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1 **Real-time monitoring the transmission potential of COVID-19 in Singapore, March 2020**

2

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31

32 **Abstract**

33 **Background**

34 As of March 31, 2020 the ongoing COVID-19 epidemic that started in China in December 2019
35 is now generating local transmission around the world. The geographic heterogeneity and
36 associated intervention strategies highlight the need to monitor in real time the transmission
37 potential of COVID-19. Singapore provides a unique case example for monitoring transmission,
38 as there have been multiple disease clusters, yet transmission remains relatively continued.

39

40 **Methods**

41 Here we estimate the effective reproduction number, R_t , of COVID-19 in Singapore from the
42 publicly available daily case series of imported and autochthonous cases by date of symptoms
43 onset, after adjusting the local cases for reporting delays as of March 17, 2020. We also derive the
44 reproduction number from the distribution of cluster sizes using a branching process analysis that
45 accounts for truncation of case counts.

46

47 **Results**

48 The local incidence curve displays sub-exponential growth dynamics, with the reproduction
49 number following a declining trend and reaching an estimate at 0.7 (95% CI: 0.3, 1.0) during the
50 first transmission wave by February 14, 2020 while the overall R based on the cluster size
51 distribution as of March 17, 2020 was estimated at 0.6 (95% CI: 0.4, 1.02). The overall mean
52 reporting delay was estimated at 6.4 days (95% CI: 5.8, 6.9), but it was shorter among imported
53 cases compared to local cases (mean 4.3 vs. 7.6 days, Wilcoxon test, $p < 0.001$).

54

55 **Conclusion**

56 The trajectory of the reproduction number in Singapore underscores the significant effects of
57 successful containment efforts in Singapore, but it also suggests the need to sustain social
58 distancing and active case finding efforts to stomp out all active chains of transmission.

59

60 **Keywords**

61 SARS-CoV-2, COVID-19, Singapore, Transmission potential, Transmission heterogeneity,
62 Reproduction number, Cluster distribution, Reporting delay

63 **Background**

64 The ongoing COVID-19 pandemic started with a cluster of pneumonia cases of unknown etiology
65 in Wuhan, China back in December 2019 (1, 2). The initial cases have been linked to a wet market
66 in the city of Wuhan, pointing to an animal source of the epidemic (3). Subsequently, rapid human-
67 to-human transmission of the disease was confirmed in January 2020, and the etiological agent
68 was identified as severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) due to
69 its genetic similarity to the SARS-CoV discovered in 2003 (4, 5). The total global case tally has
70 reached 750,890 infections including 36,405 deaths and involving 199 countries as of March 31,
71 2020 (6). As the virus continues to spread in the human population, obtaining an accurate “real-
72 time” picture of the epidemic’s trajectory is complicated by several factors including reporting
73 delays and changes in the case definition (7, 8). Although the COVID-19 case incidence in China
74 has substantially declined, active transmission is now occurring in multiple countries around the
75 world (2). Epidemiological data from these countries can help to monitor transmission potential of
76 SARS-CoV-2 in near real-time.

77
78 Outside of China, Singapore, where the first symptomatic imported case (66 years old Chinese
79 male) was reported on January 23, 2020, has been able to maintain relatively low COVID-19
80 incidence levels through active case finding and strict social distancing measures. Up until March
81 31, 2020, Singapore has reported 926 laboratory confirmed cases, including 24 reported case
82 importations from Wuhan China and 501 non-Wuhan related case importations (9). Imported cases
83 include six individuals who were evacuated from China between January 30 and February 9, 2020
84 and multiple citizens and long term Singapore pass holders returning from Asia, Europe and North
85 America in late March 2020 (9-11). Moreover, Singapore has reported 3 deaths as of March 31,
86 2020 (9). On February 4, 2020, the Ministry of Health of Singapore reported its first local cluster
87 of COVID-19, which was linked to the Yong Thai Hang shop (12). A total of 18 clusters with 2 or
88 more COVID-19 cases have been reported thus far. Table 1 summarizes the characteristics of the
89 6 largest clusters in Singapore.

90
91 Although large-scale community transmission has not been reported in Singapore, the novel
92 coronavirus can rapidly spread in confined and crowded places, as illustrated by large clusters of
93 COVID-19 cases linked to the Grace Assembly of God Church, the Life Church and Missions

94 Singapore, Wizlearn Technologies and the SAFRA Jurong cluster (13, 14). In China, substantial
95 hospital-based transmission of SARS-CoV-2 has been reported, with approximately 3400 cases
96 involving healthcare workers (15). This pattern aligns well with past outbreaks of SARS and
97 MERS (16), including substantial nosocomial transmission during the 2003 SARS outbreak in
98 Singapore (17). To minimize the risk of hospital-based transmission of SARS-CoV-2, the Ministry
99 of Health of Singapore has restricted the movement of patients and staff across hospitals (18).
100 Also, because multiple unlinked COVID-19 cases have been reported in the community (19) and
101 the recognition that a substantial proportion of asymptomatic cases may be spreading the virus
102 (20-22), strict social distancing measures have been put in place including advising the public
103 against large social gatherings in order to mitigate the risk of community transmission (23, 24).
104 These social distancing measures reduce the risk of onward transmission not only within
105 Singapore, but also beyond the borders of this highly connected nation (25). A recent influx of
106 imported cases from Asia, Europe and North America into Singapore has triggered travel bans and
107 restrictions for travelers and citizens (9).

108
109 The reproduction number is a key threshold quantity to assess the transmission potential of an
110 emerging disease such as COVID-19 (26, 27). It quantifies the average number of secondary cases
111 generated per case. If the reproduction number is below 1.0, infections occur in isolated clusters
112 as self-limited chains of transmission, and persistence of the disease would require continued
113 undetected importations. On the other hand, reproduction numbers above 1.0 indicate sustained
114 community transmission (16, 27). Using epidemiological data and mathematical modeling tools,
115 we are monitoring the effective reproduction number, R_t , of SARS-CoV-2 transmission in
116 Singapore in real-time, and here we report the evolution of R_t by March 17, 2020. Specifically, we
117 characterize the growth profile and the effective reproduction number during the first transmission
118 wave from the daily case series of imported and autochthonous cases by date of symptoms onset
119 after adjusting for reporting delays, and we also derive an estimate of the overall reproduction
120 number based on the characteristics of the clusters of COVID-19 in Singapore.

