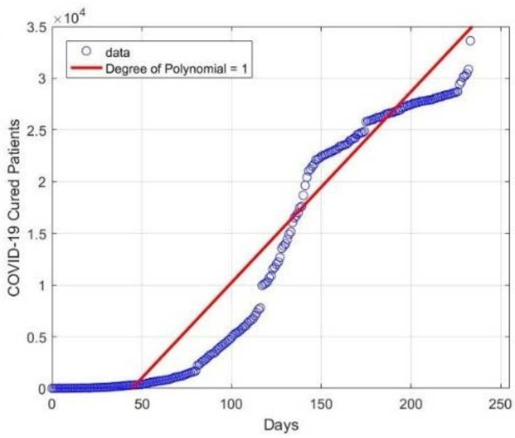


Figure 1

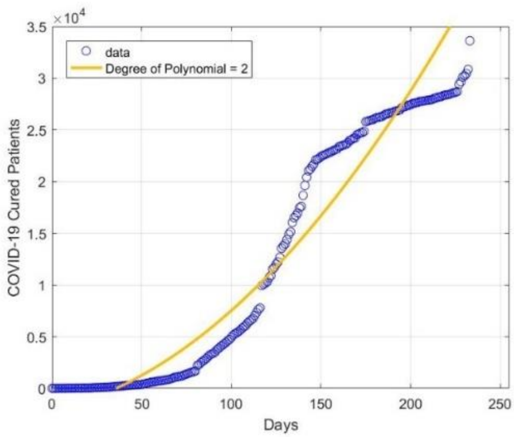
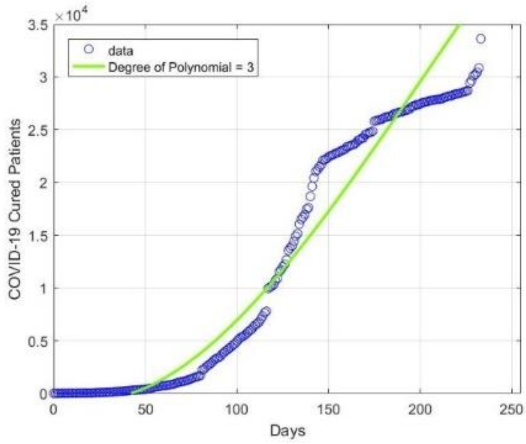


Figure 2



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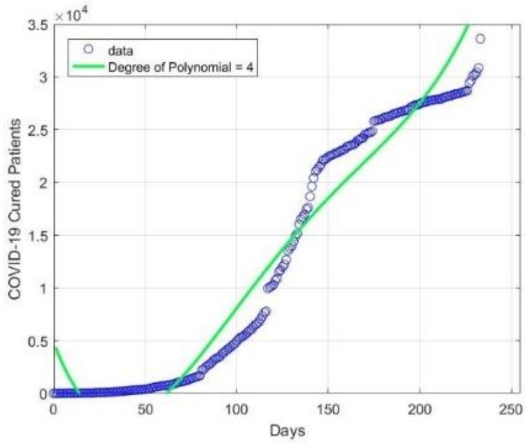

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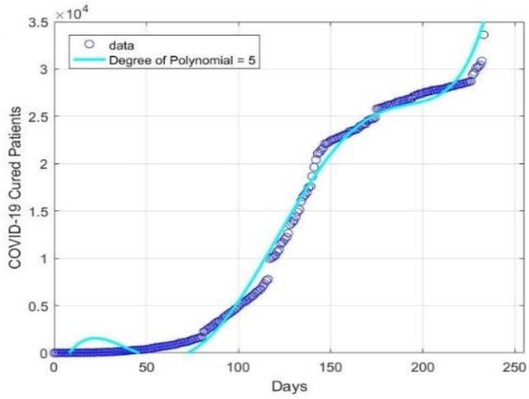
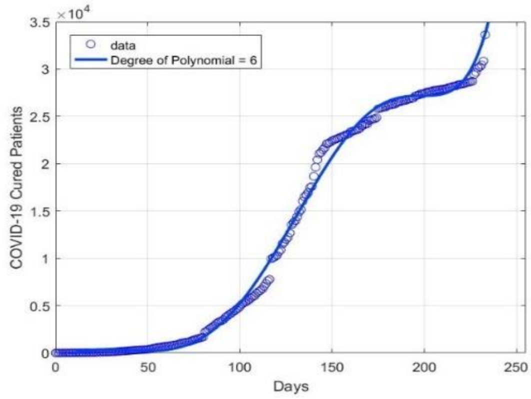


