# Dynamic Network Strategies for SARS-CoV-2 Control on a Cruise Ship

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# *Supplemental Appendix*

### 1 INTRODUCTION

This supplementary technical appendix describes the mathematical model structure, parameterization, and statistical analysis of the accompanying paper in further detail.

### **1.1 Model Framework**

The mathematical models for SARS-CoV-2 transmission dynamics presented in this study are networkbased transmission models in which uniquely identifiable relational contact dyads were simulated and tracked over time. This contact structure is represented through the use of temporal exponential-family random graph models (TERGMs). On top of this dynamic network simulation, the epidemic model represents demography (exits, and aging), interhost epidemiology (disease transmission), intrahost epidemiology (disease progression), and clinical epidemiology (disease diagnosis and treatment and prevention interventions). Individual attributes related to these processes are stored and updated in discrete time over the course of each epidemic simulation.

### **1.2 Model Software**

The models in this study were programmed in the R and C++ software languages using the *EpiModel*  [http://epimodel.org/] software platform for epidemic modeling. *EpiModel* was developed by the authors for simulating complex network-based mathematical models of infectious diseases.(1) *EpiModel* depends on *Statnet* [http://statnet.org/], a suite of software in R for the representation, visualization, and statistical analysis of complex network data.(2)

*EpiModel* allows for a modular expansion of its built-in modeling tools to address novel research questions. We have developed a set of extension modules into a software package called *EpiModelCOVID*. This software is available for download, along with the scripts used in the execution of these models. The tools and scripts to run these models are contained in two GitHub repositories:

- [http://github.com/EpiModel/EpiModelCOVID] contains the general extension software package. Installing this using the instructions listed at the repository homepage will also load in *EpiModel* and the other dependencies.
- [http://github.com/EpiModel/COVIDCruiseShip] contains the scripts to execute the models and to run the statistical analyses provided in the manuscript.

### **1.3 Core Model Specifications**

We started with a network size of 3711 persons on the Diamond Princess Cruise Ship. Age was represented as a continuous attribute, with initial distributions drawn from empirical distributions: passengers averaged 69 years old (interquartile range: 62–73) and crew averaged 36 years old (interquartile range: 29–43). The network size was allowed to decrease with departures related to mortality. We used a two-stage simulation framework, first calibrating the model to diagnosed cases on the ship (Stage 1), and then simulating the reference and counterfactual intervention scenarios for 30

days in most scenarios. The time unit used throughout the simulations was one day. Unless otherwise noted, all rate-based parameters listed below are to be interpreted as the rate per day and all durationbased estimates are to be interpreted as the duration in days.

# 2 NETWORKS OF SOCIAL CONTACTS

We modeled networks of three interacting types of network contacts relations: passenger to passenger, passenger to crew, and crew to crew. We first describe the methods conceptually, including the parameters used to guide the model and their derivation, and then present the formal statistical modeling methods. Consistent with our parameter derivations, all contacts are defined as those in which respiratory exposure is expected to occur at least once.

### **2.1 Conceptual Representation of Networks**

Our modeling methods aim to preserve certain features of the cross-sectional and dynamic network structure as observed in our primary data, while also allowing for mean contact durations to be targeted to those reported for different groups and relational types. Our methods do so within the context of changing population size (due to deaths and departures from the population) and changing composition by attributes such as age.

This model involved representing three types of contact networks at two distinct time points. The three networks represented passenger-passenger, passenger-crew, and crew-crew contacts. We modeled these as three overlapping networks with a shared node set but differing edges (instead of one large network) to provide maximal flexibility in model parameterization and intervention design. The three modeled networks were also doubled to represent a "pre-lockdown" and "post-lockdown" composition. Although the core network features remained the same, the density and determinants of the network structure varied between these time points.