121

122 **Methods**

123

124 *Data*

125 We obtained the daily series of 247 confirmed COVID-19 cases in Singapore between January 23-
126 March 17, 2020 from public records of the Ministry of Health, Singapore as of March 17, 2020
127 (9). Individual-level case details including the dates of symptoms onset, the date of reporting, and
128 whether the case is autochthonous (local transmission) or imported are publicly available. Clusters
129 consisting of two or more cases according to the infection source were also assembled from case
130 descriptions obtained from field investigations conducted by the Ministry of Health, Singapore
131 (9). Single imported cases are analyzed as clusters of size 1 whereas unlinked cases were excluded
132 from the cluster analysis.

133

134 ***Transmission clusters***

135 As of March 17, 2020, 18 different clusters of COVID-19 cases with 2-48 cases per cluster have
136 been reported in Singapore. A schematic diagram and characteristics of the COVID-19 clusters in
137 Singapore are given in Figure 1 and Table 1. The geographic location of the six clusters accounting
138 for 45.3% of the total cases is shown in Figure 2 whereas the corresponding distribution of cluster
139 sizes is shown in Figure 3.

140

141 ***Yong Thai Hang cluster***

142 This cluster with 9 cases was the first to be reported in Singapore. It has nine traceable links,
143 including eight Chinese and one Indonesian national associated with the visit of Chinese tourists
144 to the Yong Thai Hang health products store, a shop that primarily serves the Chinese population,
145 on January 23, 2020. Four shop employees and the tour guide were first identified as a cluster on
146 February 4, 2020 (12, 28, 29). The tour guide subsequently infected her husband, a newborn and
147 the domestic helper (29). No further cases have been added to this cluster as of February 8, 2020.

148

149 ***Grand Hayatt hotel***

150 This cluster with 3 local cases was the second cluster to receive international attention, as it
151 originated from a business meeting held at the Grand Hayatt hotel attended by Singaporean locals
152 and the Chinese visitors from Hubei (30). Four international cases associated with this cluster had
153 left Singapore before the onset of symptoms. All Singaporean residents associated with this cluster
154 have recovered as of February 19, 2020 (30). No additional cases have been added to this cluster
155 as of February 8, 2020.

156 ***Seletar Aerospace Heights cluster***

157 This cluster with 5 Bangladeshi work pass holders was identified on February 9, 2020. No further
158 cases have been added to this cluster as of February 15, 2020.

159

160 ***The Life Church and Missions and The Grace Assembly of God cluster***

161 The biggest Singaporean cluster is composed of 33 cases, including two imported cases and 31
162 local cases. The cluster started during The Life Church and Missions service event in Paya Lebar
163 on January 19, 2020. This event was apparently seeded by two visitors from Wuhan China who
164 infected a couple with SARS-CoV-2 at the church. The infected couple likely passed the infection
165 to another case during a Lunar New Year's celebration on January 25, 2020. This case had
166 subsequently infected Grace Assembly of God church staff at the Tanglin branch, generating
167 secondary cases by the time he was reported on February 14, 2020. Two branches of the Grace
168 Assembly of God church at Tanglin and Bukit Batok have been included in this cluster (28, 31).
169 This church serves an average of 4800 people in attendance over the weekend. While the church
170 has momentarily closed, field investigations have not led to conclusive evidence regarding super-
171 spreading transmission (32). No further cases have been added to this cluster as of March 9, 2020.

172

173 ***SAFRA Jurong cluster***

174 The largest cluster composed of 48 local cases is linked to a private dinner function at SAFRA
175 Jurong restaurant on February 15, 2020. The restaurant was closed for cleaning from February 16-
176 February 19, 2020 following the dinner function. The latest case was added to this cluster on March
177 16, 2020.

178

179 ***Wizlearn Technologies cluster***

180 This cluster which comprises of 14 cases, was identified on February 26, 2020. Wizlearn
181 Technologies is an e-learning solutions company. The latest case was added to this cluster on
182 March 3, 2020.

183

184 ***Church of Singapore cluster***

185 The first case of this cluster was identified on March 14, 2020, originating as a secondary case
186 from a case in the SAFRA Jurong cluster. This cluster is composed of 3 local cases. No further
187 cases have been added to this cluster since March 16, 2020.

188

189 ***Boulder gym cluster***

190 The first case of this cluster was identified on March 8, 2020, also linked to the SAFRA Jurong
191 cluster. This cluster is composed of 3 local cases. No further cases have been added to this cluster
192 since March 10, 2020.

193

194 ***Cluster A***

195 The first case of this cluster was identified on February 14, 2020. The cluster comprise of 3 local
196 cases. No further cases have been added in this cluster as of February 18, 2020.

197

198 ***Cluster B***

199 The first case of this cluster was identified on February 19, 2020. This cluster is composed of two
200 local cases. No further cases have been added in this cluster since February 21, 2020.

201

202 ***Cluster C***

203 This first case of this cluster was identified on March 3, 2020. This cluster is composed of 2 local
204 cases. No further cases have been added to this cluster since March 6, 2020.

205

206 ***Cluster D***

207 The first case of this cluster was identified on March 7, 2020. The two cases (one imported and
208 one local) in this cluster are related to each other. No further cases have been added in this cluster
209 since March 8, 2020.

210

211 ***Cluster E***

212 The two cases (an imported and a local case) of this cluster were identified on March 11, 2020. No
213 further cases have been added in this cluster since March 11, 2020.

214

215 ***Cluster F***

216 The first case of this cluster was identified on March 11, 2020. This cluster is composed of 3 local
217 cases. No further cases have been added to this cluster since March 13, 2020.

218

219 ***Cluster G***

220 This cluster is composed of 5 cases, including 4 imported cases. The first case of this cluster was
221 identified on March 10, 2020. No further cases have been added to this cluster since March 13,
222 2020.

223

224 ***Cluster H***

225 The first case of this cluster was identified on March 14, 2020, a secondary case generated from a
226 case at SAFRA Jurong cluster. This cluster is composed on 3 local cases. No further cases have
227 been added to this cluster since March 16, 2020.

228

229 ***Cluster I***

230 The first case of this cluster was identified on March 14, 2020. This cluster is composed of one
231 local and one imported case. No further cases have been added to this cluster since March 15,
232 2020.

233

234 ***Cluster J***

235 The first case of this cluster was identified on March 15, 2020. This cluster is composed of one
236 imported and one local case. No further cases have been added to this cluster since March 16,
237 2020.

