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Understanding Pandemics: A Systematic Review of Epidemiological Modelling of the COVID-19 Pandemic in Southern Africa

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Abstract

The (re-)emergence of global health crises, such as COVID-19, has highlighted the importance of epidemiological modelling. The aim of this review paper was to give an overview of the epidemiological models which inform policy and action that support the planning and COVID-19 response efforts in Southern Africa. Fourteen relevant records were reviewed. The process of identification followed the PRISMA approach. The review showed a diversity of models used, differing in type, form, use and scope. No single model can explain all the aspects of the disease; each should be interpreted within the context of its assumptions. While modelling has informed policy, it has occasionally been misused to justify decisions. Despite this, modelling has been vital in fighting against COVID-19. Also, in spite of challenges in forecasting future pandemics, predictive modelling provides a precautionary guide. Therefore, there is a need to increase infectious disease modelling literacy among users.

Keywords: *COVID-19, SIR, SEIR, Epidemiological Modelling, Pandemics.*

Introduction

In March 2020, the World Health Organisation (WHO) declared the coronavirus disease (COVID-19) outbreak a global pandemic. The disease is caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), novel species of the *betacoronavirus genus* (Paulo, Fontinele, & Cintra, 2020) of the family, Coronaviridae. The novel virus was first discovered in Wuhan (China) in December 2019. From there, the virus spread to other Asian countries and, consequently worldwide, causing a public health emergency of international concern whose declaration ended in May 2023. Ranked against other epidemics, COVID-19 was rated as the fifth deadliest.

Since the onset of the pandemic, the virus has been evolving with several variants being detected in diverse countries: alpha, B.1.1.7 (U.K.), Beta, B.1.351 (South Africa), Delta, B.1.617.2 (India), Gamma, P.1 (Brazil) and Omicron, B.1.1.529 (Botswana). Such variants were

associated with varied infection rates and, hence, characteristic epidemic waves (peaks).

Many interventions have been implemented in Africa in order to contain the spread and reduce associated mortality and morbidity rates. These interventions involved travel restrictions, flight and events cancellations, physical or social distancing, mandatory wearing of masks, among others. However, authorities have been issuing sometimes conflicting policy statements and advice about some of these intervention strategies, owing to little knowledge. In such times of uncertainty, quantitative methodologies have sometimes been relied upon to invoke decision-making on the level of risk and safe interactions in various settings (Nyabadza, Chirove, Chukwu & Visaya, 2020). In the context of epidemics, predictive mathematical or infectious disease modelling has been relied upon in assessing disease dynamics such as populations at risk, reproduction numbers and evaluating effectiveness of intervention measures such as pharmaceutical and non-pharmaceutical interventions. Though informative, mathematical modelling has been linked with incomplete available knowledge due to a lack of analogous experimental measures (Mushanyu, Madubueze, Chukwu, Chazuka, Mudzingwa & Ogbogbo, 2022). These models may be based on real data or sometimes on hypothetical scenarios.

Mathematical models on COVID-19 pandemic can be categorised into early/initial, mid- and late epidemiological models, depending on the time series of COVID-19 progression or evolution. Shankar et al (2021) undertook a systematic review on predictive mathematical models of the COVID-19 pandemic and analysed the initial epidemiologic models on the disease from January to June 2020. The current review sought to analyse predictive epidemiological models published from the year 2020 to 2023, covering the whole spectrum of such models, that is, initial, mid- and late epidemiological models. However, the review did not attempt to classify these as such.

Several models describing various aspects of the COVID-19 epidemic have been proposed. However, the magnitude and complexity of such models often evades reality and would-be consumers of the information are sometimes left, generally, in a messy situation. The current review focused mainly on disease transmission dynamics regardless of whether they are institutionalised or not. It was aimed at providing a glimpse of the diversity of mathematical or infectious disease modelling that invoked decision-making during the COVID-19 pandemic in Southern Africa.

Methods

In this systematic review, quantitative empirical studies were assessed. The studies used a variety of designs to model infection rates, disease transmission dynamics as well as evaluate effects of intervention strategies during the COVID-19 outbreak in Southern Africa.

Figure 1 shows the structure for the search and screening strategy. Records search and identification were performed through database searches. Backwards and forwards citation search was also done to identify additional records. The search was not only limited to journals indexed in certain databases such as PubMed, Scopus or Web of Science.