Figure 5



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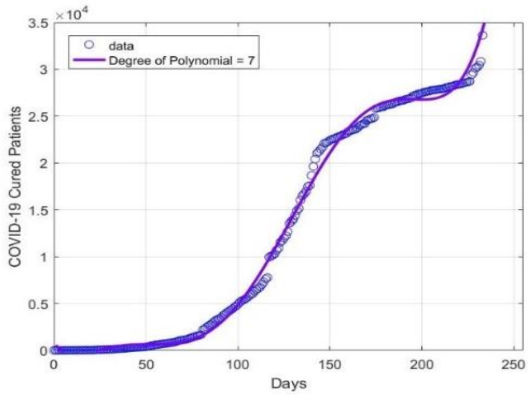


Figure 7

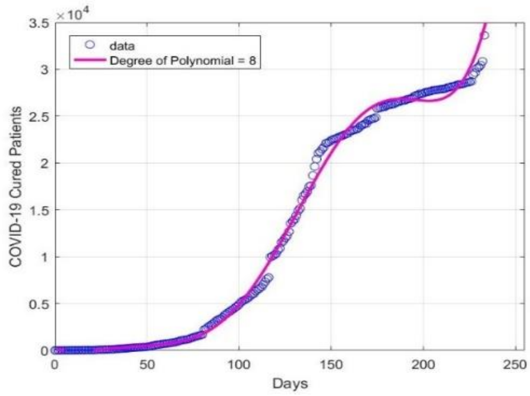


Figure 8

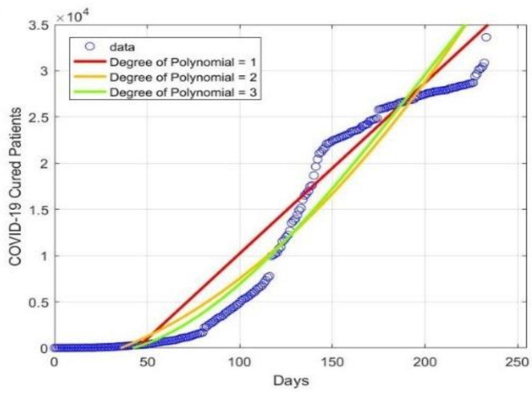


Figure 9

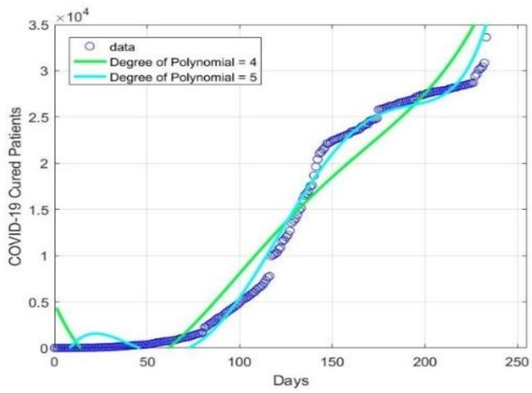


Figure 10