238

239 ***Adjusting for reporting delays***

240 As an outbreak progresses in real time, epidemiological curves can be distorted by reporting delays
241 arising from several factors that include: (i) delays in case detection during field investigations,
242 (ii) delays in symptom onset after infection, (iii) delays in seeking medical care, (iv) delays in
243 diagnostics and (v) delays in processing data in surveillance systems (33). However, it is possible
244 to generate reporting-delay adjusted incidence curves using standard statistical methods (34).
245 Briefly, the reporting delay for a case is defined as the time lag in days between the date of onset
246 and date of reporting. Here we adjusted the COVID-19 epidemic curve of local cases by reporting

247 delays using a non-parametric method that employs survival analysis known as the Actuaries
248 method for use with right truncated data, employing reverse time hazards to adjust for reporting
249 delays as described in previous publication (35-37). The 95% prediction limits are derived
250 according to Lawless et al. (38). For this analysis, we exclude 7 imported cases and 5 local cases
251 for which dates of symptoms onset are unavailable.

252

253 ***Effective reproduction number from case incidence***

254 We assess the effective reproduction number over the course of the outbreak, R_t , which quantifies
255 the temporal variation in the average number of secondary cases generated per case during the
256 course of an outbreak after considering multiple factors including behavior changes, cultural
257 factors, and the implementation of public health measures (16, 27, 39). Estimates of $R_t > 1$ indicate
258 sustained transmission; whereas, $R_t < 1$ implies that the outbreak is slowing down and the incidence
259 trend is declining. Hence, maintaining $R_t < 1$ is required to bring an outbreak under control. Using
260 the reporting delay adjusted incidence curve, we estimate the most recent estimate of R_t for
261 COVID-19 in Singapore by characterizing the early transmission phase using a phenomenological
262 growth model as described in previous publications (40-42). Specifically, we first characterize
263 daily incidence of local cases for the first transmission wave (January 21- February 14, 2020) using
264 the generalized logistic growth model (GLM) after adjusting for imported cases. This model
265 characterizes the growth profile via three parameters: the growth rate (r), the scaling of the growth
266 parameter (p) and the final epidemic size (K). The GLM can reproduce a range of early growth
267 dynamics, including constant growth ($p=0$), sub-exponential or polynomial growth ($0 < p < 1$), and
268 exponential growth ($p=1$) (43). We denote the local incidence at calendar time t_i by I_i , the raw
269 incidence of imported cases at calendar time t_i by J_i , and the discretized probability distribution
270 of the generation interval by ρ_i . The generation interval is assumed to follow a gamma distribution
271 with a mean of 4.41 days and a standard deviation of 3.17 days based on refs. (44, 45). Then, we
272 can estimate the effective reproduction number by employing the renewal equation given by (40-
273 42)

$$274 \quad R_{t_i} = \frac{I_i}{\sum_{j=0}^i (I_{i-j} + \alpha J_{i-j}) \rho_i}$$

275 In this equation the numerator represents the new cases I_i , and the denominator represents the total
276 number of cases that contribute to the new cases I_i at time t_i . Parameter $0 \leq \alpha \leq 1$ represents the

277 relative contribution of imported cases to the secondary disease transmission. We perform a
278 sensitivity analyses by setting $\alpha = 0.15$ and $\alpha = 1.0$ (46). Next, in order to derive the uncertainty
279 bounds around the curve of R_t directly from the uncertainty associated with the parameters
280 estimates (r , p , K), we estimate R_t for 300 simulated curves assuming a Poisson error structure
281 (47).

282

283 ***Reproduction number (R) from the analysis of cluster sizes***

284 A second method of inferring the reproduction number applies branching process theory to cluster
285 size data to infer the degree of transmission heterogeneity (48, 49). Simultaneous inference of
286 heterogeneity and the reproduction number has been shown to improve the reliability of confidence
287 intervals for the reproduction number (50). In the branching process analysis, the number of
288 transmissions caused by each new infection is modeled as a negative binomial distribution. This
289 is parameterized by the effective reproduction number, R , and the dispersion parameter, k . The
290 reproduction number provides the average number of secondary cases per index case, and the
291 dispersion parameter varies inversely with the heterogeneity of the infectious disease. In this
292 parameterization, a lower dispersion parameter indicates higher transmission heterogeneity.

293

294 Branching process theory provides an analytic representation of the size distribution of cluster
295 sizes as a function of R , k and the number of primary infections in a cluster (as represented in
296 equation of 6 of the supplement of (51)). This permits direct inference of the maximum likelihood
297 estimate and confidence interval for R and k . In this manuscript, we modify the calculation of the
298 likelihood of a cluster size to account for the possibility that truncation of case counts at a specific
299 time point (i.e. March 17, 2020) may result in some infections being unobserved. This is
300 accomplished by denoting x as the sum of the observed number of serial intervals in a cluster. Then
301 the likelihood that an observed cluster of size j containing m imported cases is generated by x
302 infectious intervals is given by:

303

$$304 \quad l_{m \rightarrow j}^C(R_{eff}, k, x) = \frac{m}{j} l_{x \rightarrow (j-m)}(R_{eff}, k) \quad (1)$$

305 Where the likelihood of a i infections causing j infections is given by:

306

307
$$l_{i \rightarrow j}(R_{eff}, k) = \frac{\Gamma(j+ki)}{\Gamma(j+1)\Gamma(ki)} \left(\frac{k}{R_{eff}+k}\right)^{ki} \left(\frac{R_{eff}}{R_{eff}+k}\right)^j \quad (2)$$

308 where Γ is the gamma function.

309

310 To determine the number of observed serial intervals we observe in each cluster, we first estimate
311 the cumulative probability distribution of the serial interval. We assume the serial interval is a
312 gamma distribution, with a mean of 4.7 days and a standard deviation of 2.9 days (44). This
313 translates to a shape parameter of 2.63 and a scale parameter of 1.79. We then use the difference
314 between the onset data and the end of our study (March 17, 2020) to determine how much of the
315 infectious period was observed. For cases that only have a report date, but no onset date, we assume
316 an onset date that is six days earlier than the reporting date. This is based on the average duration
317 between onset date and report date that was observed in the data. When applied to the case series,
318 we are able to assign a total size, the number of imported cases and the observed number of
319 infectious periods for each cluster in the case series. When no imported cases are known to be in
320 a cluster, we assign the number of imported cases to be one as the cluster must have been initiated
321 by someone (e.g. the index case had contact with a foreign visitor).

322

323 When equation 1 is applied to the table of cluster size characteristics, the likelihood of the data can
324 be calculated as a function of R and k . Minimizing the likelihood produces the maximum
325 likelihood estimates of R and k . Applying the likelihood ratio test by profiling and R and k ,
326 produces confidence intervals (52). Code was run in R version 3.6.1.

