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Logistic Approximations for Characterizing Novel Outbreak Patterns in the 2020 COVID-19 Pandemic

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Abstract: ***This study employs the logistic growth model to analyze COVID-19 pandemic mortality data across multiple countries. Daily death statistics from China, Iran, Italy, South Korea, Spain, and the United States were fitted to logistic functions to characterize outbreak dynamics. Based on current pandemic growth trajectories, our model predicts final death tolls of 3,277-3,327 in China, 2,035-2,107 in Iran, 120-134 in South Korea, 11,227-12,793 in Italy, and 6,217-7,405 in Spain. The analysis reveals distinct secondary outbreaks within individual countries, particularly Iran, China, and the United States. Among the studied countries, South Korea exhibited the lowest mortality growth rate (0.14701±0.00923), followed by China (0.16667±0.00284). Italy (0.22594±0.00599) and Spain (0.31213±0.02337) demonstrated the highest growth rates, with Iran's second wave reaching 0.37893±0.02712. This work was submitted to arXiv with data available through April 2020, and subsequent validation with modern data confirms the continued applicability of this technique for detecting multiple outbreak patterns throughout the extended pandemic period.***

Keywords: logistic growth model, COVID-19 mortality, secondary outbreaks, epidemiological modeling, pandemic prediction

1. Introduction

COVID-19 was first identified in Wuhan, Hubei Province, China, in November 2019 [1]. The infection rapidly disseminated across Asian countries before reaching other continents by early February 2020 [2]. The main modes of contagion are respiratory droplets and contact with contaminated surfaces, with the virus demonstrating remarkable persistence on various materials [3]. This characteristic facilitates global spread via transportation networks carrying both infected individuals and contaminated cargo. The disease exhibits heightened lethality among elderly populations and individuals with underlying health conditions [4].

Despite World Health Organization (WHO) recommendations for comprehensive testing of suspected cases, many countries adopted selective testing strategies. Additionally, authorities in some regions advised low-risk individuals to avoid seeking medical attention, resulting in substantial underreporting of infections. Consequently, case numbers across countries lack reliability due to varying testing methodologies and protocols. This disparity contributes to observed differences in COVID-19 mortality rates globally. However, death statistics present greater reliability, as post-mortem COVID-19 testing is routinely performed in most healthcare systems, providing more accurate mortality data and death dates.

2. Methodology

Data Sources and Processing

Mortality data were obtained from the World Health Organization database at the time of manuscript submission [5]. It is assumed in this study that government interventions do not significantly alter mortality growth rates during the study period.

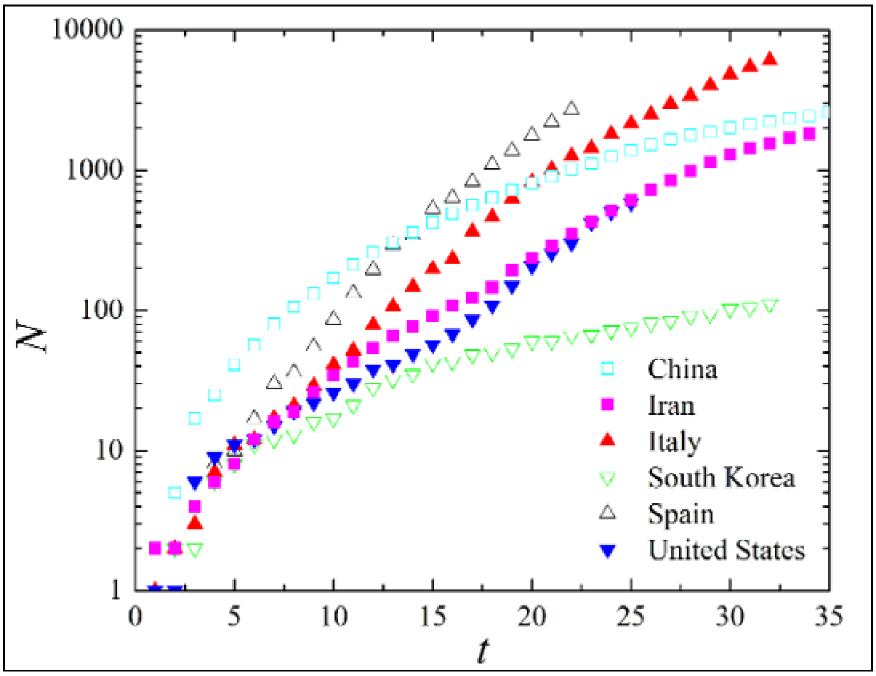

Figure 1: Cumulative total deaths, N, versus days since the first demise, t, for several countries.

