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# MARITIME DISEASE SPREAD MODELING USING SUSCEPTIBLE-INFECTED-RECOVERED (SIR) MODELS

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**Abstract**

The COVID-19 (C-19) epidemic aboard the Diamond Princess Cruise Ship offers a unique chance to assess its initial transmissibility through the basic reproduction number (Ro) and the efficacy of quarantine strategies. The research formulated a standard dynamic equation-based Susceptible-Infected-Recovered (SIR) framework with Bayesian foundations to calculate the primary variable of Ro, defined by transmission values, incubation duration, and recovered rate. The Probabilistic Markov Chain Monte Carlo (MCMC) estimate approach addressed the uncertainty factors arising from the C-19 epidemic in a few individuals on a cruise vessel. The expanded stratified SIR framework was presented to clarify the heterogeneity in communication routes based on the deck levels of customers and crew members. The total model projected Ro to be as high as 6.75. The complete duration of the pandemic without restrictions was roughly 48 days, culminating in a peak one month after the index incidence. The partial confinement method decreased the number of affected travelers by 64%. The deck-specific SIR approach revealed the variety of R estimations for each board. The projected Ro values were 5.25 for guests, primarily due to within-deck delivery, and 2.5 for crew members, predominantly from between-deck communication. Modeling the dynamics of C-19 on the cruise vessel offers insights into prompt evacuations, early loneliness, and confinement, while clarifying the relative impacts of various dissemination modalities using the deck-stratified SIR framework.

**Keywords – Disease Spread, Susceptible-Infected-Recovered, Maritime, COVID-19**

## 1. INTRODUCTION

The COVID-19 (C-19) pandemic, which is disrupting healthcare systems globally, has been triggered by infections with the severe acute respiratory syndrome coronavirus 2 (CoV-2). Numerous phylogenetic analyses have identified the ancestor of this zoonotic virus, as well as the probable hosts and amplifying species, particularly among mammals [1]. The initial report of C-19 infection occurred in December 2019 in China. The global proliferation CoV-2 was unavoidable due to its facile transmission via droplets, ostensibly low fatality rate, and significant prevalence of asymptomatic cases (≥16.2% of affected individuals).

Within three months, 62% of nations reported C-19, notably across Europe. C-19 illness was recorded throughout North America, followed by Brazil, Ecuador, and Chile one week later. The lethality of C-19 has been put at 4-7%, with fatality rates ranging from 1-2.8%, with severe illness occurring in at least 5.3% of confirmed cases. The predicted recovery period varies from 8 to 12.4 days, contingent upon many conditions. The Ecuadorian Ministry of Public Health announced the initial case of C-19 in February 2020. An Ecuadorian woman traveled from Guayaquil to Spain on an airplane, where a welcoming group greeted her [2]. More instances emerged near the northeast and southern boundaries, probably from Colombia and Peru. As of early June, official data indicated at least 44.2k confirmed instances, predominantly among those aged 21 to 62 years, with a morbidity rate of 5 to 8.1% and a fatality rate of less than 2%.

Mathematical designs, such as the Susceptible, Infected, and Recovered (SIR) model, are employed to forecast various scenarios about epidemiological components and potential results to evaluate epidemic propagation [3][20]. The replication number (Ro) estimates the potential for individual viral transmission. The actual reproduction amount (Re or Rt) denotes the quantity of infected individuals within a specific time frame, contingent upon the basic Ro. The susceptible proportion (Fso) considers the proportion of infected individuals in an epidemic. These indicators illustrate the correlation between an individual and a virus, facilitating forecasts and evaluating repercussions at a particular time [9].

The C-19 outbreak aboard the Diamond Princess Cruise (DPC) offers a unique chance to analyze its initial transmission and propagation through four distinct epidemic-related features [4]. The terms susceptible, interaction, dissemination, and infected period are explicitly delineated based on a specific cohort of worldwide passengers and personnel residing at various deck levels within the confined environment of this vessel [10][19].

