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Evaluating infectious disease outbreak potential and mitigation effectiveness on cruise ships

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A R T I C L E I N F O

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A B S T R A C T

The cruise ship sector is a major part of the tourism industry, and an estimated over 30 million passengers are transformed worldwide each year. Cruise ships bring diverse populations into proximity for many days, facilitating the transmission of respiratory illnesses. The objective of this study is to develop a modeling framework to inform the development of viable disease risk management policies and measures to control disease outbreaks on cruises. Our model, parameterized and calibrated using the data of the COVID-19 outbreak on the Diamond Princess cruise ship in 2020, is used to assess the impact of the mitigation measures such as mask wearing, vaccination, on-board and pre-traveling testing measures. Our results indicate mask wearing in public places as the cheapest and most affordable measure can drop the number of cumulative confirmed cases by almost 50%. This measure along with the vaccination by declining the number of the cumulative confirmed cases by more than 94% is the most effective measure to control outbreaks on cruises. According to our findings, outbreaks are more predominant in the passenger population than the crew members, however, the protection measures are more beneficial if they are applied by both crew members and passengers. Regarding the testing measure, pre-traveling testing is more functional than the on-board testing to control outbreaks on cruises.

1. Introduction

Cruise ships carry a large number of people in confined spaces providing an environment for transmission of infections. Hence, analyzing the impact of protection measures to control infectious diseases on cruises, the objective of this project, is crucial to public health policy decision makers and private companies. Cruise and passenger ships are the most affected segment by the COVID-19 pandemic amongst the global maritime shipping industry. Comparing the 2020 mobility levels to those in prior years, cruise and passenger ships showed a reduction in mobility ranging from 19.57% to 42.77% ([Zhou et al.](#page-9-0), [2023\)](#page-9-0). In the present study, we go over policies to control outbreaks on cruise ships, with insight into and from the COVID-19 outbreak that occurred on the Diamond Princess cruise ship in 2020. The Diamond Princess cruise ship completed a 16-day voyage on February 4, 2020, which was started on January 20, with 2666 passengers and 1045 crew

members from a combined total of 56 countries, and the average age of passengers was 66 years. The ship departed from Yokohama Port, Japan on January 20, 2020, and a passenger who disembarked in Hong Kong on January 25 was confirmed to be infected with SARS-CoV-2 on February 1. The Diamond Princess cruise ship anchored at Yokohama port since February 4, 2020. On February 5, the first 10 confirmed RT-PCR tests were reported, and they rose to 634 by February 20 as illustrated in [Fig.](#page-1-0) [1.](#page-1-0) Japan National Emergency Medical Team (N-EMT), and Japan Disaster Medical Assistance Team (DMAT) were dispatched and managed the medical operation for Diamond Princess (DP) passengers and crew members ([Kondo et al.](#page-8-0), [2023](#page-8-0)).

Various aspects of the COVID-19 outbreak occurred on the Diamond Princess cruise ship have already been analyzed. Chen et al. used computational textual analytical tools—topic modeling and sentiment analysis to understand what kind of messages and how customers

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Fig. 1. Cumulative numbers of confirmed infected (asymptomatic and symptomatic) passengers and crew members on the Diamond Princess cruise ship over Feb 5 - Feb 20, 2020, including double tests [\(Nakazawa et al.,](#page-9-1) [2020;](#page-9-1) [Mizumoto et al.,](#page-9-2) [2020\)](#page-9-2).

onboard conveyed during their direct experience of the crisis. They studied how communication of Diamond Princess cruise with the public affected the tourists on the endured the COVID-19 crisis and contributed in health crisis management [\(Chen et al.,](#page-8-1) [2022](#page-8-1)). Azimi et al. developed a modeling framework and leveraged the information from the Diamond Princess cruise ship outbreak to evaluate the relative importance of multiple transmission routes for SARS-CoV-2. The study modeled 21,600 scenarios to figure out for eight unknown or uncertain epidemic and mechanistic transmission factors. The results show that "aerosol inhalation was likely the dominant driving factor of COVID-19 transmission among the passengers, even considering a conservative assumption of high ventilation rates and no air recirculation conditions for the cruise ship. Moreover, close-range, and long-range transmission likely contributed similarly to disease progression aboard the ship, with fomite transmission playing a smaller role. The passenger quarantine also affected the importance of each mode, demonstrating the impacts of the interventions'' ([Azimi et al.](#page-8-2), [2021\)](#page-8-2). Um and Adhikari applied the combination of bootstrap partial filtration(PF) and Markov chain Monte Carlo (MCMC) algorithms within a Bayesian framework with modeling considerations informed by the simulations, to the study of COVID-19 outbreak on Diamond Princess cruise ship and examined the age-dependent effects on transmission rates, with considerations for different networks of crew and passengers and limited COVID-19 testing ([Um and Adhikari,](#page-9-3) [2024\)](#page-9-3).