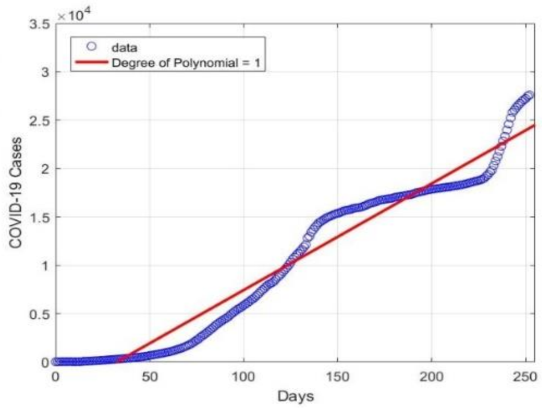
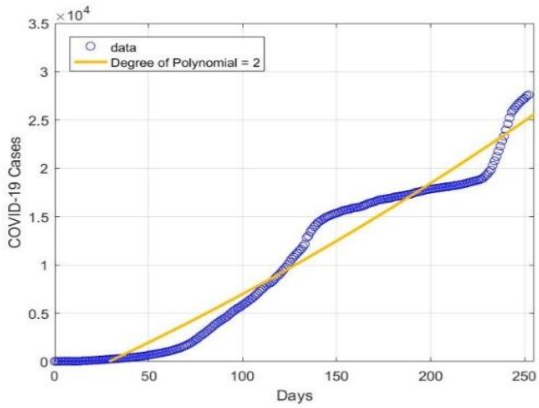


Figure 11



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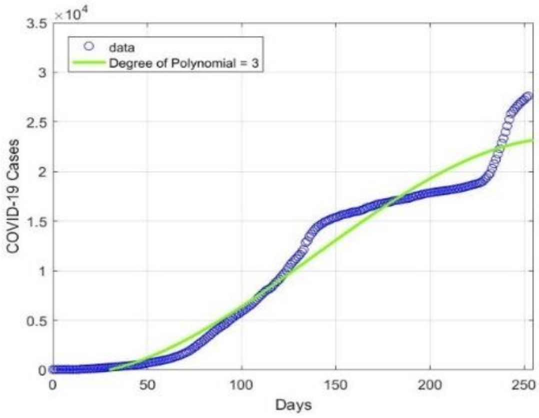

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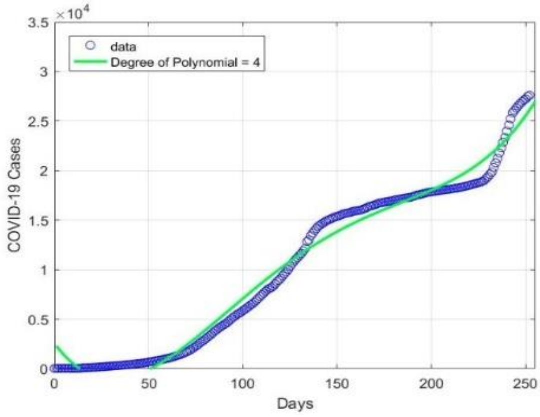