327

328 **Results**

329

330 ***Incidence data and reporting delays***

331 The COVID-19 epidemic curve by the date of reporting, stratified for local and imported incidence
332 case counts is shown in Figure 4. It shows that the majority of the imported cases are concentrated
333 at the beginning of the outbreak (January 23, 2020 - February 3, 2020) and after March 10, 2020
334 in Singapore, with an average of ~ 12 new cases reported per day between March 1, 2020 and
335 March 17, 2020 (Figure 4). Out of 88 imported cases, only 14 cases have been linked to secondary

336 cases. Meanwhile, a total of 159 autochthonous cases have been reported as of March 17, 2020
337 including 27 cases that are unlinked to any known transmission chains.

338
339 The reporting-delay adjusted epidemic curve of local cases by date of symptoms onset roughly
340 displays two small waves of transmission reflecting the occurrence of asynchronous case clusters
341 (Figure 5). Moreover, the gamma distribution provided a reasonable fit to the distribution of
342 reporting delays for all cases, with a mean reporting delay at 6.4 days (95% CI: 5.8, 6.9) (Figure
343 6). We also found that imported cases tend to have shorter reporting delays compared to local cases
344 (mean 4.3 vs. 7.6 days, Wilcoxon test, $p < 0.001$), as imported cases tend to be identified more
345 quickly. The mean of reporting delays for the six large clusters ranged from 4.8-13.6 days (Figure
346 7).

347
348 **Reproduction Numbers**

349 For the first small wave of transmission comprising the first 25 epidemic days, the delay-adjusted
350 local incidence curve displays sub-exponential growth dynamics with the scaling of growth
351 parameter p at 0.7 (95% CI: 0.4, 1.0), the intrinsic growth rate r estimated at 0.6 (95% CI: 0.3, 1.1)
352 and parameter K estimating the wave size estimated at 95 (95%CI: 56, 230). Because of the sub-
353 exponential growth dynamics, the effective reproduction number followed a declining trend with
354 the latest estimate at 0.7 (95% CI: 0.3, 1.0) when $\alpha = 0.15$ (Figure 8). This estimate was not
355 sensitive to changes in parameter α .

356
357 Based on the entire distribution of cluster sizes, we jointly estimated the overall reproduction
358 number R and the dispersion parameter k as of March 17, 2020. Fitting the negative binomial
359 distribution to the cluster data in the empirical distributions of the realizations during the early
360 stages of the outbreak in Singapore, the reproduction number is estimated at 0.61 (95% CI: 0.39,
361 1.02) after adjusting for the truncation of the time series leading to the possibility that some
362 infected cases might still cause new infections after March 17, 2020. The dispersion parameter is
363 estimated at 0.11 (95% CI: 0.05, 0.25) consistent with SARS-CoV-2 transmission heterogeneity.

364
365 **Discussion**

366 Overall, current estimates of transmission potential in Singapore, based on two different data
367 sources and different methods, suggest that temporary local transmission potential of SARS-CoV-
368 2 has occurred in Singapore while our most recent estimate of the effective reproduction number
369 is below the epidemic threshold of 1.0 whereas the overall reproduction number derived from the
370 distribution of cluster sizes just barely crosses 1.0 ($R_t = 0.61$ (95% CI: 0.39, 1.02)). Temporary
371 sustained transmission in the beginning of the epidemic can be partly attributed to multiple case
372 importations and initiation of local transmission in the region. While large-scale local transmission
373 has not been reported in Singapore, the fact that asymptomatic and subclinical cases are now well
374 documented for COVID-19 (53) suggests that our estimates could be underestimated (54). On the
375 other hand, it is not clear if asymptomatic or subclinical cases are as infectious as symptomatic
376 cases. Indeed, we have reported that multiple local cases have yet to be traced to existing
377 transmission chains. Additional data collected during the course of the outbreak will help obtain
378 an improved picture of the transmission dynamics (55). These findings emphasize the need to
379 strengthen public health interventions including active case contact tracing activities in countries
380 with emerging transmission of SARS-CoV-2 (56). It is worth noting that imported cases have
381 minor contribution to secondary cases in Singapore, with most of the imported cases dating back
382 to the early phase of the epidemic and between March 10-17, 2020. However, there are examples
383 such as the Grant Hayatt Singapore cluster and the Yong Thai Hang cluster that were linked to
384 imported sources, and the original sources had left Singapore before these local clusters emerged
385 (30, 57).

386
387 Our R_t estimates for Singapore are substantially lower than mean estimates reported for the
388 COVID-19 epidemic in other parts of the world (58-66). This indicates that containment efforts
389 have a significant impact in Singapore (Table 2). However, some differences in the reproduction
390 numbers reported for the epidemic in China may result from different methods, differences in data
391 sources, and time periods used to estimate the reproduction number. Similarly, a recent study has
392 shown an average reporting delay of 6.1 days in China (67) which agrees with our mean estimate
393 for cases in Singapore (6.4 days). Moreover, the scaling parameter for growth rate (p) indicates a
394 sub-exponential growth pattern in Singapore, reflecting the effective isolation and control
395 strategies in the region. This is consistent with a sub-exponential growth pattern for Chinese

396 provinces excluding Hubei ($p \sim 0.67$), as estimated by a recent study (68); whereas, an exponential
397 growth pattern was estimated for Hubei ($p \sim 1.0$) (68).

398
399 A previous study on the 2015 MERS outbreak in South Korea reported substantial potential for
400 superspreading transmission despite a subcritical R_t (69). The lower estimate of the dispersion
401 parameter in our study also indicate significant transmission heterogeneity in Singapore. Super-
402 spreading events of MERS-CoV and SARS-CoV associated with nosocomial outbreaks are well
403 documented and driven largely by substantial diagnostic delays (16, 37). Although the average
404 delay from onset of symptoms to diagnosis for COVID-19 patients in Singapore is at 6.4 days and
405 no super-spreading events has been observed yet, the dispersion parameter, $k < 1$, indicates the
406 probability of observing large clusters and the potential for super-spreading such as the SAFRA
407 Jurong cluster (49, 69). Therefore, public health measures enacted by public health authorities in
408 Singapore that advise the public to avoid mass gatherings and confined places are crucial to prevent
409 disease amplification events. However, the presence of asymptomatic cases in the community
410 represent an ongoing threat (70, 71) although it is not currently known if subclinical cases are less
411 infectious. This highlights the need for rapid testing of suspected cases to quickly isolate those that
412 test positive for the novel coronavirus. To achieve this goal, public health authorities in Singapore
413 are reactivating 900 general practitioner clinics (72). While new clusters emerge in Singapore,
414 some clusters including the Yong Thai Hang cluster, Seletar Aerospace cluster, Wizlearn
415 Technologies and the Grand Hayatt cluster have stabilized (no recent additional cases in most
416 clusters). The “Grace Assembly of God and the Life Church and Missions” cluster and the
417 “SAFRA Jurong” cluster continue to be consolidated (57, 73).