Zhang et al. estimated that the Maximum-Likelihood (ML) value of reproductive number (R_0) in the early stage of COVID-19 outbreak in Diamond Price cruise by fitting a gamma distribution to the reported serial interval (mean and standard deviation). They also simulated plausible cumulative epidemic trajectories and future daily incidence by fitting the data of existing daily incidence, a serial interval distribution, and the estimated R_0 into a model based on the assumption that daily incidence obeys approximately Poisson distribution determined by daily infectiousness [\(Zhang et al.,](#page-9-4) [2020a\)](#page-9-4). Russell et al. estimated the infection and case fatality ratio for coronavirus disease using ageadjusted data from the outbreak on the Diamond Princess cruise ship ([Russell et al.,](#page-9-5) [2020](#page-9-5)). In addition to calculating the transmission rates and the basic reproduction numbers for the first and second part of the voyage conducted in most existing studies, a statistical model was employed in [Mizumoto et al.](#page-9-2) ([2020](#page-9-2)) and asymptomatic proportion was estimated. Zhang et al. studied the impacts of the central airconditioning on the peak time of infection, the number of the infections caused by the Hong Kong passenger, and the basic reproduction number [\(Zhang et al.,](#page-9-6) [2020b\)](#page-9-6). Rocklöv et al. analyzed the counterfactual scenario in absence of countermeasures and creates a model stratified by crew and guests to study the effects of differential contact rates

among the groups [\(Rocklöv et al.,](#page-9-7) [2020](#page-9-7)). The present study is an extension of the previous studies, and here we focus on analyzing the mechanism of the COVID-19 outbreak and the effectiveness of various protection measures on the cumulative number of confirmed cases over Jan 20–Feb 19, 2020 on the Diamond Princess cruise ship. We hope this study provides a model framework which is generic enough to be adopted for infection risk assessment and intervention effectiveness of many respiratory infectious diseases with transmission routes similar to those of the COVID-19, and in general cruise ships.

2. Methods

According to requirements of the Ministry of Health, Labor and Welfare of Japan, as of February 5, all passengers on the Diamond Princess cruise ship had to be quarantined in their cabins for 14 days. Japan's emergency measures, which kept passengers isolated in cruise cabins but continued to circulate the air through the central airconditioning, were questioned by many experts. During the quarantine period, passengers and crew members were tested in batches randomly, and individuals confirmed to be positive for COVID-19 disembarked for treatment at designated institutions in Japan. The number of RT-PCR– confirmed COVID-19 cases hit its peak on February 18. Meanwhile, as of February 17, other countries began to evacuate their nationals on chartered flights. As of February 19, passengers who completed 14 days without sharing a cabin with a confirmed case, had a negative result for a SARS-CoV-2 by RT-PCR test in the final days of the period and had no relevant symptoms identified during a medical screening on the final day of the period were allowed to disembark. A total of 3011 respiratory specimens were tested until the end of February 19. Out of them, 619 cases have been confirmed positive, including 82 crew members and 537 passengers. Two people had two confirmed positive tests. Therefore, the total number of confirmed positive tests was 621. Initially, testing focused on high-risk persons. On February 11, the strategy shifted toward testing all passengers by RT-PCR test for SARS-CoV-2. Testing began with passengers over 80 years old, then over 75, then over 70, etc. After all passengers had been tested, the focus shifted to testing crew members. As of February 27, the crew members of the cruise ship began to disembark and were sent to Saitama prefecture and Hikari city in Japan to be isolated for 14 days. By March 1, all the people had disembarked from the cruise ship. Eventually, a total of 721 on the Diamond Princess cruise ship were reported to be infected with SARS-CoV-2 ([Nakazawa et al.,](#page-9-1) [2020](#page-9-1); [Mizumoto et al.](#page-9-2), [2020;](#page-9-2) [Zhang](#page-9-6) [et al.](#page-9-6), [2020b;](#page-9-6) [of Infectious Disease](#page-9-8), [2020;](#page-9-8) [Pavli et al.,](#page-9-9) [2016;](#page-9-9) [Yamahata](#page-9-10) [et al.,](#page-9-10) [2020](#page-9-10)).

We model the COVID-19 outbreak on the Diamond Princess cruise ship on two-time intervals Jan 20–Feb 4, the first part of the voyage,

Table 1

Parameters, descriptions, and values.

and Feb 5–Feb 19, the second part of the voyage, with two different systems of ordinary differential equations. The population is segregated into two main clusters, passengers and crew members clusters. In this framework, we aim to assess the impacts of protection measures in each cluster. To this end, we need to connect the clusters together, hence, we assume the populations of crew members and passengers move from one to another at rates v_1 and v_2 . In which parameter v_1 denotes the rate of progress from the crew members cluster to the passengers cluster and v_2 indicates the counterwise direction. For the first part of the voyage, we study the mechanism of the outbreak under two alternative scenarios—with and without the on-board testing measures with scenario-specific models, each with or without on-board testing. In the scenario with on-board testing, we assume that the rapid antigen(RA) test is used to detect symptomatic and asymptomatic individuals on the third day of the voyage, and those with positive testing confirmation are isolated in their cabins. This will be contrasted with the alternative scenario without on-board testing. For the second part of the voyage, as people are selected to get RT-PCR test daily and randomly, and as individuals with the confirmed positive tests are unloaded, we design the model accordingly so that no isolation sub-cluster is incorporated for this part of the voyage.