Secondly, this communication mode within the secluded setting of the cruise ship facilitates robust human-to-human community-based infections in close quarters, differing from transmission modes observed in households or hospitals, while evaluating the spread of this newly arising infectious illness [5][17]. The third point is that the infected people on board comprise multinationals, providing a clearer understanding of C-19's transmission among different ethnic groupings. The fourth point is that modeling the variation of distribution across various deck quantities with travelers and crew provides insight into the relative contributions of various dissemination options, such as aerosols and fomite delivery, by evaluating whether the primary route of transmission occurs using within-deck or between-deck communication [11]. Based on these four features, three unresolved concerns about the manner of transmission aboard the cruise ship are presented. Can the research assess and forecast the epidemic curve to establish prompt containment strategies and flight protocols? What is the efficacy of containment procedures for confinement and quarantine for sick travelers before escape? What is the primary mode of infection that caused the C-19 epidemic aboard the cruise ship? Addressing these three inquiries is essential for determining the planning and implementation of protective measures for upcoming cruise ships vulnerable to the epidemic [12]. Addressing these three inquiries necessitates formulating a computational framework to estimate the fundamental reproduction number of the outbreak aboard a cruise vessel.

## 2. BACKGROUND

### 2.1 Information on the epidemic aboard the DPC liner

The information regarding the journey of the DPC, the documented number of verified instances, and the isolation procedures was obtained from freely available sources, such as the DPC web page of Carnival Corporation and the web page of the Ministry of Health. Auxiliary data sources, comprising general media, academic news, and online descriptions, were utilized to verify case counts, quarantine precautions, and evacuation procedures following the epidemic aboard the DPC. A retrospective observational method was used to assess the spread of C-19 during the epidemic [6][13].

### 2.2 Epidemic on the DPC

The DPC set sail from Yokohama in January 2020. The total subjects was 3.8k, comprising 2.7k travelers from eleven nations and 1.1k crew members aboard the DPC. The epidemic originated from a traveler from Hong Kong who participated in part of the cruise and landed in January 2020 [16]. The incident was verified as a C-19 case by testing in a laboratory. The DPC has been grounded at Yokohama port since its arrival in February 2020. After the index case, 11 C-19 instances were documented on February 6th, 2020, signaling the epidemic that resulted in 762 cases in the following weeks. As of February 28th, the C-19 epidemic on the DPC has resulted in six fatalities [14].

The variability in CoV-2 dissemination by the deck was assessed using information on the overall number of C-19 instances up to February 15th, along with summed data regarding the placement of C-19 instances between travelers and crew on every level during the initial phase of the C-19 outbreak on the DPC [7].

### 2.3 Mitigation Strategies for C-19 Dissemination on the DPC

During the isolation procedure, personal protective equipment was supplied to crew workers. Passengers and team members were directed to self-monitor their body temperatures. Subjects exhibiting a body temperature over 38.4 degrees Celsius or manifesting any sickness were directed to the ship's medical facility, where medical treatments and tests for C-19 were conducted.

Several crew members remained to provide necessary yet restricted services during quarantine to sustain the ship's activities [8]. This symptom-based strategy started when the ship docked in Yokohama on February 7th. Beginning February 1st, the progressive enhancement of laboratory resources allowed quarantine officials to methodically administer tests based on testing capabilities, covering asymptomatic travelers starting February 16th.

## 3. PROPOSED MARITIME DISEASE SPREAD MODELING USING SIR

### 3.1 Assumptions

Several presumptions have been established. Efforts have been taken to ensure that the incidence of reinfections is minimized in the estimation. The following are the presumptions:

- A significant delay in healing occurs, lasting 28 days.
- The period of incubation was estimated to be 6 days.
- The model disregards social separation and protection, attributing an identical infection likelihood to everyone.
- Some infections have been documented due to insufficient testing, incorrect diagnosis, or asymptomatic cases.
- Diseases and cures are not documented on the day of their occurrence.
- There is no departure from, or emigration to, an area of interest.
- The model presupposes a uniform population size, devoid of social structure (e.g., a comparable number of inhabitants per home).