418
419 Beyond Singapore, COVID-19 cases are now being reported in 204 countries including
420 identifiable clusters in many parts of the world (2, 74-77). Moreover, Singapore has also produced
421 secondary chains of disease transmission beyond its borders (25). Although Singapore has been
422 detecting and isolating cases with diligence, our findings underscore the need for continued and
423 sustained containment efforts to prevent large-scale community transmission including
424 nosocomial outbreaks. Overall, the current situation in Singapore highlights the need to investigate
425 the imported, unlinked and asymptomatic cases that could be a potential source of secondary cases
426 and amplified transmission in confined settings. Although Singapore has a world-class health

427 system including a highly efficient contact tracing mechanism in place that has prevented to
428 outbreak from getting out of control (25, 78), continued epidemiological investigations and active
429 case finding efforts are needed to contain the outbreak.

430
431 Our study is not exempt from limitations. First, the outbreak is still ongoing and we continue to
432 monitor the transmission potential of COVID-19 in Singapore. Second, onset dates are missing for
433 twelve cases, which were excluded from our analyses. Third, we cannot rule out that additional
434 cases will be added to existing clusters, which may lead to underestimating the reproduction
435 number based on the cluster size distribution. Fourth, some of the cases are associated with
436 generating secondary chains in more than one cluster, which were included in the most relevant
437 cluster.

438

439 **Conclusion**

440 This is a real-time study to estimate the evolving transmission potential of SARS-CoV-2 in
441 Singapore. Our current findings point to temporary sustained transmission of SARS-CoV-2, with
442 our most recent estimate of the effective reproduction number lying below 1.02. These estimates
443 highlight the significant impact of containment efforts in Singapore while at the same time suggest
444 the need to maintain social distancing and active case finding efforts to stomp out all active or
445 incoming chains of transmission.

446

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457

458 **List of abbreviations**

459 COVID-19

460 SARS-CoV-2

461

462 **Ethics approval and consent to participate**

463 Not applicable

464

465 **Consent for publication**

466 Not applicable

467

468 **Conflict of Interest**

469 The authors declare no conflicts of interest.

470

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474

475 **Data declaration**

476 All data are publicly available.

477

478 **Author Contributions**

479 A.T, S.B., P.Y. and G.C. analyzed the data. A.T. , Y. L, P.Y and S.M. retrieved and managed data;

480 A.T and G.C wrote the first draft of the manuscript. All authors contributed to writing and revising

481 subsequent versions of the manuscript. All authors read and approved the final manuscript.

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Cluster name	Cluster location	Cluster size	Number of Imported Cases linked to the cluster	Number of local cases linked to the cluster	Number of secondary cases in the cluster	Reporting date for the first case linked to cluster	Reporting date for the last case linked to cluster
Yong Thai Hang cluster	Yong Thai Hang Medical Store on Cavan Road	9	0	9	1	February 4, 2020	February 8, 2020
Grand Hayatt cluster	Grand Hayatt hotel in Orchard	3	0	3	0	February 6, 2020	February 8, 2020
The Life Church and Missions and The Grace Assembly of God cluster	The Life Church and Missions at Paya Lebar and The Grace Assembly of God Church at Tanglin and Bukit Batok	33	2	31	10	January 29, 2020	March 9, 2020

Seletar Aerospace Heights construction cluster	Seletar Aerospace Heights construction site	5	0	5	4	February 9, 2020	February 15, 2020
Wizlearn Technologies cluster	Wizlearn Technologies in Science park	14	0	14	8	February 26, 2020	March 3, 2020
SAFRA Jurong cluster	SAFRA Jurong restaurant	48	0	48	29	February 27, 2020	March 16, 2002

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696 Table 1: Characteristics of the largest COVID-19 outbreak in Singapore as of March 17, 2020.

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Date	Event
1/23/2020	First imported case of SARS-CoV-2 confirmed
1/23/2020-1/26/2020	Flights to Wuhan cancelled by the Singaporean government
1/29/2020	Travelers from Hubei denied entry in Singapore
2/1/2020	New visitors with recent travel history to mainland China within the last 14 days denied entry into Singapore, or transit through Singapore
2/1/2020	Distribution of masks by the government
2/4/2020	First cases of local SARS-CoV-2 transmission
2/6/2020	First recovered patient in Singapore
2/7/2020	Singapore's outbreak response level upgraded from yellow to orange
2/17/2020	Stay at home notices issued for 14 days for all Singapore residents and long term work pass holders returning from China
2/23/2020	Travel advisory extended to visitors from South Korea
2/25/2020	Links between Grace Assembly of God cluster and The Life Church and Missions cluster established
2/26/2020	Ban on visitors arriving from Cheongdo and Daegu in South Korea.
2/28/2020	Singapore company Biotech introduced COVID-19 test kit for in-vitro case diagnosis
3/4/2020	Ban implemented on visitors arriving from South Korea, Iran and Italy
3/10/2020	600 passengers disembarked from the Italian cruise ship, Costa Fortuna and social distancing measures announced
3/12/2020	First two deaths from COVID-19 reported

3/15/2020	Ban implemented on visitors arriving from Italy, France, Spain and Germany
3/18/2020	Announcement made for all visitors entering Singapore from March 20, 2020 onwards to observe a 14 day quarantine
3/22/2020	Ban implemented on all short term visitors arriving or transiting from Singapore from March 23, 2020 onwards
3/23/2020	Announcement made for travelers including Singapore citizens required to submit a health declaration before entering Singapore
3/24/2020	Social distancing measures reinforced including bans on large gatherings and social events
3/26/2020	Punishments announced for individuals breaching the stay at home notices