On Feb 19, the number of cumulative confirmed cases for crew members and passengers was 82 and 537 respectively. Moreover, two people had confirmed positive results in a double testing process. We distribute double tests to the crew members and passengers, resulting in a total of 83 crew members and 538 passengers confirmed positive tests. For this period we estimate some parameters with the least square method (See [Table](#page-2-0) [1](#page-2-0)) to calculate the cumulative number of confirmed cases for the first part of the voyage (See [Appendix](#page-8-8) [A](#page-8-8) [Fig.](#page-8-9) [8\)](#page-8-9). In the next step, we develop an extended SEAIR model (See [Fig.](#page-3-0) [2\)](#page-3-0) to simulate different scenarios and compare the results to actual data to investigate the effectiveness of each measure. First, we analyze the impacts of the protection measures such as mask wear, vaccination, pre-traveling RA and RT-PCR testing, and on-board RA testing measures on the cumulative number of infected on the Diamond Princess cruise ship over Jan 20 to Feb 19. We also estimate the number of infected for each cluster of crew members and passengers under different scenarios for each protection measure (See [Figs.](#page-6-0) [6](#page-6-0) and [7](#page-7-0)). Regarding the testing measure, we suppose all the individuals get either RT-PCR or RA test two days or half a day before starting the voyage, respectively, and those with confirmed negative results are allowed to board. Also, all

the aboard individuals get an RA test on the third day of the voyage, and those who have confirmed positive results transfer to the isolation sub-cluster and stay there for 14 days. The findings suggest that using mask wear is the simplest and most cost-effective way to reduce the total number of confirmed cases by roughly 50% and it is the most effective method to control respiratory outbreaks when it is aligned with vaccination by declining the number of cumulative confirmed cases by more than 94%.

2.1. Model description

We develop a deterministic compartmental SEAIR model to study the transmission mechanism of the COVID-19 outbreak on the Diamond Princess cruise ship that occurred on Jan 20–Feb 19, 2020 as follows

$$
\dot{S}_{ji} = v_{i+1}S_{j(i+1)} + (\omega_{j1} - \omega_{j2} - A_{ji})S_{ji} - v_iS_{ji},
$$
\n
$$
\dot{E}_{0_{ji}} = v_{i+1}E_{0_{j(i+1)}} + A_{ji}(1-q)S_{ji} - \epsilon_0E_{0_{ji}} - v_iE_{0_{ji}},
$$
\n
$$
\dot{E}_{1_{ji}} = v_{i+1}E_{1_{j(i+1)}} + A_{ji}qS_{ji} - \epsilon_1E_{1_{ji}} - v_iE_{1_{ji}},
$$
\n
$$
\dot{A}_{0_{ji}} = v_{i+1}A_{0_{j(i+1)}} + (1-p)\epsilon_0E_{ji} - rA_{0_{ji}} - v_iA_{0_{ji}},
$$
\n
$$
\dot{I}_{0_{ji}} = v_{i+1}I_{0_{j(i+1)}} + p\epsilon_0E_{0_{ji}} - rI_{0_{ji}} - v_iI_{0_{ji}},
$$
\n
$$
\dot{A}_{1_{ji}} = v_{i+1}A_{1_{j(i+1)}} + (1-p)\epsilon_1E_{1_{ji}} - \epsilon_2A_{1_{ji}} - v_iA_{1_{ji}},
$$
\n
$$
\dot{I}_{1_{ji}} = v_{i+1}I_{1_{j(i+1)}} + p\epsilon_1E_{1_{ji}} - \epsilon_2I_{1_{ji}} - v_iI_{1_{ji}},
$$
\n
$$
\dot{A}_{2_{ji}} = v_{i+1}A_{2_{j(i+1)}} + \epsilon_2A_{1_{ji}} - rA_{2_{ji}} - v_iA_{2_{ji}},
$$
\n
$$
\dot{I}_{2_{ji}} = v_{i+1}I_{2_{j(i+1)}} + \epsilon_2I_{1_{ji}} - rI_{2_{ji}} - v_iI_{2_{ji}},
$$
\n
$$
\dot{A}_{I_{j0_{ji}}} = v_{i+1}R_{I_{j(i+1)}} + r(A_{0_{ji}} + I_{0_{ji}} + A_{2_{ji}} + I_{2_{j}i}) - v_iR_{ji},
$$
\n
$$
\dot{A}_{I_{j0_{ji}}} = v_{i+1}I_{I_{j0_{j(i+1)}} - rI_{I_{j0_{ji}}} - v_iI_{I_{j0_{ji}}},
$$
\n
$$
\dot{R}_{I_{j0_{ji}}} = v_{i+1}I_{I_{j0_{j(i+1)}} - rI_{I_{j0_{ji}}} - v_i
$$

with the non-negative initial conditions given by

$$
S_{jn}(0) = S_{jn0}, \quad E_{kjn}(0) = E_{kjn0}, \quad A_{mjn}(0) = A_{mjn0}, \quad I_{mjn}(0) = I_{mjn0},
$$

$$
R_{jn}(0) = R_{jn0}, \quad A_{Iso_{jn}}(0) = A_{Iso_{jn0}}, \quad I_{Iso_{jn}}(0) = I_{Iso_{jn0}}, \quad R_{Iso_{jn}}(0) = R_{Iso_{jn0}},
$$

(2)

where $k \in \{0, 1\}$, $m \in \{0, 1, 2\}$, and $n \in \{i, i + 1\}$.