3. Theoretical Framework

Population dynamics modeling has a rich history across physics, biology, and mathematics [6]–[9]. Epidemic modeling faces particular challenges during initial outbreak phases, as models typically assume continuous population fields. Furthermore, data reliability for small case numbers limits model-data agreement. Disease-specific factors, including population health status, transmission mechanisms, and environmental conditions, influence outbreak characteristics.

An often-overlooked factor in epidemic studies is the topology of population interaction networks [10]. While static agent-based models inadequately describe complex realities, hybrid dynamic-static approaches demonstrate that zero-order models provide reasonable approximations when dealing with large infected populations [11]–[13].

Multiple zero-order population growth models for epidemics have been proposed since Verhulst's foundational logistic model [14]–[17]. Recent work by Castorina and colleagues applied similar methodologies to infection data [18]. These models share common characteristics for determining population number N (deceased individuals in this context): presumed equilibrium K, growth rate r, and initial population $N_0 = N(t = 0)$. Parameter K represents the saturation capacity of deceased individuals, essentially the limit for the at-risk population. Growth rate r is expressed in units of day^{-1}.

The mortality growth rate depends on healthcare system capacity and at-risk population size:

Equation 1:

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right)$$

This differential equation yields a three-parameter function:

Equation 2:

$$N(t) = \frac{K}{1 + Ce^{-rt}}$$

where $C \equiv (K - N_0)/N_0$.

Equation 2 was fitted to WHO-reported data to extract K and r parameters for each country.

Data Analysis

Data processing and curve fitting were performed using Python programming language [19] with scipy.optimize simplex iterative methods [20], employing a minimum of 1000 iterations and convergence criteria of 10^{-9} for parameter estimation.

4. Results and Discussion

Single-Outbreak Countries

Italy: Despite declining daily mortality rates, equilibrium has not been reached. Model projections indicate concerning final totals of $K = 12{,}010.76 \pm 783.39$ deaths with growth rate $r = 0.22594 \pm 0.00599$.

Spain: While initially exhibiting higher growth rates than Italy, Spain's mortality acceleration has subsequently decreased (see Figure 2). Current projections suggest equilibrium at $K = 6{,}811.95 \pm 593.71$ deaths ($r = 0.31213 \pm 0.02337$).

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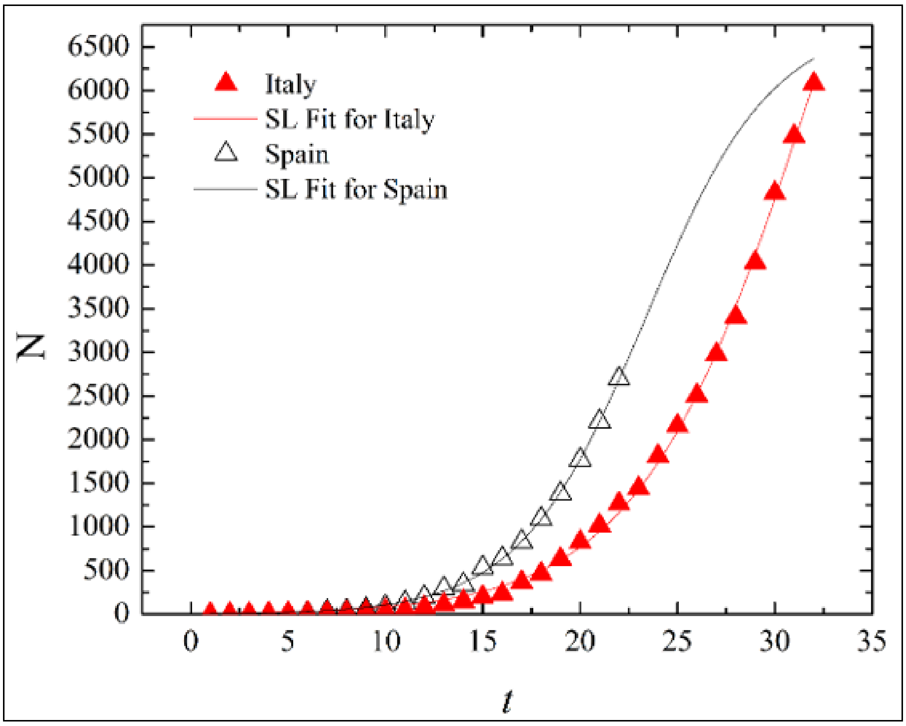

Figure 2: Cumulative total deaths, N, versus days since the first demise, t, for Italy and Spain. Although visually the growth rate of deaths in Spain appears to be higher than in Italy, the model's curve adjustments show that the equilibrium in Spain is lower than in Italy.