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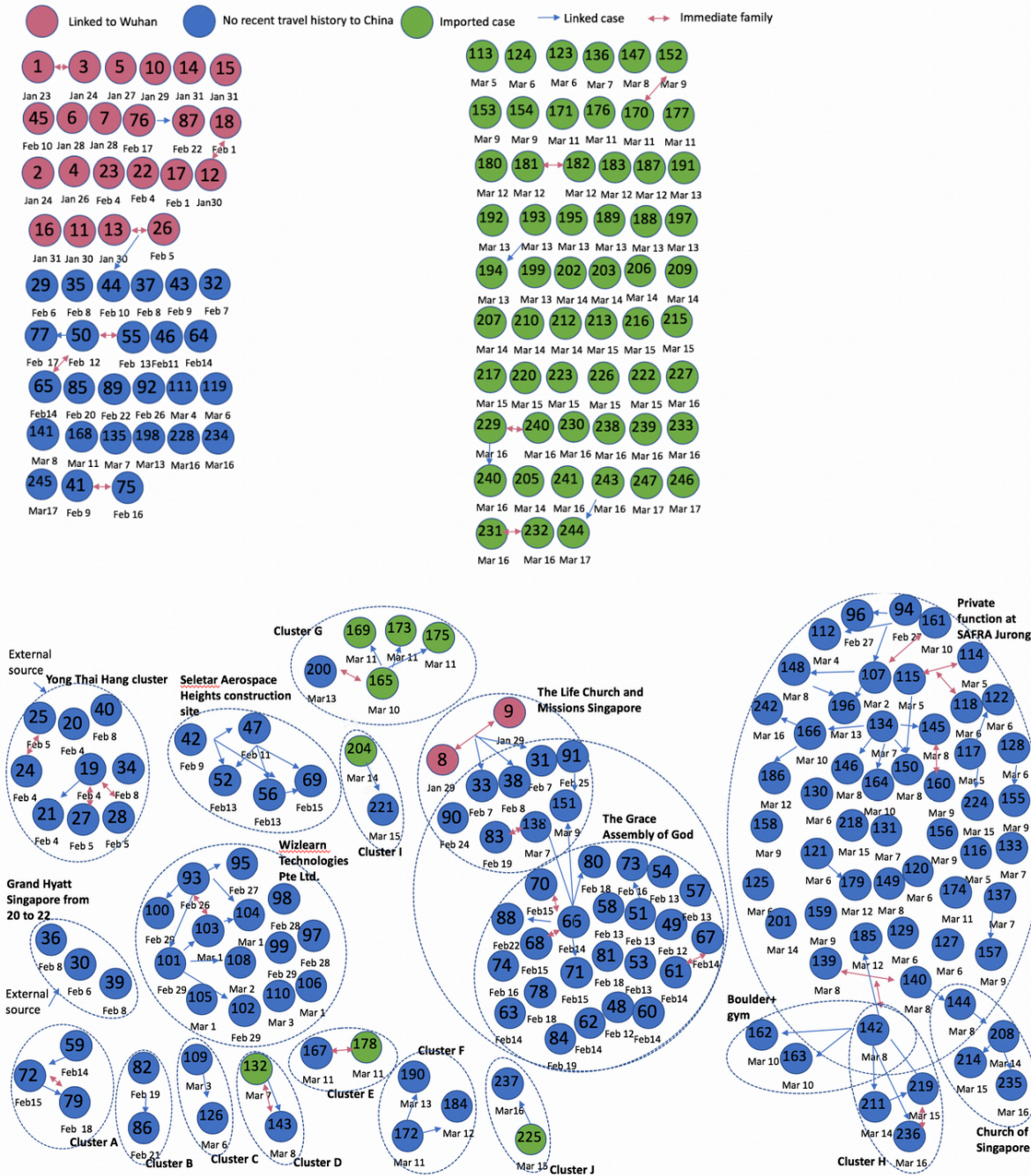
714 Table 2: Timeline of COVID-19 epidemic in Singapore as of March 31, 2020.

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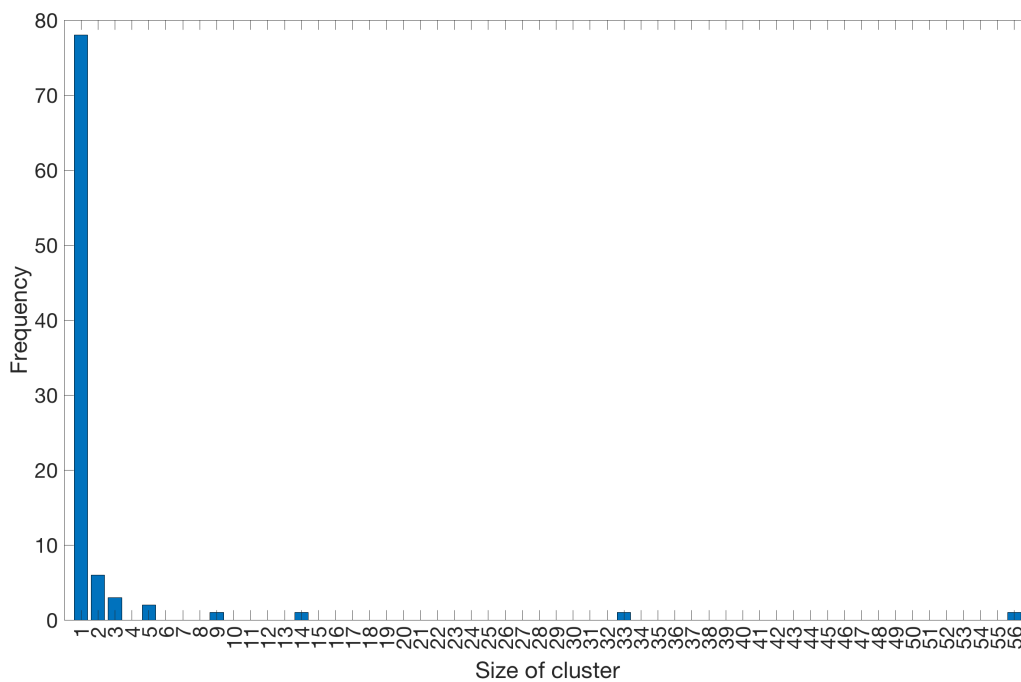
721 Figure 1: Cluster network of the cases in Singapore for the COVID-19 global pandemic as of
 722 March 17, 2020 . The pink circles represent the cases linked to Wuhan, the green circles represent
 723 the non-Wuhan related case importations and the blue circles represent cases with no travel history
 724 to China. The larger dotted circles represent the COVID-19 disease clusters. Each blue arrow

725 represents the direction in which the disease was transmitted. Pink arrows represent immediate
726 family. Dates below the circles are the dates of case reporting.
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730 Figure 2: Map depicting the spatial distribution of the 6 largest COVID-19 clusters in Singapore;
731 Grand Hayatt cluster, Yong Thai Hang cluster, Seletar Aerospace cluster, Wizlearn Technologies
732 cluster, SAFRA Jurong cluster and The Grace Assembly of God Church and Life Church and
733 Missions cluster as of March 17, 2020.