### 3.2 The Prototype

The approach is founded on the compartmental SIR structure (Fig. 1), distinguishing between first and subsequent infections, culminating in a 6-state paradigm (susceptible, infected, recovered, attacked [two or more times], healed [two or more times], and died). Daily infection and mortality figures were sourced from national data (as previously outlined).

Recovery statistics were utilized when accessible; alternatively, recoveries were estimated using a 30-day lag duration, with the total amount of recovery reflecting those who survived the 30-day healing period. Persons classified as "recovered" were randomly picked from the people of the regions 30 days earlier, “infected persons from the communities of the regions 6 days earlier (accounting for the incubating time), and “deceased” individuals from the communities of the regions 1 day earlier.

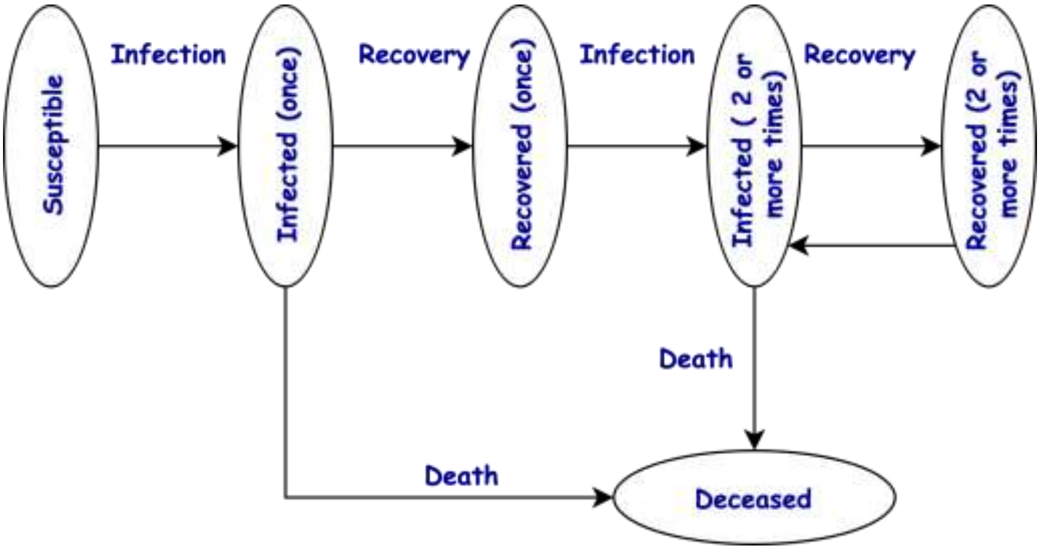

Fig. 1. Workflow of the SIR model

The simulation presumed that every condition's disease rates, recuperation, and mortality were independent of the number of prior viruses a host had experienced. The initial number of vulnerable individuals, N, was defined as the demographics of the area of interest. Following the tally of diseases, turnarounds, and fatalities for a day, the duration of the experiment was incremented by one, t → t + 1, up to Emax. The experiment was conducted 10,000 times to get expected values and variances for the count of persons identified as recurrent.

By aggregating the cases of individuals afflicted (two or more instances), healed (two or more instances), and dying (after two or more illnesses) after the simulations, the research derived a figure of the anticipated number of recurrence This figure denotes the entire population that has experienced the infectious condition (two or more occasions) by the conclusion of the experiment. Unless specified otherwise, the models utilized have a mean recuperation duration of 30 days, as this exceeds the mean recovery period indicated in the Expedition assessment of C-19.

## 4. RESULTS

Three estimating approaches were applied to the daily recorded instances to get the transmission factor and Ro for the C-19 epidemic aboard the DPC. Using the deterministic technique, the Ro and propagation coefficient (ß) were calculated at 5.3 and 0.8 each day, respectively, based on instances up to February 19, 2020. The value of 0.78/day represents the transmission factor, which considers immediate changes in the SIR framework as illustrated in a sequence of differential equations, in opposition to the mean rate of 0.3/day for C-19 occurrences up to February 18. The research utilized the Bayesian SIR framework to calculate the spreading coefficient, considering the dynamic fluctuations in the counts of infectives, exposed, infected, and recovering individuals. The maximum likelihood estimations for Ro and Β were determined to be 5.43 and 0.78 per day, respectively. The numbers obtained from the Bayesian Equation-based SIR framework were 5.8 and 0.8/day, respectively. The point estimations of Ro and ß were consistent across the three estimating techniques.