Fig. 2. Schematic representation of the COVID-19 transmission dynamics model on the Diamond Princess cruise ship. In the figure and the model, S_{ii} is the umber of the susceptible individuals in the jth part of the voyage of the main cluster i ; E_{0ji} is the number of the exposed individuals under the untested on-board scenario in the jth part of the voyage of the main cluster i; E_{1ji} is the number of the exposed individuals under the tested on-board scenario in the jth part of the voyage of the main cluster i; A_{0ji} is the number of the asymptomatic individuals under the untested on-board scenario in the jth part of the voyage of the main cluster i ; A_{1ji} is the number of the asymptomatic individuals in RA test detectable phase in the jth part of the voyage of the main cluster i; A_{2ii} is the number of the asymptomatic individuals after RA test detectable phase in the jth part of the voyage of the main cluster i; I_{0ji} is the number of the symptomatic individuals under the untested on-board scenario in the jth part of the voyage of the main cluster i; I_{1ji} is the number of the symptomatic individuals in RA test detectable phase in the jth part of the voyage of the main cluster i ; I_{2ji} is the number of the symptomatic individuals after RA test detectable phase in the jth part of the voyage of the main cluster i; R_{ji} is the umber of the recovered individuals in the jth part of the voyage of the main cluster i; $A_{Iso_{ji}}$ is the number of the asymptomatic individuals in the jth part of the voyage of the isolation sub-cluster i; $I_{iso_{\mu}}$ is the number of the symptomatic individuals in the jth part of the voyage of the isolation sub-cluster *i*; $R_{Iso_{ji}}$ is the number of the recovered in the *j*th part of the voyage of the isolation sub-cluster *i*.

The model is developed for two parts of the voyage, Jan 20–Feb 4, and Feb 5–Feb 19. In this model, we integrate two main clusters and two isolation sub-clusters of crew members and passengers in [Fig.](#page-3-0) [2](#page-3-0) where index $j = \{1, 2\}$ denotes the section of the voyage and $i = \{c, p\}$ where c and p represent the clusters of crew members and passengers, respectively. When i refers to crew members, then $i + 1$ corresponds to passengers, and conversely, when i refers to passengers, then $i + 1$ corresponds to crew members.

To explore the effects of the protection measures on cumulative numbers of the infectees for the first part of the voyage, Jan 20–Feb 4, we simulate the model under two alternative scenarios, i.e.,

- all the aboard individuals are tested $(q = 1)$,
- no aboard individual is tested $(q = 0)$.

Parameter q , $0 \leq q \leq 1$, denotes the proportion of the individuals who get tested on board for each main cluster, crew members, and passengers.

We assume the number of the total population remains constant for both clusters of crew members, $N_c = 1045$ and passengers, $N_p =$ 2666, over Jan 20–Feb 4, implying the rate of embarking, ω_{11} , and the rate of disembarking, ω_{12} , are equal. In the first part of the voyage, qS_{1i} aboard susceptible individuals are tested and $(1 - q)S_{1i}$ aboard susceptible individuals are untested in each cluster. $(1 - q)S_{1i}$ aboard untested individuals of the cluster i are infected by asymptomatic and symptomatic individuals in compartments $A_{0_{1i}}$ and $I_{0_{1i}}$, respectively, of the aboard untested individuals. $(1 - q)S_{1i}$ aboard untested individuals can also be infected by asymptomatic and symptomatic individuals of RA detectable and the mid-infection stages, and the isolation subcluster $A_{1_{1i}}, A_{2_{1i}}, I_{1_{1i}}, I_{2_{1i}}, A_{iso_{1i}},$ and $I_{iso_{1i}}$, accordingly, of the on-board testing stream with the force of infection function

$$
A_{1i} = \lambda_{1i} k_v k_m, \tag{3}
$$

where

$$
\lambda_{1i} = \beta_1 \left(\frac{A_{0_{1i}} + I_{0_{1i}} + \sum_{l=1}^2 (A_{l_{1i}} + I_{l_{1i}})}{1 + c_1 (A_{0_{1i}} + I_{0_{1i}} + \sum_{l=1}^2 (A_{l_{1i}} + I_{l_{1i}}))} + \theta \frac{A_{Iso_{1i}} + I_{Iso_{1i}}}{N} \right),
$$
(4)

and transfer to exposed state $E_{0_{1i}}$ of main cluster *i*. Force of infection function ([4](#page-3-1)) describes the saturation feature of the epidemic transmission and the fraction $1/1 + c_1(A_{0_{1i}} + I_{0_{1i}}) + \sum_{l=1}^{2} (A_{l_{1i}} + I_{l_{1i}})$ represents the inhibition of the transmission in the infected contacts, $c_1 \in \mathbb{R}^+$ is the saturation constant, β_1 is the transmission rate for the first part of the voyage, and $0 \le \theta \le 1$ is the rate of reduction in transmission due to the isolation. Since the air circulates through the central air-conditioning, we consider $\theta = 1$ in the simulations. Also, N is a number of the total population for each cluster, either crew members or passengers, N_c or N_p . In Eq. [\(3\)](#page-3-2), the coefficients