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739 Figure 3: Distribution of COVID-19 cluster sizes in Singapore as of March 17, 2020.

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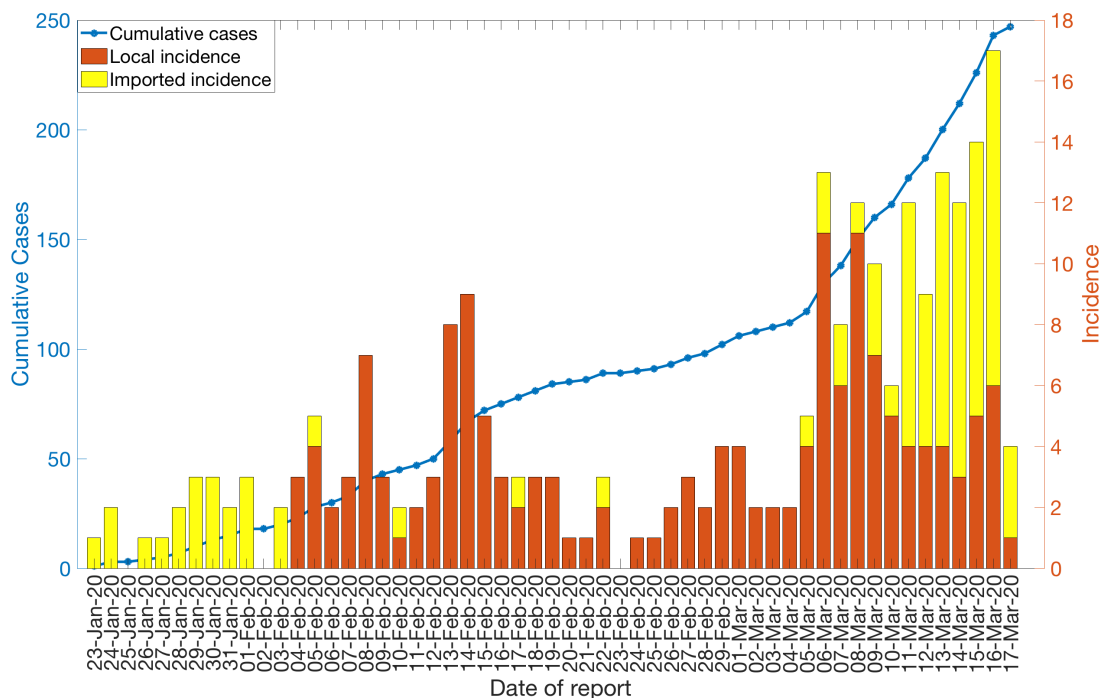
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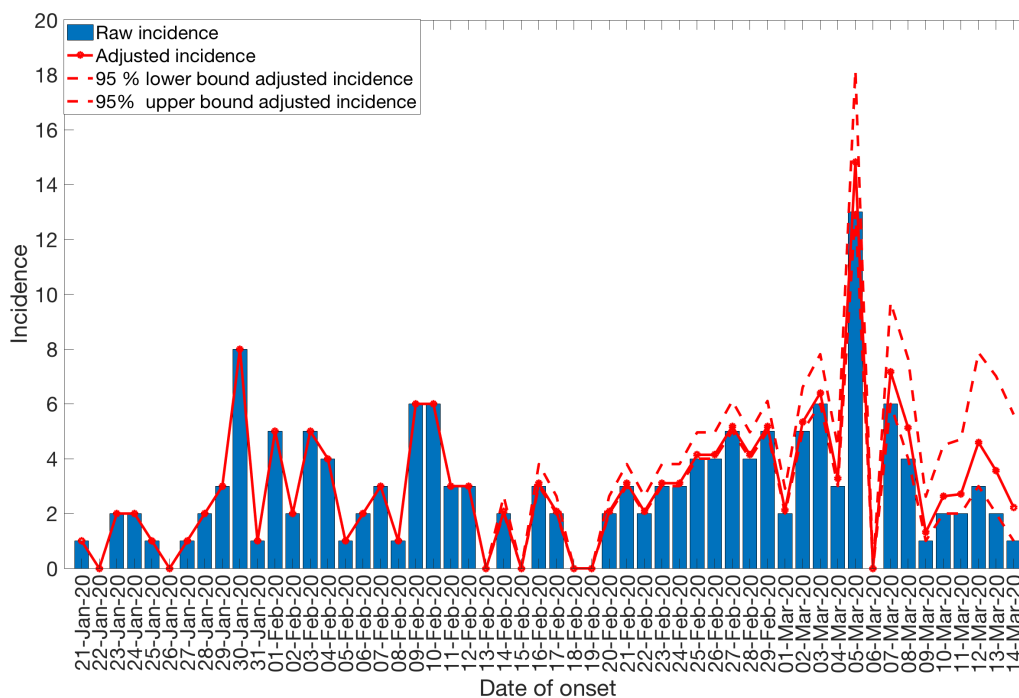
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749 Figure 4: Local and imported incidence cases by date of reporting as of March 17, 2020. The solid
750 blue line represents the cumulative case count for the COVID-19 cases in Singapore.
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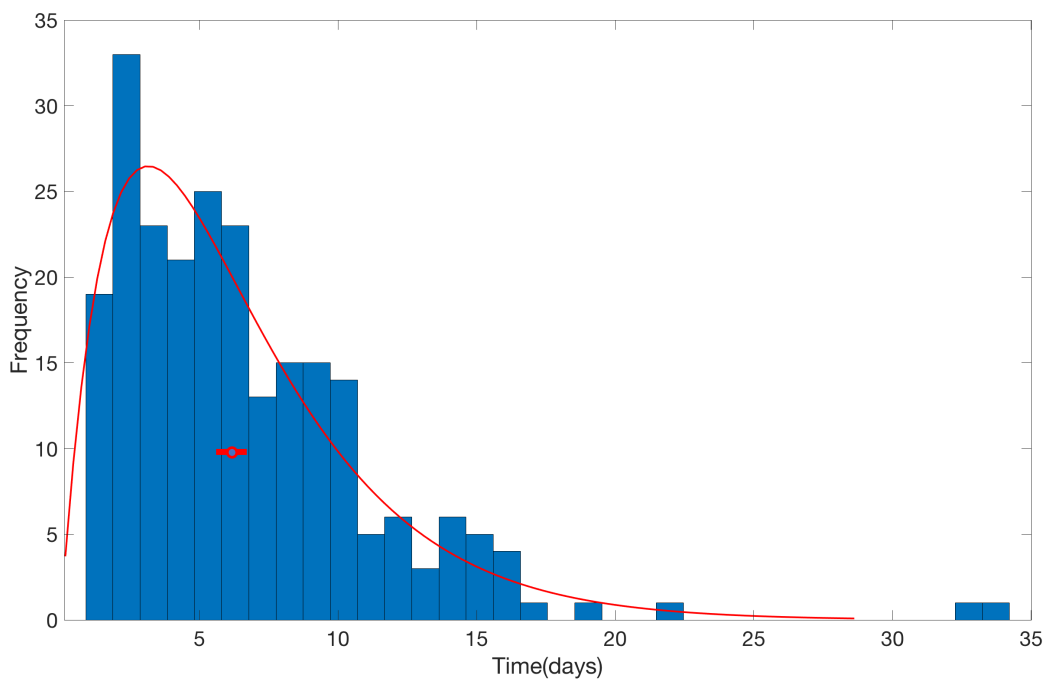