Consistent findings were obtained during the reported pandemic at several periods, with the calculated Ro fluctuating between 5.6 and 5.8, accompanied by overlapped 93% credible intervals. The Bayesian expression-based SIR model exhibited a commendable match utilizing data before February 21, 2020.

Despite the similarity of point estimations across the three techniques, the deterministic strategy failed to account for the unpredictability of the three factors. The method accounted for the unpredictability of the transmission factor, neglecting the rate of regeneration and incubation duration due to identifiability issues found while concurrently estimating all three variables. Both nuisance variables (recuperation rate and incubation duration) were treated as fixed figures. In contrast, the primary variable of the dissemination factor was calculated using the Maximum Likelihood Estimation (MLE) approach. By obtaining valid assumptions for the recuperation rate and incubating duration, the Bayesian technique produced three-point estimations with the appropriate 95% credible intervals for the three variables.

This addresses the absence of a Confidence Interval (CI) for the ß and Ro utilizing the deterministic strategy, as well as the narrow CIs for both variables derived from the MLE method, in contrast to the broader 95% credible interval obtained through the Bayesian Markov Chain Monte Carlo (MCMC) technique, which accounted for the joint ambiguity of three variables.

The fitted scenarios for cumulative instances obtained from the Bayesian expression-based SIR approach, with the comprehensive fitted cumulative cases. According to the propagation factor derived from the empirical information between January 21st and February 20th, the projected total instances for February 21st are 635, closely aligning with the actual cumulative cases of 625.

The graphic figure depicting cumulative examples offers a clear, smooth picture. It illustrates the 95% anticipated credible period, effectively representing the joint ambiguity of the three variables in the posterior distribution over time. Fig. 2 illustrates the calculated curve of C-19 derived from the findings of MLE and the deterministic technique.