$$
k_v = 1 - \eta_v, \quad v = \{s, b\} \quad \text{and} \quad k_m = 1 - \eta_m \tag{5}
$$

take into account the impacts of vaccine efficacy and mask wear measures with parameters η_v and η_m , respectively, in which η_s is the rate of the vaccine efficacy of two-dose Moderna (mRNA- 1273) vaccination against a symptomatic infection for the ancestral strain of SARS-CoV-2 infection and η_b indicates the rate of a bivalent mRNA booster against a sever infection (hospitalization) for those who are 65 years old or older. Parameters η_v and η_m are zero in the baseline. $E_{0_{1i}}$ exposed individuals can progress to the compartment of symptomatic individuals, $I_{0_{1i}}$, at rate $p\epsilon_0$ or they can progress to the compartment of asymptomatic individuals, $A_{0_{1i}}$, at rate $(1 - p)\varepsilon_0$ of the main cluster *i*. Here, *p* is the probability of becoming symptomatic and ε_0 is the rate of the progression from the early latent phase to the infectious phase. Then infectees transfer to the recovery stage R_{1i} of main cluster *i* with rate .

Under the on-board testing scenario of the first part of the voyage, qS_{1i} aboard tested individuals are infected by asymptomatic and

(b) The impacts of protection measures for only one part of the voyage

Fig. 3. The simulated impact of the protection measures on the number of cumulative confirmed cases with no RA testing measure on board.

Table 2

Testing measure policies.				
Test	-2 Day	-0.5 Day	3 Day	Everyday
PCR Test		$-$		Feb5-Feb 19
RA Test	-			-

symptomatic aboard individuals of main cluster i in RA detectable and the mid-infection stages, $A_{1_{1i}}$, $A_{2_{1i}}$, $I_{1_{1i}}$ and $I_{2_{1i}}$, respectively. Also, qS_{1i} aboard tested individuals are infected by the asymptomatic and symptomatic individuals of the isolation sub-cluster *i*, $A_{Iso_{1i}}$ and $I_{Iso_{1i}}$, respectively and $A_{0_{1i}}$, $I_{0_{1i}}$ of the aboard untested individuals with the force of infection function ([3](#page-3-2))–[\(4\)](#page-3-1) and transfer to the exposed state, $E_{1_{1i}}$, of the main cluster *i*. Then the exposed individuals of the main cluster i progress to the RA test detectable stage at a rate $p\varepsilon_1$ in which parameter ϵ_1 is the rate of progression from the early latent phase to the RA detectable stage. The asymptomatic and symptomatic individuals of the main cluster i get RA tested on board on the third day of the voyage, and the individuals with the confirmed positive results transfer to the asymptomatic and symptomatic components of the isolation subclusters with RA test sensitivity for symptomatic and asymptomatic individuals, ξ , and ξ of each cluster *i*, respectively. Under this scenario, we suppose, the individuals are isolated in their cabins without any symptomatic or asymptomatic individuals. The symptomatic individuals who are not diagnosed with RA test transfer to the mid-infection stage, $I_{2_{1i}}$ component at rate ε_2 , the rate of progression from the incubation phase to the mid-infection phase after the RA test, and then they can progress to the recovery stage, R_{1i} at rate r. Asymptomatic individuals follow the same procedure. For the second part of the voyage, Feb 5–Feb 19, the total number of the population is non-constant since the rate of embarking, ω_{21} , vanishes and the rate of disembarking, ω_{22} , is estimated in [Table](#page-2-0) [1.](#page-2-0) Moreover, the aboard individuals with confirmed positive RT-PCR tests are evacuated for treatment as of Feb 5 hence, there is no isolation sub-cluster for this part of the voyage. Therefore, we consider the model without an on-board testing scenario, $(q = 0)$, for the second part of the voyage. Under this scenario, the susceptible individuals get infected by asymptomatic and symptomatic individuals of the main cluster *i*, $A_{0_{2i}}$ and $I_{0_{2i}}$, respectively with the force of infection function

$$
\Lambda_{2i} = \lambda_{2i} k_v k_m, \tag{6}
$$

where

$$
\lambda_{2i} = \frac{\beta_2 (A_{0_{2i}} + I_{0_{2i}})}{1 + c_2 (A_{0_{2i}} + I_{0_{2i}})}
$$
\n(7)

and $c_2 \in \mathbb{R}^+$ is the saturation number for main cluster *i*.

It is noticeable that, based on the evidence, the total number of individuals remains constant over the first part of the voyage. Therefore, we assume ω_{11} and ω_{12} are equal, regardless of their values, since in model (1), their influence vanishes. Regarding the force of infection functions, during the first part of the voyage, as the total population remains constant throughout, we could have utilized the standard form of the force of infection. However, recognizing that the force of infection with the saturation structure provides a more accurate interpretation of infectious disease transmission mechanisms, we employed it for this segment for the main clusters. For the second part of the voyage, where the number of individuals fluctuates due to confirmed cases disembarking for treatment, the force of infection with saturation structure becomes preferable as it varies with the number of infected individuals. As the saturation numbers, c_1 and c_2 , are not directly accessible, we estimated them through a data fitting process detailed in [Appendix](#page-8-8) [A.](#page-8-8) Initially, we estimated c_1 and c_2 for both parts of the voyage in the baseline scenario without any testing measures for main clusters. We then applied them in testing scenarios. For the isolation scenario, treated as an assumption occurring on-board without direct data access, we aimed to employ a different force for the isolation clusters, however, we could not perform the data fitting process to estimate the saturation number for the force of infection of the isolation clusters. Consequently, we resorted to using the standard form. Furthermore, we make the assumption that the asymptomatic and symptomatic transmission rates are equal.