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755 Figure 5: Reporting delay adjusted local incidence for the COVID-19 outbreak in Singapore as of
756 March 17, 2020. Blue bars represent the raw incidence, red solid line represents the adjusted
757 incidence, red dotted lines represent the 95% lower and upper bound of the adjusted incidence.

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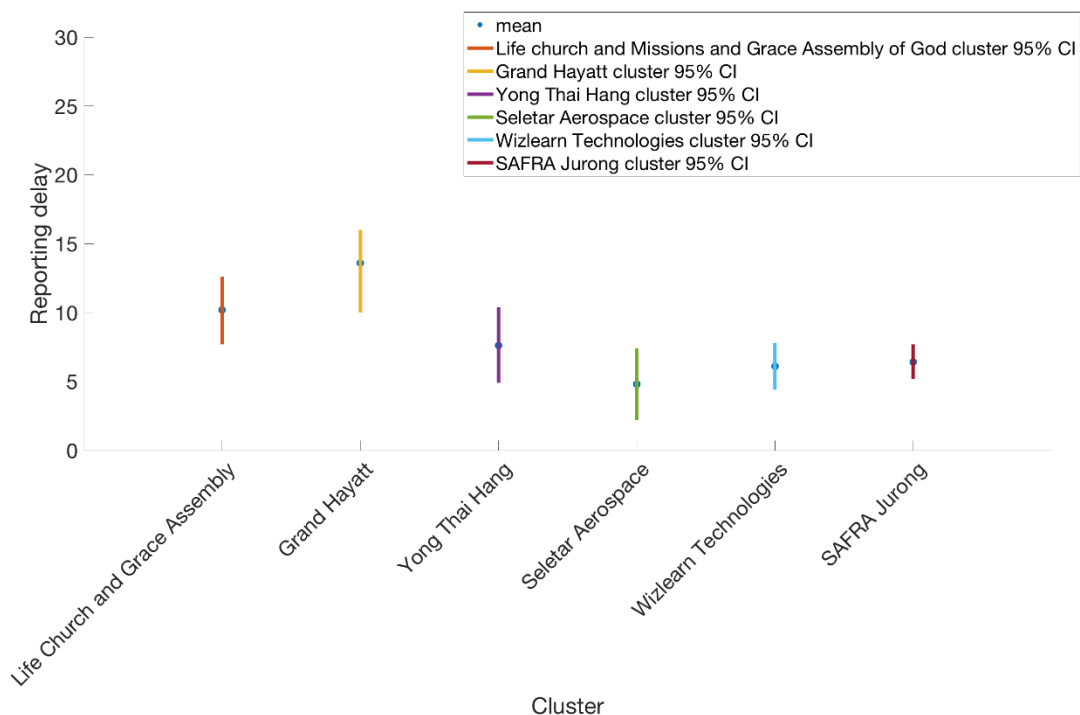


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761 Figure 6: The distribution of reporting delays for all cases as of March 17, 2020. The red line
762 represents the fit of a gamma distribution to the data. The red circle represents the mean of gamma
763 distribution and the horizontal line represents the 95% CI.

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782 Figure 7: Reporting delay distribution with mean (blue circle) and 95% CI (vertical lines) for each
783 big cluster in Singapore; Grand Hayatt cluster, Yong Thai Hang cluster, Seletar Aerospace cluster,
784 Wizlearn Technologies cluster, SAFRA Jurong cluster and The Grace Assembly of God Church
785 and Life Church and Missions cluster as of March 17, 2020.

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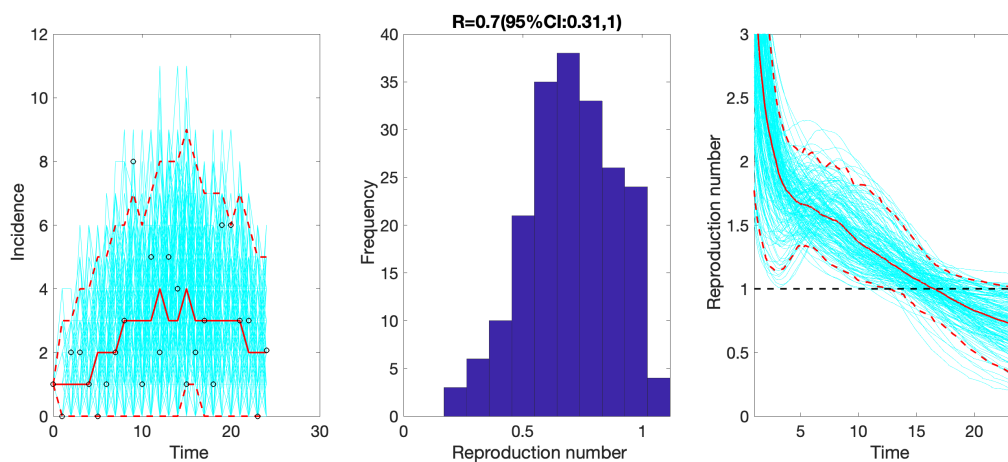
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799 Figure 8: The effective reproduction number reproduction number with 95% CI estimated by
800 adjusting for the imported cases $\alpha = 0.15$ during the first transmission wave by February 14, 2020.

801 The effective reproduction number followed a declining trend with the latest estimate at 0.7 (95%
802 CI: 0.3,1.0) by February 14, 2020.