South Korea: Demonstrating the most effective pandemic response, South Korea achieved parameters of $K = 127.44 \pm 6.99$ deaths and $r = 0.14701 \pm 0.00923$. This success reflects comprehensive testing strategies, with the Korean government having tested more than 270,000 people by that time without implementing broad quarantine measures [21]. Using South Korea's more reliable 5.27% fatality rate for populations aged 65+ [22], and considering Lombardy's demographic composition (23.1% over 64 years among 10 million residents [23]), approximately 105,000 deaths would occur in Italy without treatment interventions.

Multiple-Outbreak Analysis

Geographic factors significantly influence outbreak patterns. Larger countries with greater territorial extent face higher risks of developing multiple epidemic centers, as new regions become infected independently.

Iran: Given Iran's substantial territory (1.648 million km²) compared to Italy (301,338 km²) and South Korea (100,210 km²), multiple outbreak centers were anticipated. The model confirms this hypothesis, with each center following distinct growth curves that sum to produce the national trajectory.

For multiple outbreaks, Equation 2 is modified to accommodate temporal delays (τ) between centers:

Equation 3:

$$N(t) = \frac{K}{1 + Ce^{-r(t-\tau)}}$$

Iran's secondary outbreak manifests clearly around day 19 (Figure 3). First outbreak parameters: $K = 857.97 \pm 598.19$ deaths, $r = 0.21497 \pm 0.01974$. Second wave parameters: $K = 1{,}214.93 \pm 36.42$ deaths, $r = 0.37893 \pm 0.02712$, with $\tau = 22.48 \pm 29.35$ days.

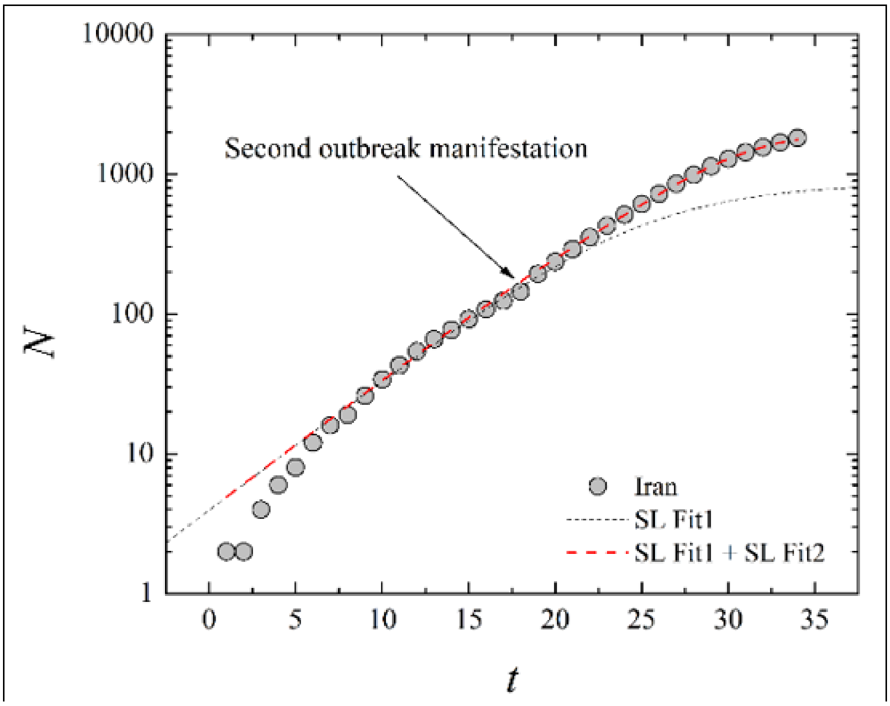

Figure 3: Cumulative total deaths, N, versus days since the first demise, t, for Iran. The data shows a clear manifestation of a second outbreak around the 19th day.

China: A behavioral shift occurs around day 39, suggesting a secondary outbreak outside Wuhan (Figure 4). Primary outbreak characteristics: $K = 3{,}170.76 \pm 40.10$ deaths, $r = 0.16667 \pm 0.00284$. Secondary outbreak parameters: $K = 103.795 \pm 13.62$ deaths, $r = 0.38478 \pm 0.6480$. Total projected deaths range between $3{,}277 - 3{,}327$, assuming no additional epidemic centers emerge.