Parameters of model ([1](#page-2-1)) are assigned in the following table.

3. Results

In this section, we report the simulation on the impact of different protection measures such as mask wear, vaccination, and testing measures on the number of the cumulative confirmed cases on the Diamond Princess cruise ship. For this aim, the effects of mask wear and vaccine measures are taken into account with the force of infection functions ([3](#page-3-2))–[\(6\)](#page-4-0) for the first and second part of the voyage, respectively. The impact of pre-traveling RT-PCR and RA tests is considered two days and half a day before the starting day of the voyage, respectively, under the assumption all the individuals get tested. Under the on-board testing scenario for the first part of the voyage, we suppose all the aboard individuals get the RA test on the third day of the voyage and those who have confirmed positive RA test are isolated in their cabins without any infectee. For the second part of the voyage, Feb 5- Feb 19, the individuals get RT-PCR tests daily and randomly and the individuals

(b) The impacts of the isolation with RA testing measure on board

Fig. 4. The impacts of the protection measures without and with RA testing measure on board.

with the positive confirmed tests disembark for treatment. The testing policy is recapped in [Table](#page-4-1) [2.](#page-4-1)

3.1. Impacts of protection measures

Following figures illustrate the impact of the protection measures on the number of cumulative confirmed cases when there is no RA test on board.

[Fig.](#page-4-2) [3\(a\)](#page-4-2) indicates that the mask wearing with the vaccination measures is the most effective factor to control the outbreak, since it drops the number of cumulative confirmed cases by almost 94% in the non-pre-traveling test measure and 97% in pre-traveling RT-PCR test measure. Vaccination, booster and mask, and booster measures come in the second, third, and fourth rank to decrease the number of cumulative confirmed cases, respectively. As the mask wear solely declines the number of cumulative numbers dramatically by more than 53% for each policy, non-pre-traveling test, pre-traveling RA, and pre-traveling RT-PCR testing measures, it is considered the most affordable and cheapest measure to control the outbreak on the cruise. According to the results, pre-traveling RT-PCR test is more effective than pre-traveling RA test in controlling the outbreak. [Fig.](#page-4-3) [3\(b\)](#page-4-3) depicts employing the protection measures only for the second part of the voyage declines the number of the cumulative confirmed cases almost by four times in comparison to applying the protection measures only for the first part of the voyage. This means that the impacts of the protection measures of the second part of the voyage are predominant in the protection measures of the first part of the voyage when there is no testing measure on board. Even though the transmission rate in the second part of the voyage is less than the transmission rate of the first part of the voyage, the numbers of the infected in the second part of the voyage are greater than the peer numbers in the first part of the voyage. The latter could be a reason for this dominance, implying the protection measures of the second part of the voyage are more effective in controlling the outbreak.

3.2. Exploring the effects of protection measures combined with isolation

[Fig.](#page-5-0) [4](#page-5-0) shows the impacts of the different protection measures on the number of cumulative confirmed cases when all the aboard individuals get RA test on the third day of the voyage.

[Fig.](#page-5-1) [4\(a\)](#page-5-1) compares the effects of RA testing measure on board to without RA testing measure on board. Under the former scenario, we suppose all the aboard individuals get an RA test on board on the third day of the voyage and those with confirmed positive RA tests are isolated in their cabins without any infectee for 14 days.

Since the air circulates through the air-conditioner, we consider $\theta =$ 1 in force of infection ([4](#page-3-1)). According to the results, the number of cumulative confirmed cases for both scenarios, with and without RA testing measures on board, is almost the same. [Fig.](#page-5-2) [4\(b\)](#page-5-2) showcases the effect of the isolation on the number of cumulative confirmed cases without any protection measures, including mask wear and vaccination measure. We suppose all the aboard individuals get RA test and those with positive confirmed cases are isolated in their cabins without any infectee. Parameter θ in force of infection ([4\)](#page-3-1) denotes the rate of reduction in transmission due to the isolation evaluated with $0 \le \theta \le 1$. As it is visualized in [Fig.](#page-5-2) [4\(b\),](#page-5-2) when the isolation works perfectly and the virus does not spread through the air-conditioning, $\theta = 0$, the number of cumulative confirmed cases drop 0.09%, and the decline is 0.04% for $\theta = 0.5$. The results denote increasing the value of θ from 0 to 1, does not affect the number of cumulative confirmed cases appreciably. This means that the on-board testing measure and the isolation are not very effective factors in controlling the outbreak compared to the pre-traveling testing and other protection measures.

3.3. Examining the effects of various population coverage rates on protection measures

The following figure illustrates the effects of protection measures at varying population coverage levels.