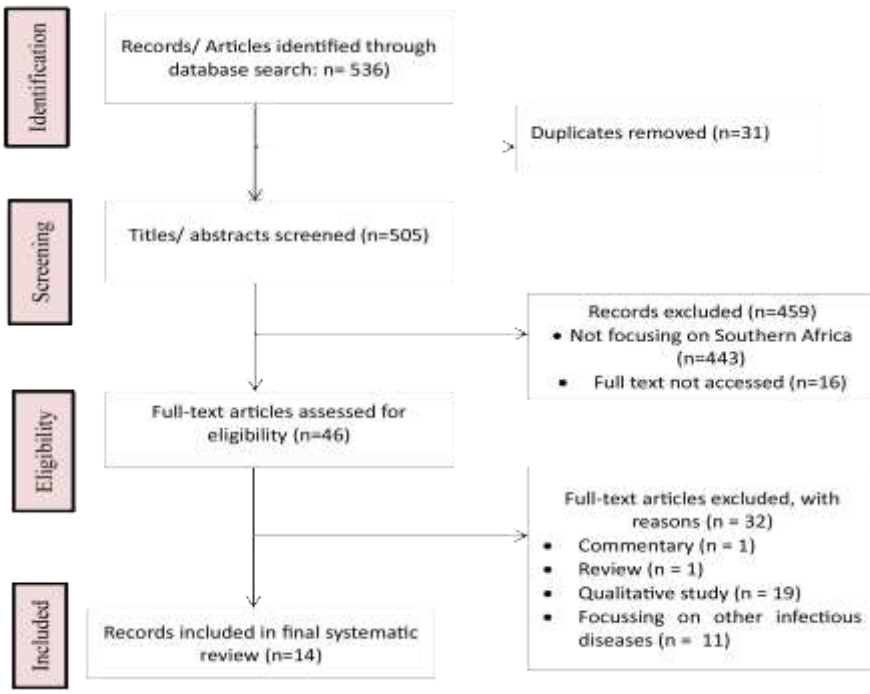

Figure 1: Search and screening strategy using PRISMA approach

The process of records identification and screening followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) approach (Moher et al., 2015) as shown in Figure 1. The articles considered in this review included case-control, cross-sectional as well as cohort (prospective and retrospective) studies published between the years 2020 and 2023. The publication period was chosen so as to include publications that were motivated or driven by the evolution of the pandemic.

The search strategy was aimed at identifying publications that mentioned the following mesh terms or concepts in their titles, abstract and/or keyword lists: SARS, OR Severe Acute Respiratory Syndrome, OR COVID-19, OR Coronavirus, OR novel Coronavirus, OR 2019-nCoV, OR SARS-CoV-2, Epidemiological Modelling, OR Mathematical Modelling, OR Infectious Disease Modelling, OR Transmission Dynamics, Southern Africa, OR Zimbabwe, OR South Africa, OR Mozambique, OR Angola, OR Zambia, OR Lesotho, OR Swaziland/ Eswatini, OR Namibia, OR Madagascar, and OR Botswana. Some adaptations to key words were made during literature search, and such adaptations were based on their definitions as previously used in similar studies. Because of an anticipated diversity of articles, a data extraction form could not be developed before-hand. However, filters were used such that publications from 2020 to 2023 and focusing on Southern Africa could be retrieved.

For the inclusion criteria, the following were considered:

- Empirical studies using quantitative methodologies;
- Studies in English language, or in other languages with an English translation; and
- Studies focusing on COVID-19, transmission and dynamics and effects of certain interventions.

The exclusion criteria used were:

- Studies using qualitative methodologies;
- Studies in other languages and without an English translation;
- Studies not focusing on Southern Africa; and
- Reviews, meta-analyses, commentaries, books or book chapters, theses and editorials.

As a result, only those empirical studies meeting the inclusion and exclusion criteria were considered for the final analysis.

The titles and/or abstracts of all the identified publications were screened for eligibility, and only those meeting the inclusion and exclusion criteria were subjected to full-text eligibility assessment. Some publications were excluded based on limited relevance. These included records such as commentaries (n = 1), reviews (n = 1), qualitative studies (n = 19), and focusing on other infectious disease dynamics (n = 11). As shown in Figure 1, only eligible publications, meeting all the screening criteria (n = 14), were selected for the final review.

The publications were coded and analysed on the basis of author, year, country, model formulation, data sources and model fitting, parameter estimation, simulation, and sensitivity analyses. Methodological care of the selected publications was also analysed according to the principles set out in the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) (Vandenbrouke et al., 2007). It contains 22 items that include title and abstract, introduction (background and objectives), method (study design, setting, participants, variables, measurement, bias, study size, quantitative variables and data analysis), results (participants, descriptive data, outcome data, main results and other analyses), discussion (key results, limitations, interpretations, and generalizability) and other information (funding). The rationale and meaning of each item were used as outlined by Vandenbrouke et al. (2007) in the STROBE statement. STROBE facilitates the critical appraisal and interpretation of cohort, case-control and cross-sectional studies. In this review, each publication was assessed against the provisions of the STROBE statement.