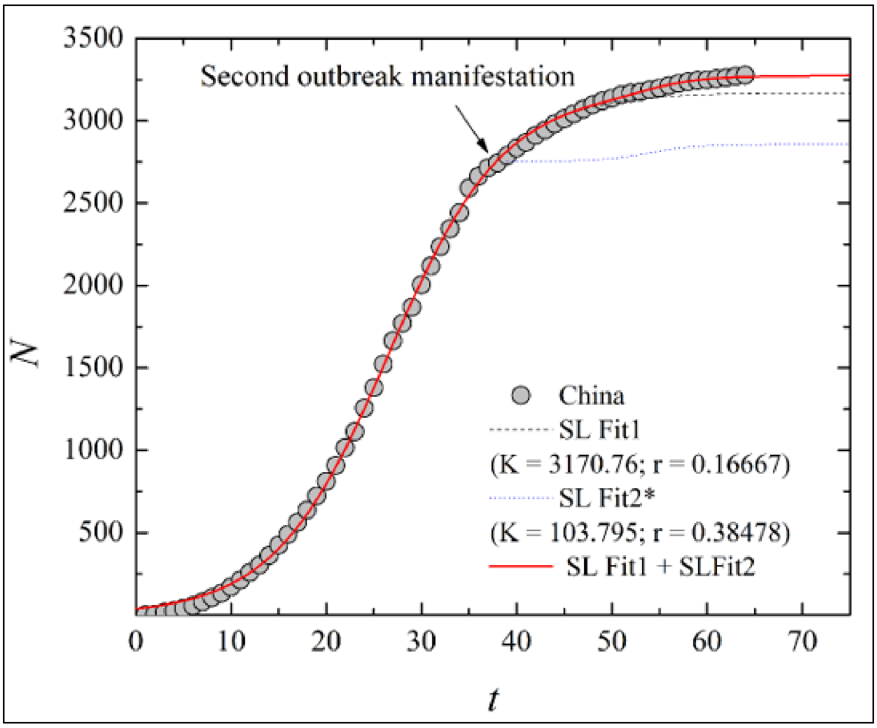

Figure 4: Cumulative total deaths, N, versus days since the first demise, t, for China. The data are better adjusted when we add two logistic curves. This shows that there may have been a second outbreak. The adjustment of the second outbreak in the graph is shown plus the data value for the thirty-ninth day for aesthetic effects.

United States: Mortality patterns suggest multiple outbreak centers, particularly in New York, Washington D.C., and California. Since infection spread is a geographic issue, accurate modeling through the logistic approach is not feasible at this stage due to the complexity of multiple simultaneous outbreaks.

Comparative Analysis

Table 1: Summarizes presumed equilibrium values and growth rates for all studied countries:

Country	Presumed Equilibrium (deaths)	r (day^{-1})
China	3,277-3,327	not defined*
Iran	2,035-2,107	not defined*
Italy	11,227-12,793	0.22594±0.00599
South Korea	120-134	0.14701±0.00923
Spain	6,217-7,405	0.31213±0.02337

*Multiple outbreak dynamics preclude single r-value definition

Epidemic control appears successful in China, South Korea, Japan, and Singapore during the study period.

5. Conclusions

This logistic model provides a simplified framework for describing epidemic mortality progression. Assumptions regarding fixed mortality growth rates hold validity only when healthcare systems remain unchanged or when disease evolution occurs rapidly, as potentially observed with COVID-19. Nevertheless, multiple proposed models for mortality growth follow equations analogous to Verhulst's formulation.

Successful data fitting across diverse countries demonstrates the logistic model's utility. The analysis confirms that countries with extensive territories are susceptible to multiple epidemic outbreaks, emphasizing the critical importance of georeferenced surveillance systems for defining regional equilibrium populations and growth rates.

This work was submitted to arXiv with data available through April 2020. With updated COVID-19 data from Our World in Data [24], numerous large and small outbreaks have been verified to this day using the technique presented here. The difficulties continue to be the correct reporting of deaths properly diagnosed as COVID-19, which remains a persistent challenge for accurate epidemic modeling and surveillance.

With Europe, the Americas, Oceania, and Africa still confronting pandemic onset during this study period, our findings suggest that containment strategies successfully implemented by China and South Korea should be rigorously replicated where feasible to reduce mortality growth rates.