[Fig.](#page-6-1) [5](#page-6-1) shows that 10% population coverage for any of the protection measures produces a negligible reduction in cumulative confirmed cases, while the change is noticeable for 50% of protection measures for which it drops to more than 42% for booster and mask, vaccine, and vaccine and mask. Booster and mask wear comes in the late ranks with 35% and 23% decrease, respectively. The decline is noticeable for applying 90% of protection measures, implying more than 80% decline in the number of the cumulative confirmed cases with vaccination alone and vaccination with masking. The other measures like booster and mask, booster, and mask drop this number by 76%, 64%, and 43%, respectively. A comparison among various percentages for the protection measures illustrates the impacts of the two last measures, vaccination alone and vaccination with masking, are almost two times more than the impacts of the mask measure. According to the results, vaccination alone and vaccination with masking are the most effective factors to control the outbreak. This implies mask wear measure as the cheapest measure to control the outbreak is not sufficient to control the outbreak, while vaccination is considered the most expensive and effective measure to control the outbreak, and it is more efficient when it is aligned with mask wear guidelines.

Fig. 5. The impacts of protection measures when covering different percentages of the population.

(b) The impacts of protection measures for either crew members and passengers

Fig. 6. The impacts of whole population protection measures on the number of cumulative confirmed cases for the crew and passengers without testing measures.

3.4. Assessing the influence of protection measures on crew members and passenger cohorts

In this section, we examine the effects of protection measures on both crew members and passenger groups.

[Fig.](#page-6-0) [6](#page-6-0) shows the impacts of whole population protection measures for the crew members and passengers in absence of testing measures. [Fig.](#page-6-2) [6\(a\)](#page-6-2) illustrates the impacts of the protection measures on the number of cumulative confirmed cases for both crew members and passengers, and [Fig.](#page-6-3) [6\(b\)](#page-6-3) visualizes the number of cumulative confirmed cases for each measure for either the crew members or passengers. The baseline results correspond with our assumption that the number of the cumulative confirmed cases of the crew members is 83 and passengers is 538, including double tests on Feb 19. This implies the number of cumulative confirmed cases for the passengers is six times more than the peer number for the crew members, while the number of the total population of the passengers is two times more than the number of the total population for the crew members. This proportion is more noticeable for vaccine and vaccine and mask measures for which the number of the cumulative confirmed numbers for the passengers is 10.6 and 18 times, respectively, more than the number of the cumulative confirmed cases for the crew members. These protection measures decline the number of cumulative cases by almost 97% for the crew members and 93% for the passengers with the most effective measure, vaccine, and mask-wear policy. The results show the outbreak is more predominant in the passenger population than the crew members population, most likely as they have more contacts and public activities.

(b) The impacts of protection measures when applied to the crew members only.

Fig. 7. The impacts of applying protection measures to a single sub-population on the number of cumulative confirmed cases for the crew members and passengers, without testing measures.

[Fig.](#page-7-0) [7](#page-7-0) illustrates the impacts of the protection measures on the number of cumulative confirmed cases for either the crew members and passengers without the testing measure on board when the protection measures are employed only for one cluster. [Fig.](#page-7-1) [7\(a\)](#page-7-1) visualizes the impacts of the protection measures when the protection measures are applied just for the passengers. According to the results, the number of the cumulative confirmed cases of the crew members remains almost the same for all the measures while the peer number of the passengers declines by almost 80% for vaccination and vaccination along with mask measures. The other measures like booster and mask, booster, and mask come in the second, third, and fourth orders with 74%, 62%, and 46% decline, respectively. [Fig.](#page-7-2) $7(b)$ shows by employing the protection measures only on the crew, the number of the cumulative confirmed cases of the crew members drops by more than 90% for the vaccination and vaccination along with mask wear measures. The decline is 88% for booster and mask wear, 73% for booster, and 54% for mask wear. Under this scenario, the protection measures affect the number of the cumulative confirmed cases of passengers very slightly for which the passengers have 10% decline in the most effective measures, vaccination and vaccination along with mask wear. The other measures come in the late ranks with 9%, 8%, and 5% for booster along with mask wear, booster, and mask wear, respectively. The research findings imply following the protection measures by passengers affects the outbreak control noticeably since their population is more crowded and active. Moreover, the protection measures will be more useful if they are followed by both clusters, the crew members and passengers (compare $7(a)$ and $7(b)$ to $6(b)$).

4. Discussion

In this work, we have proposed a deterministic mathematical model SEAIR in the form of differential equations to quantify the impacts of the protection measures on infectious disease outbreaks on cruise ships. For this aim, we benefit from the insights into the COVID-19 outbreak that occurred on the Diamond Princess cruise ship from Jan 20 to Feb 19, 2020. To do so, we split the voyage into two parts, the first part Jan 20–Feb 4, and the second part, Feb 5–Feb 19. The first part of the voyage is studied under two scenarios with constant population sizes for crew members and passengers, i.e., with and without on-board testing measures. Under the on-board testing scenario, we suppose all the aboard individuals get RA test on the third day of the voyage and those with positive results are isolated in their cabins without any infectee for 14 days and compare the results with no on-board testing measure. For the second part of the voyage, Feb 5–Feb 19, the individuals get RT-PCR