Conceptually, the 6 network models are defined as follows:

- Passenger-Passenger Network
	- o Pre-Lockdown
		- § Contacts between passengers, with most contacts occurring with passenger in same cabin. Average daily degree of 5.
		- Contacts prohibited with crew members in this network.
	- o Post-Lockdown
		- § All passenger-passenger contacts limited to within-cabin. Same within-cabin daily degree (average degree of 1) but no contacts with passengers outside of cabin.
		- Contacts prohibited with crew members in this network.
- Passenger-Crew Network
	- o Pre-Lockdown
		- § Contacts between passengers and crew, with an average daily degree of 8.
- § 50% of contacts restricted to passenger-crew pairs within same ship sector.
- No contacts within person type permitted.
- o Post-Lockdown
	- § Contacts limited to 2 daily visits to each cabin (for cleaning and meal services)
	- § 98% of contacts restricted to passenger-crew pairs within the same ship sector.
- Crew-Crew Network
	- o Pre-Lockdown
		- Contacts between crew, with an average daily degree of 10.
		- Contacts prohibited with passengers in this network.
	- o Post-Lockdown
		- Contacts between crew, with an average daily degree of 2.
		- 98% of contacts restricted to crew-crew pairs within same ship sector.
		- Contacts prohibited with passengers in this network.

Algorithmically, we implemented the swap of network models from pre-lockdown to post-lockdown by implementing a deterministic time step at which the appropriate network model was selected as input for the simulation.

### **2.2 Statistical Representation of Contact Networks**

Exponential-family random graph models (ERGMs) provide a foundation for statistically principled simulation of local and global network structure given a set of target statistics from empirical data. Social contacts were modeled using modeled using cross-sectional ERGMs.(3) This allowed for more flexibility in relational dissolution than temporal ERGMs, in which this is a stochastic process. Repeated contacts within the same dyads (e.g., passenger cabinmates) were allowed through mixing constraints in the cross-sectional network composition.

Formally, our statistical models for relational dynamics can be represented as a set of six equations for the conditional log odds (logits) of relational existence at time *t*:



where:

•  $Y_{i,j,t}$  = the relational status of persons *i* and *j* at time *t* (1 = in relationship/contact, 0 = not).

- $\bullet$   $Y_{i,j,t}^C$  = the network complement of *i,j* at time *t*, i.e. all relations in the network other than *i,j.*
- $g(y)$  = vector of network statistics in each model (the empirical statistics defined in the tables above).
- $\theta$  = vector of parameters in the model.

For  $g(y)$  and  $\theta$ , the subscript indicates the contact network type. For  $Y_{i,j,t}$  the subscript differentiates the pre- and post-lockdown times corresponding to day 15. The recursive dependence among the relationships renders the model impossible to evaluate using standard techniques; we use MCMC in order to obtain the maximum likelihood estimates for the  $\theta$  vectors given the  $q(y)$  vectors.

Converting the statistics into our fully specified network models consists of the following steps:

- 1. Construct a cross-sectional network of 3711 persons with no contacts (an empty network).
- 2. Assign persons demographics (age) based on ship census data, as well as a passenger type (corresponding to passenger or crew). For passengers, individuals were assigned a cabin number (and thus cabin mate). Both passengers and crew were assigned a sector on the ship to which the cabin and crew were assigned.
- 3. Calculate the target statistics (i.e., the expected count of each statistic at any given moment in time) associated with the terms in the existence model.
- 4. Estimate the coefficients for the existence model that represent the maximum likelihood estimates for the expected cross-sectional network structure.

Steps 1–4 occur within the *EpiModel* software and used the ERGM methods therein. They are completed efficiently by the use of an approximation in Step 4 (4). During the subsequent model simulation, we use the method of Krivitsky (5) to adjust the coefficient for the first term in each model at each time step, in order to preserve the same expected mean degree (relationships per person) over time in the face of changing network size and nodal composition. At all stages of the project, simulated partnership networks were checked to ensure that they indeed retained the expected cross-sectional structure and relational durations throughout the simulations.

## 3 MODEL CALIBRATION

We used Bayesian approaches to define a select set of model parameters with uncertain values, construct prior distributions for those parameters, and fit the model to diagnosed SARS-CoV-2 case data to estimate the posterior distributions of those parameter values.