Results and Discussion

The search strategy yielded 536 records. The screening of titles yielded 505 abstracts, of which 459 records did not meet the eligibility

assessment criteria. Finally, 14 articles were analysed in this systematic review.

The majority of the articles (86%) contained predictive epidemiological modelling based on the Susceptible, Exposed, Infectious and Recovered (SEIR) model. One article (7%) was based on the Susceptible, Infectious and Recovered (SIR) model, while one article (7%) was based on other mathematical models, as shown in Table 1. According to Shankar et al. (2021), epidemiological or compartmental models divide the population into various groups or compartments whose movement from one compartment to another can be explained using differential equations. These models can either be stochastic or deterministic. In this review, only 29% of the authors exclusively identified their models as deterministic, while the others did not identify articles as either stochastic or deterministic. In modelling the dynamics of infectious diseases, epidemiological models take into account the transmission dynamics of the disease as well as having the ability to include several variables affecting the transmission dynamics. These other variables include behavioural and disease factors like re-infection, pharmaceutical and non-pharmaceutical interventions like quarantine, isolation, and vaccination. As observed, all the articles reviewed were based on real data of either the infected, recovered and/or deaths.

The distribution of the included articles is as shown in Table 1. Most of the analysed articles were predictive models for South Africa (64%), followed by Zimbabwe (14%). While most articles presented models focusing on a single country (93%), one article focused on multiple countries (7%). Of the included articles, two articles (14%) explicitly modelled the 2019 nCoV-2 variants: one article modelled a single variant (Omicron), while the other modelled three variants (Beta, Delta and Omicron). While the articles considered in this review cover the whole spectrum of COVID-19 evolution in Southern Africa, the articles were neither classified as long-term/ short-term nor early/late prediction models.

Table 1: Analysis of Articles Included in the Systematic Review

Author (Year), Country	**Model Formulation**	**Data Source/ Model fitting**	**Numerical Simulation**	**Determine DFE/ Ro**	**Sensitivity Analysis Method**
1. (Garba, Lubuma & Tsanou, 2020), South Africa.	SEAIJRP; P being contaminated environment: stools, droplets	Mortality data for S. Africa: March 2020 – June 2020 (3 months)	Yes	Yes	Partial Rank Correlation Coefficient (PRCC)
2. (Assan & Nyabadza, 2023), South Africa	SEI_aI_sR	COVID-19 data, South Africa (Python)	Yes	Yes	Not explicit
3.(Nyabadza, Chirove, Chukwu & Visaya, 2020), S. Africa	SEIR, incorporating immigration	COVID-19 data, South Africa (Matlab)	Yes	Yes	Latin Hypercube Sampling (LHS)
4.(Nyabadza, Mushanyu, Mbogo & Muchatibaya, 2023), S. Africa	$SEI_dI_uR_dR_u$, incorporating human behaviour	COVID-19 data from first wave, Nelder-Mead simplex algorithm	Yes	Yes	Jacobian sMatrix
5. (Paulo, Fontinele & Cintra, 2020), Mozambiq ue	SEIRD Included compartment D, death	Infected/ case data, Mozambique. Non-linear Least squares Method (Python)	Yes	Yes	Not explicit
6. (Mushanyu, et al, 2022), Zimbabwe.	$SQ_1Q_2EII_dR$ D	Zimbabwe COVID-19 data 30 March 2020-30 June 2020	Yes	Yes	Normalised forward sensitivity index; PRCC
7. (Ndlovu, Moyo & Mpofu, 2022), Zimbabwe	SVI_aI_sR	COVID-19 data, Zimbabwe	Yes	Yes	Jacobian Matrix
8. (Mukandav Nyabadza, Malunguza, Shiri & Musuka, 2020), South Africa	SEIR, with ire, vaccination potential Cuadros,	COVID-19 data, South Africa Markov Chain Monte Carlo (MCMC)	Yes	Yes	Not explicit

9. (Khan & $SEI_aI_SI_OR$, Atangana, incorporating 2022), vital South dynamics Africa		COVID-19 case data from South Africa,	Yes	Yes	Next Generation Approach
10. (Gatyeni, Chukwu, Chirove, Fatmawati & Nyabadza, 2022), South Africa	SEI_uI_dR, Included active screening	COVID-19 case data from South Africa,	Yes	Yes	Not explicit, stated elsewhere
11. (Kinyili, Munyakazi & Makhtar, 2021), S. Africa.	$SS_VEI_SI\Lambda R$;	Cumulative positive case data for South Africa	Yes	Yes	Maximum Likelihood
	Incorporate vaccination		Next Generation Matrix		Estimation (in fitR package)
12. (Yu, Liu, Zhao & He, 2022), South Africa	SEIHRD & COVID-19 EIHRD deaths, South Africa Plug-and-play Likelihood-based inference framework		Yes Negative Binomial	Yes	Not explicit
13. (Amouzouvi, Assamagan, Azote, et al, 2021), African Countries	SIDARTHE	COVID-19 data, South Africa, Zambia, Madagascar, Mozambique	Yes	Yes	Not explicit
14. (Mulenga, 2020), Zambia	Data Driven Mathematical Model	COVID-19 data from Zambia Multiple regression analysis	N/A	N/A	N/A