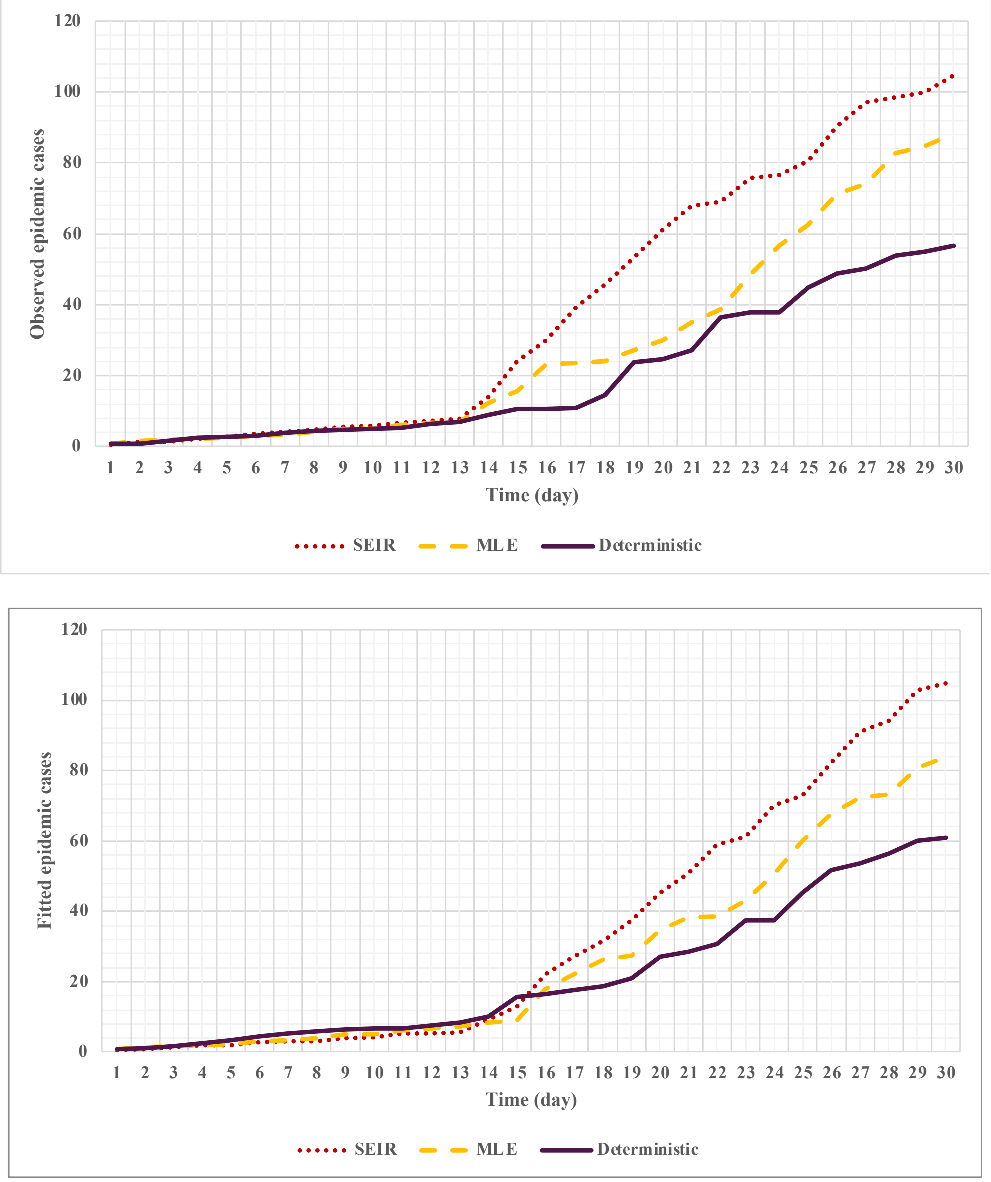

Fig. 2. Observed and fitted epidemic curve.

## 5. CONCLUSION

The fundamental reproductive number in this situation was calculated at 5.8, notably higher than the transmission of C-19, where the projected Ro ranges from 2 to 4. The exceptionally elevated value of Ro is consistently seen during the onset of many C-19 outbreaks, as well as the succeeding early pandemic waves in Europe and the USA. The elevated value of Ro contributes to the rapid increase in confirmed infections recorded over a brief timeframe, attributed to faster propagation exacerbated by a series of clustering incidents resulting from public gatherings. The current epidemics instigated by clustering occurrences involving long-term care institutions have similar trends. The virus's excellent transmission can significantly surge C-19 cases, placing immense strain on medical facilities and the economy.

The SIR approach does not account for a latent period. However, the SIR approach incorporates this aspect by adding the exposed (E) space, representing the delay from the vulnerable's exposure to the onset of spread in the infectious component (I). This update enhances the SIR algorithm's specificity in representing the C-19 epidemic aboard the DPC, considering the significant percentage of symptomatic and presymptomatic individuals.

The compartmentalized model facilitates the representation of immediate shifts using a sequence of differential equations governing the course of infectious diseases. The propagation coefficient obtained from the Bayesian SIR framework accounts for the dynamic fluctuations in the numbers of infectives, revealed, infected, and healed individuals. The value of 0.8 per day represents the transmission rate. The suggested Bayesian SIR model offers a flexible method to clarify the propagation of C-19 by utilizing collected information on cases reported with low precision. The proposed Bayesian structure and MCMC estimates enable data integration regarding disease features, such as incubation and dissemination periods, derived from previous research into the models through prior payments, accommodating the ambiguity of variables from those studies. The variables derived from the synthesis of noticed information alongside contemporary knowledge on disease patterns can illuminate the evolution of disease patterns, which is essential for using resources and formulating approaches to manage potential outbreaks on incoming passenger vessels.

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