### **3.1 Calibration Methods**

We used Approximate Bayesian Computation with sequential Monte Carlo sampling (ABC-SMC) methods (6, 7) to calibrate \ parameters in which there was measurement uncertainty in order to match the diagnosed cases. The details of ABC depend on the specific algorithm used, but in this case, ABC-SMC proceeded as follows.

For each candidate parameter,  $\theta$ , to be estimated, we:

- 1. Sampled a candidate  $\theta^i$  from a prior distribution  $\pi(\theta)$
- 2. Simulated the epidemic model with candidate value,  $\theta^i$ .
- 3. Tested if a distance statistic,  $d$  (e.g., the difference between observed HIV prevalence and model simulated prevalence) was greater than a tolerance threshold,  $\epsilon$ .
	- a. If  $d > \epsilon$  then discard
	- b. If  $d < \epsilon$  then add the candidate  $\theta^i$  to the posterior distribution of  $\theta$ .
- 4. Sample the next sequential candidate,  $\theta^{i+1}$ , either independently from  $\pi(\theta)$  (if 3a) or from  $\theta^i$  plus a perturbation kernel with a weight based on the current posterior distribution (if 3b).

### **3.2 Justification of Calibration to Cumulative Incidence Data**

We calibrated the model to match the target statistics the cumulative positive SARS-CoV-2 diagnoses on the Diamond Princess ship. Given the potential for overestimating the precision of fitted parameters when using cumulative incidence data  $(8, 9)$ , we experimented with fitting the model to both raw daily cases and cumulative daily cases. While we appreciate the theoretical advantages of fitting to raw cases suggested in this literature, the procedures were not practical here for four reasons.

First, daily case counts were low because the underlying target population on the ship was small. This is in contrast with the modeling work in King (8) and Towers (9), where the target population was country wide and the daily case counts numbered in the hundreds or thousands. Attempting to calibrate our model to raw case counts simply failed because of the noisiness of the data and algorithms.

Second, the observed cases on the Diamond Princess were a function of diagnosis campaigns with relatively wide temporal fluctuation (i.e., there were waves of diagnoses on certain days). This was in contrast to the Ebola case data in King and Towers, where the diagnoses were more slowly ramping up as the outbreak progressed. If we fit to the daily cases in our model, we could end up overfitting our screening rate parameters versus our more parsimonious approach of calibrating periods of screening rates as they increased over the outbreak (see Supplemental Table 1).

Third, in contrast to the compartmental models featured in King and the statistical time-series models in Towers, our individual-based models have inherently more model stochasticity as a function of model structure. Thus, our model prediction intervals reflect the additional uncertainty involved in stochastic outbreaks in small population settings.

Finally, in contrast to both King and Towers, our primary goal was not parameter estimation (e.g., both of those papers used models to estimate  $R_0$ ) but counterfactual intervention scenario projection. Of course, the uncertainty of our projections is related to the precision of the parameter estimates, but in a much more indirect way than the direct parameter estimation experiments of King and Towers.

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#### **3.3 Calibration Results**

We calibrated the model to cumulative daily counts (see Supplemental Figure 1) using calibration prior distributions in Supplemental Table 1. Overall, the model fit well to the cumulative data as well as the raw daily case counts. The estimates of the posterior distribution medians and 95% credible intervals are provided in Supplemental Table 1. For primary analyses, we used the maximum likelihood estimates (medians) from the posterior estimates for model selection purposes. For sensitivity analyses (Supplemental Figures 3–5), we sampled from across the posterior distribution to evaluate the correlation between these estimated parameters and cumulative incidence.

#### **3.4 Post-Calibration Sensitivity Analyses**

To evaluate the sensitivity of the primary outcome (cumulative incidence) to the fitted parameters, we conducted a probabilistic sensitivity analysis by sampling from the full posterior distributions of each parameter. This involved drawing from the posterior distributions 10,000 times and recording the cumulative incidence with each parameter set. The bivariate comparisons between each sampled parameter and the outcome are visualized in Supplemental Figures 3–5. The model outcomes are more closely correlated with the infection probability and contact intensity parameters than the screening rate parameters in these bivariate comparisons.