tests daily and irregularly in the second part of the voyage and those with negative results unload for the treatment, hence the number of the total population is non-constant and we employ the untested on-board model for this section of the voyage. For both models, we consider the impacts of pre-traveling testing measures. For this goal, we assume all the individuals get RA and RT-PCR tests half a day and two days before the boarding, respectively and those with confirmed negative results are allowed to board. Also, the effectiveness of mask wear and vaccination is investigated. According to the study's findings, the easiest and most cost-effective way to cut the total number of confirmed cases by about 50% is to wear a mask, and when it is combined with vaccination, it is the best technique to manage respiratory outbreaks by decreasing the number of the cumulative confirmed cases by more than 90%. Since the passenger population is more crowded and active, employing the protection measures is more effective in controlling the outbreak and the results are more outstanding when the protection measures are used by both clusters, crew members, and passengers. Moreover, Pre-travel testing is more effective than on-board RA testing in controlling the outbreak. These research findings can be used to control the next outbreak on cruise ships.

In this study, we face data limitations. Specifically, we do not have access to the number of passengers boarding and disembarking the cruise during the first part of the voyage, nor do we have data on the number of passengers disembarking the cruise during the second part of the voyage. Additionally, transmission rates for both segments of the voyage and the number of incidents during the initial phase of the voyage are unavailable. Consequently, we have estimated the inaccessible parameters through the data fitting process (See [Appendix](#page-8-8) [A\)](#page-8-8).

5. Conclusion

We start with a remark that the conclusion drawn in this study is qualitative rather than quantitative. This is due to the fact that the estimates are heavily reliant on assumptions and are subject to sensitivity analyses.

Our study recommends that private insurance companies use these research findings to refine their policies and risk assessments for cruise operators, while also emphasizing that public health organizations can leverage these results in policymaking. Additionally, we strongly advise shipping companies to incorporate these results into their safety protocols, benefiting passenger safety and overall confidence in the industry.

The research results provide insights on the impacts of protection measures against infectious diseases on cruise ships, and these insights are considered invaluable for private insurance companies and shipping companies. Private insurers can use these findings to refine their policies and risk assessments, aligning coverage options with the level of risk mitigation in place. This can also lead to more accurate premium pricing and comprehensive coverage options, benefiting both insurance companies and cruise operators. Shipping companies can integrate the research results into their operational instructions and safety protocols, enabling them to develop more effective strategies for passengers and crew members safety. These insights inform decisions on screening, hygiene practices, medical facilities, and emergency response plans, enhancing their preparedness and passenger confidence. Ultimately, a collaboration between researchers, private companies, and policymakers can create safer and more resilient cruise experiences for all stakeholders.

CRediT authorship contribution statement

Rahele Mosleh: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Mortaza Baky-Haskuee:** Writing – review & editing, Validation, Investigation, Conceptualization. **Abbas Ghasemi:** Writing – review & editing, Validation, Investigation, Conceptualization. **Martin Grunnill:** Writing – review & editing, Validation, Investigation, Conceptualization. **Julien Arino:** Supervision, Conceptualization. **Mohammadali Tofighi:** Writing – review & editing, Validation, Investigation, Conceptualization. **Edward W. Thommes:** Supervision, Conceptualization. **Jianhong Wu:** Writing – review & editing, Supervision, Investigation, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Data fitting process

We utilize the least square method to estimate the model parameters, as detailed in [Table](#page-2-0) [1](#page-2-0). This involves applying the basic model with $q = 0$ to both the first and second segments of the voyage and consequently calculating the cumulative confirmed cases at time $t = 31$. For this aim, we employ the *fminsearch* ([Inc.,](#page-8-10) [2023\)](#page-8-10) function from the MATLAB optimization toolbox to refine these parameters. For each parameter, we access the corresponding data range and calculate a 95% confidence interval by computing the average and standard deviation of the dataset. Subsequently, we derive the 95% confidence interval based on the normal distribution using the formula

$$
CI = \bar{x} \pm 1.96 \frac{s}{\sqrt{N}},\tag{8}
$$

where \bar{x} is the mean of the corresponding data range, s denotes the standard deviation of the corresponding data range, and N represents the size of the corresponding data range. Throughout this process, we ensure that the confidence interval encompasses the estimated parameter; if not, we identify and exclude outlier data points to obtain

Fig. 8. The fitted data over Jan 20–Feb 19, 2020.

a confidence interval that accurately covers the estimated parameter. Our objective is to ensure that the cumulative confirmed cases predicted by the model for both voyage segments closely align with the actual data recorded from January 20th to February 19, 2020, as illustrated in [Fig.](#page-8-9) [8,](#page-8-9) showcasing the model's alignment with actual observations. The estimated parameters suggest that the reproduction number (R_0) for the early stage of the voyage is approximately 3.24, while for the second part of the journey, it stands at around 1.96. These calculations consider a single cluster encompassing both crew members and passengers for each voyage segment.

Appendix B. Well-posedness

Given the initial conditions, it could be mathematically proved that a unique solution of the model exists and preserves the non-negativity for all $t \ge 0$. This results in system $(1)-(2)$ $(1)-(2)$ $(1)-(2)$ $(1)-(2)$ is well-posed over the given time interval of Jan 20–Feb 19, 2020.

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