From Table 1, most of the reviewed articles used the modified SEIR model because of its ability to model several variables. However, it is not without limitations, especially when estimating parameter values. For instance, as pointed out by Nyabadza, Chirove, Chukwu and Visaya (2020), model parameters need to be measured appropriately as they vary according to demography and geographic region. As such, interpretation and use of results of mathematical modelling should be done within the confines of the circumstances under which the model was formulated. The various modifications to the SEIR and SIR models used by articles reviewed in this analysis are as shown in Table 2.

Table 2: Expressions for the Population Total in Modified SEIR and SIR Models

Author (Year)	Population Total, N(t)
1. (Garba, Lubuma, & Tsanou, 2020)	N(t)=S(t)+E(t)+A(t)+I(t)+J(t)+R(t), (+P); Susceptible, S; Exposed, E; Asymptomatic infectious, A; symptomatic infectious, I; isolated/ hospitalised, J; recovered, R; P being contaminated environment: stools, droplets
2. (Assan & Nyabadza, 2023)	N(t)=S(t)+E(t)+Ia(t)+Is(t)+R(t) Susceptible, S; Exposed, E; asymptomatic & undiagnosed, confirmed positive, Ia; symptomatic & confirmed positive, Is; recovered, R
3. (Nyabadza, Chirove, Chukwu & Visaya, 2020)	N(t)=S(t)+E(t)+I(t)+R(t), No vital dynamics; incorporating immigration and analysed effect of social distancing
4. (Nyabadza, Mushanyu, Mbogo & Muchatibaya, 2023)	N(t)=S(t)+E(t)+Id(t)+Iu(t)+Rd(t)+Ru, Susceptible, S; Exposed/ non-infectious, E; detected, infectious, Id; undetected, infectious, Iu; recovered, recorded, Rd; recovered, unrecorded, Ru. Incorporating human behaviour No disease-induced death, but natural birth and death
5. (Paulo, Fontinele & Cintra, 2020), Mozambique	N(t)=S(t)+E(t)+I(t)+R(t)+D(t) Included compartment D, death Assumed homogeneously distributed population

As can be seen from Table 2, no single model is able to cater for all aspects of a disease and its transmission dynamics. As such, each model attempted to depict a particular attribute. Some articles modelling early COVID-19 assessed effects of non-pharmaceutical interventions like social distancing. The early models were associated with limited knowledge on the natural disease history as well as poor quality data associated with case underreporting and low rates of COVID-19 testing which missed some other cases.

Some assumptions upon which the models were based, like homogenously distributed population (Paulo, Fontinele, & Cintra, 2020), non-inclusion of vital dynamics, like natural births and deaths (Nyabadza, Chirove, Chukwu & Visaya, 2020) and non-disease-induced deaths (Nyabadza, Mushanyu, Mbogo & Muchatibaya, 2023), did not depict reality.

The available literature shows that the complexity of the models increased as the COVID-19 pandemic progressed and more knowledge about the disease increased. However, the more complex a model becomes, the less useful it becomes. Though associated with

uncertainties in making predictions, James, Salomon, Buckee and Menzies (2021) state that mathematical modelling is likely to remain prominent as new policy questions arise. As such, careful evaluation of the results of modelling is critical in order to reap the benefits associated with epidemiological modelling in the face of emerging and re-emerging infectious diseases such as COVID-19.

Conclusion

The review showed that there was a diversity of models used and these differed in their formulations, use and scope. The formulations and thrust depended mostly on the phase of the pandemic. Earlier models were simple, and later ones complex as more information and knowledge about the history of the disease improved. It was also seen that no single model can explain all aspects of the disease; each should be interpreted within the context of its underlying assumptions. Though modelling has shown a capacity to inform policy, in some scenarios they have been misused to justify decisions. While single models can be biased, their limitations can be solved by benchmarking and validation of the said model(s) by multilevel collaborations. Use can also be made of COVID-19 ensemble models. Nevertheless, despite all the limitations, modelling has played important roles in the fight against COVID-19 and other infectious disease pandemics. Though there are challenges in forecasting of future pandemics, predictive modelling provides a pre-cautionary guide. As such, future research should focus on enhancing model adaptability for emerging pandemics and endeavor to increase literacy in infectious disease modelling among users.

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