To numerically quantify the independent relationships, we fit a multivariable metamodel with linear regression, with the 10,000 simulations as individual observations. This regression model estimated the relationship between cumulative incidence and symptomatic screening at day 26, asymptomatic screening at day 26, the per-contact infection probability, and the per-dyad exposure intensity. We found no statistically significant relationships with symptomatic screening at day 26 (32.9 fewer cases per 1 unit increase in the screening rate;  $95\%$  CI: -167.3, 101.5; p = 0.63) or asymptomatic screening at day 26 (144.9 more cases per 1 unit increase in the screening rate;  $95\%$  CI: -38.7, 328.6; p = 0.12). However, the infection probability (103.3 more cases per 1 percentage point increase in the parameter; 95% CI: 99.8, 106.8; p < 0.001) and contact intensity (208.9 more cases per one unit increase in the perdyad exposures per day; 95% CI: 204.4, 213.6; p < 0.001) were strongly associated with cumulative incidence. This multivariable metamodel approach to sensitivity analysis suggests that the intervention results generally may be sensitive to the calibrated parameters related to the force of infection.

### **SUPPLEMENTAL FIGURES**

Supplemental Figure 1. Comparison of model calibration to cumulative diagnoses to raw (daily) case counts. As noted above, the daily case counts were noisy due to small population size and temporally varying screening campaigns on the ship, so we elected to calibrate to cumulative diagnoses instead with the caveat that our precision may be overestimated.



**Supplemental Figure 2.** COVID-19 transmission and disease progression is represented as transitions from an exposed latent state to either a symptomatic (clinical) or asymptomatic (subclinical) pathway. Transmissibility is reduced within the asymptomatic pathway. Disease-induced mortality occurs within the infectious, symptomatic state only.









Supplemental Figure 5. Sensitivity analysis of relationship between infection probability per contact and cumulative incidence and contact intensity (number of exposures per day per dyad) and cumulative SARS-CoV-2 incidence.

# **SUPPLEMENTAL TABLES**

### **Supplemental Table 1.** Calibrated Model Parameters



### **Supplemental Table 2.** Primary Model Parameters







**Supplemental Table 3.** Impact of Network Isolation Timing, With and Without Personal Protective Equipment (PPE), on COVID-19 Incidence and Mortality at 1 Month

<sup>1</sup> Number of infections averted relative to base scenario

<sup>2</sup> Percent of infections averted relative to base scenario

<sup>3</sup> Number of COVID-related deaths averted relative to base scenario

<sup>4</sup> Percent of COVID-related deaths averted relative to base scenario

**Supplemental Table 4.** Directionality of Transmission and Contact Intensity Reductions, with Day 15 Network Lockdown and PPE, on COVID-19 Incidence at 1 Month



*Varying Passenger-Crew Contact Intensity*





**Supplemental Table 5.** Impact of Varying Intensity of Diagnosis-Based Case Isolation, with Asymptomatic Screening Starting at Day 15, Stratified by Network Lockdown and PPE Use, on COVID-19 Incidence and Mortality at 1 Month

<sup>1</sup> Number of infections averted relative to base scenario

<sup>2</sup> Percent of infections averted relative to base scenario

<sup>3</sup> Number of COVID-related deaths averted relative to base scenario

<sup>4</sup> Percent of COVID-related deaths averted relative to base scenario

Supplemental Table 6. Impact of Timing of Mass Asymptomatic Screening and Diagnosis-Based Case Isolation, with No Network Lockdown and Stratified by PPE Use, on COVID-19 Incidence and Mortality at 1 Month



<sup>1</sup> Number of infections averted relative to base scenario

<sup>2</sup> Percent of infections averted relative to base scenario

<sup>3</sup> Number of COVID-related deaths averted relative to base scenario

<sup>4</sup> Percent of COVID-related deaths averted relative to base scenario

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