The model's ability to detect secondary outbreaks provides valuable insights for public health planning and resource allocation. The continued applicability of this logistic approach throughout the extended pandemic period demonstrates its robustness as a tool for real-time epidemic monitoring, despite ongoing challenges in data quality and reporting consistency across different healthcare systems globally. Future research should incorporate more sophisticated network models and demographic factors to enhance predictive accuracy across diverse geographic and social contexts.

References

[1] Z. Wu and J. M. McGoogan, "Characteristics of and important lessons from the coronavirus disease 2019 outbreak in China: summary of a report of 72 314 cases from the Chinese Center for Disease Control and Prevention," *Jama*, 2020.

[2] W. H. Organization and others, "Coronavirus disease 2019 (COVID-19): situation report, 51," 2020.

[3] M. Negahdaripour, "The Battle Against COVID-19: Where Do We Stand Now?," *Iran. J. Med. Sci.*, vol. 45, no. 2, pp. 81–82, 2020.

[4] R. Porcheddu, C. Serra, D. Kelvin, N. Kelvin, and S. Rubino, "Similarity in Case Fatality Rates (CFR) of COVID-19/SARS-COV-2 in Italy and China," *J. Infect. Dev. Ctries.*, vol. 14, no. 02, pp. 125–128, 2020.

[5] WHO, "Coronavirus disease (COVID-2019) situation reports." 2020.

[6] T. R. E. Southwood and H. N. Comins, "A synoptic population model," *J. Anim. Ecol.*, pp. 949–965, 1976.

[7] C. Song, S. Havlin, and H. A. Makse, "Origins of fractality in the growth of complex networks," *Nat. Phys.*, vol. 2, no. 4, pp. 275–281, 2006.

[8] A. Hastings, *Population biology: concepts and models*. Springer Science & Business Media, 2013.

[9] A. Martin and S. Ruan, "Predator-prey models with delay and prey harvesting," *J. Math. Biol.*, vol. 43, no. 3, pp. 247–267, 2001.

[10] Z. Wang et al., "Statistical physics of vaccination," *Phys. Rep.*, vol. 664, pp. 1–113, 2016.

[11] M. Barthélemy, A. Barrat, R. Pastor-Satorras, and A. Vespignani, "Dynamical patterns of epidemic outbreaks in complex heterogeneous networks," *J. Theor. Biol.*, vol. 235, no. 2, pp. 275–288, 2005.

[12] R. Pastor-Satorras and A. Vespignani, "Epidemic dynamics and endemic states in complex networks," *Phys. Rev. E*, vol. 63, no. 6, p. 66117, 2001.

[13] J. Zhou et al., "Epidemic reemergence in adaptive complex networks," *Phys. Rev. E*, vol. 85, no. 3, p. 36107, 2012.

[14] C. Viboud, L. Simonsen, and G. Chowell, "A generalized-growth model to characterize the early ascending phase of infectious disease outbreaks," *Epidemics*, vol. 15, pp. 27–37, 2016, doi: https://doi.org/10.1016/j.epidem.2016.01.002.

[15] D. Jiang, Q. Liu, N. Shi, T. Hayat, A. Alsaedi, and P. Xia, "Dynamics of a stochastic HIV-1 infection model with logistic growth," *Phys. A Stat. Mech. its Appl.*, vol. 469, pp. 706–717, 2017.

[16] Y.-H. Hsieh and C.-K. Hsiao, "Predator--prey model with disease infection in both populations," *Math. Med. Biol. a J. IMA*, vol. 25, no. 3, pp. 247–266, 2008.

[17] V. Pierre-François, "Notice sur la loi que la population poursuit dans son accroissement," *Corresp. Math. Phys*, vol. 10, pp. 113–121, 1838.

[18] P. Castorina, A. Iorio, and D. Lanteri, "Data analysis on Coronavirus spreading by macroscopic growth laws," Mar. 2020.

[19] G. van Rossum and F. L. Drake, "Python 3 Reference Manual," CreateSpace, Scotts Valley, CA, 2009.

[20] P. Virtanen et al., "SciPy 1.0: fundamental algorithms for scientific computing in Python," *Nat. Methods*, vol. 17, no. 3, pp. 261–272, 2020.

[21] D. Normile, "Coronavirus cases have dropped sharply in South Korea. What's the secret to its success?" 2020.

[22] W. So, "Fatality rate of coronavirus (COVID-19) in South Korea as of March 16, 2020, by age group." 2020.

[23] W. So, "Age distribution of the population in Italy from 2002 to 2020." 2020.

[24] E. Mathieu et al., "Coronavirus Pandemic (COVID-19)," *Our World in Data*, 2020. [Online]. Available: https://ourworldindata.org/coronavirus