Figure 14

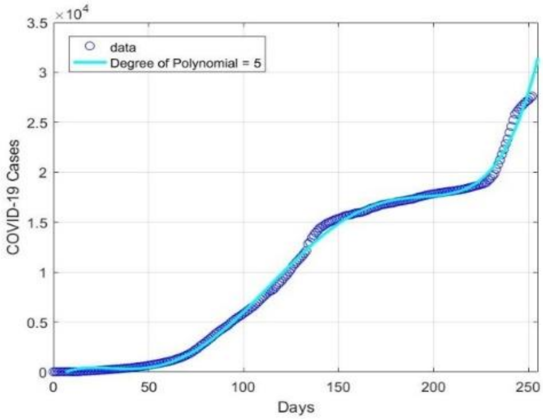

Figure 15

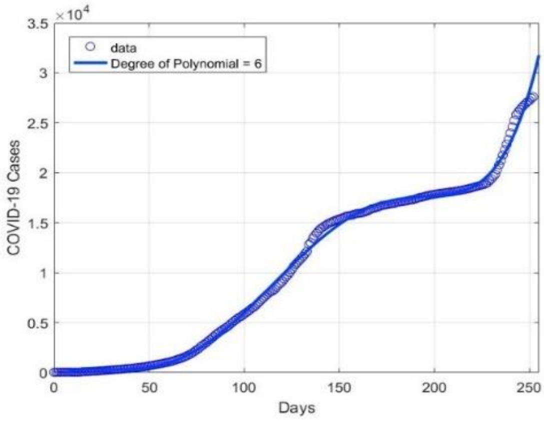

Figure 16

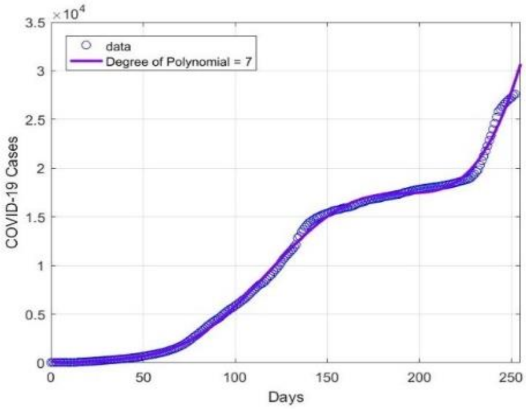

Figure 17

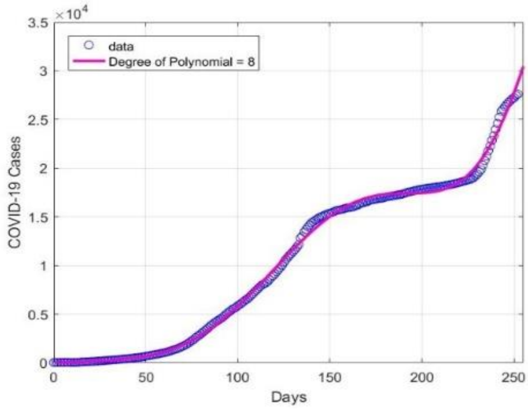

Figure 18

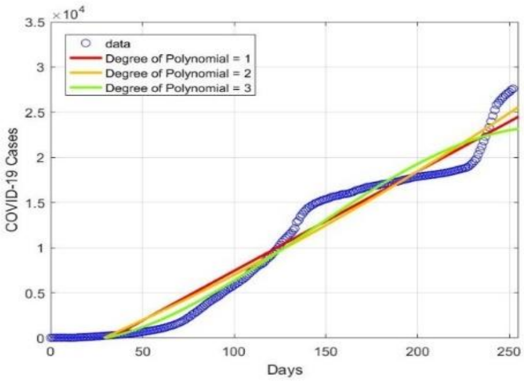

Figure 19

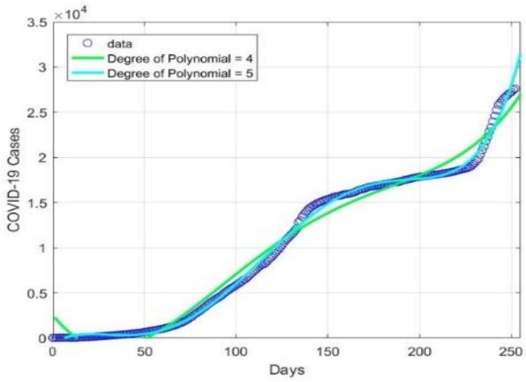

Figure 20

Conclusion:

The spline curve method has evolved into a foundational technique in mathematical modeling and data interpolation. Its historical development and widespread applications underscore its significance in various scientific and engineering disciplines. As technology advances, the spline curve method continues to play a crucial role in the analysis and representation of complex data patterns. In conclusion, our analysis using the spline method across different degrees revealed varying degrees of effectiveness in fitting the data related to daily cured and COVID-19 positive patients. Degrees 1 to 4 showed suboptimal fitting for the actual cured patient data, while degrees 5 to 8 demonstrated improved accuracy, with degrees 7 and 8 yielding the most precise results. Similarly, for COVID-19 positive patient data, degrees 5 to 8 exhibited better fitting, with degrees 7 and 8 providing the most accurate representation of the actual data. These findings underscore the importance of selecting an appropriate degree in spline interpolation for reliable modeling and prediction of disease-related datasets. Furthermore, the identified optimal degrees (7 and 8) can serve as valuable insights for future analyses and decision-making in public health contexts.

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