

1 **Version 1**

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2

3 **Title: A mathematical model for estimating the age-specific transmissibility of a novel**
4 **coronavirus**

5 **Running title: Age-specific transmissibility of SARS-CoV-2**

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36

37 **Abstract**

38 **Background:** A novel coronavirus named as "SARS-CoV-2" has spread widely in many countries since

39 December 2019, especially in China. This study aimed to quantify the age-specific transmissibility by

40 using a mathematical model.

41 **Methods:** An age-specific susceptible – exposed – symptomatic – asymptomatic – recovered –

42 seafood market (SEIARW) model was developed based on two suspected transmission routes (from

43 market to person and person to person). The susceptible people from Wuhan City were divided into

44 different age groups. We used the subscript i and j to represent age group 1 to 4 ($i \neq j$; 1: ≤ 14 years; 2:

45 15-44 years; 3: 45-64 years; 4: ≥ 65 years) and 1 to 5 ($i \neq j$; 1: ≤ 5 years; 2: 6-14 years; 3: 15-24 years; 4:
46 25-59 years; 4: ≥ 60 years), respectively. Data of reported COVID-19 cases were collected from one
47 published literature from 26 November to 22 December, 2019 in Wuhan City, China. The age-specific
48 transmissibility of the virus was estimated accordingly secondary attack rate (SAR).

49 **Results:** The age-specific SEIARW model fitted with the reported data well by dividing the population
50 into four age groups ($\chi^2 = 4.99 \times 10^{-6}$, $P > 0.999$), and five age groups ($\chi^2 = 4.85 \times 10^{-6}$, $P > 0.999$).
51 Based on the four-age-group SEIARW model, the highest transmissibility occurred from age group 2 to
52 3 ($SAR_{23} = 17.56$ per 10 million persons), followed by from age group 3 to 2 ($SAR_{32} = 10.17$ per 10
53 million persons). The lowest transmissibility occurred from age group 1 to 2 ($SAR_{12} = 0.002$ per 10
54 million persons). Based on the five-age-group SEIARW model, the highest transmissibility occurred
55 from age group 4 to 5 ($SAR_{45} = 12.40$ per 10 million persons), followed by from age group 5 to 4 (SAR_{54}
56 = 6.61 per 10 million persons). The lowest transmissibility occurred from age group 3 to 4 ($SAR_{34} =$
57 0.0002 per 10 million persons).

58 **Conclusions:** SARS-CoV-2 has high transmissibility among adults and elder people but low
59 transmissibility among children and young people.

60 **Key words:** Transmissibility; Novel coronavirus; Mathematical model; Age-specific dynamics

61

62 Introduction

63 In December 2019, a series of cases were identified by a novel coronavirus named severe acute
64 respiratory syndrome coronavirus 2 (SARS-CoV-2) was reported by Wuhan City, Hubei Province,
65 China. The disease was named as coronavirus disease 2019 (COVID-19) by the World Health
66 Organization in 11 February 2020. The patients may be related to have contacted with Huanan
67 Seafood Wholesale Market[1], and the virus can continuously transmit from person-to-person with
68 basic reproduction number (R_0) of 2.2 (95% confidence interval [CI], 1.4 to 3.9)[2]. Another research
69 estimated that the R_0 of SARS-CoV-2 was 2.68 (95% CI, 2.47 to 2.86)[3].

70 Age-related transmissibility of COVID-19 has become a public health concern. The reported cases
71 at the early stage (before 2 January 2020) of the transmission were higher than 18 years old and
72 mainly were on 25-64 years old[1]. A study with 425 patients indicated that the median age was 59
73 years (range, 15 to 89) and reported different case distributions in four age groups: 0 – 14, 15 – 44, 45
74 – 64, and ≥ 65 years[2]. However, there is not enough epidemiological evidence to classify the age
75 groups in transmission. In this study, we added another age classification scenario according to our
76 previous research on influenza that people were divided into five age groups: 0 – 5, 6 – 14, 15 – 24, 25
77 – 59, and ≥ 60 years[4], to better understand the transmissibility of the disease for different ages.

78 There were several studies focusing on mathematical modelling on COVID-19[2, 3], calculating the
79 R_0 by using the serial intervals and intrinsic growth rate[2, 5, 6], or using ordinary differential equations
80 and Markov Chain Monte Carlo methods[3]. We also developed a Bats-Hosts-Reservoir-People (BHRP)
81 transmission network model and simplified the BHRP model as Reservoir-People (RP) transmission
82 network model to calculate the transmissibility of SARS-CoV-2[7]. However, there is no age-specific
83 mathematical model for quantifying the age-specific transmissibility SARS-CoV-2.

84 In this study, based on the RP model which we developed, we built an age-specific susceptible –
85 exposed – symptomatic – asymptomatic – recovered – reservoir (SEIARW) model. The age-specific
86 SEIARW model was employed to estimate the age-specific transmissibility of SARS-CoV-2 by fitting
87 the data from 26 November to 23 December, 2019 from published literature[1].

88

89 **Methods**

90 **Data collection**

91 The data of COVID-19 were collected in Wuhan City from 26 November, 2019 to 23 December,
92 2019 from a published literature[1], including 29 COVID-19 cases with the onset date and exposure
93 history. The data of total population which were used in our model was from Wuhan City Statistics
94 Bureau. The data of age group proportions, birth rate and death rate in our model was obtained from
95 Wuhan Statistical Yearbook.

96 **Study design**

97 In this study, people were divided into 4 age groups based on the published literature[1], and 5 age
98 groups based on our previous study[4]. We used the subscript i and j to represent age group 1 to 4 ($i \neq j$;
99 1: 0 – 14 years; 2: 15 – 44 years; 3: 45 – 64 years; 4: ≥ 65 years) and 1 to 5 ($i \neq j$; 1: 0 – 5 years; 2: 6-14
100 years; 3: 15-24 years; 4: 25-59 years; 4: ≥ 60 years), respectively.

101 **Age-specific transmission model**

102 Our previous study showed that the SEIARW model could be adopted to simulate the infectious
103 diseases transmitted from reservoir (such as water or food) to people and from person to person[8, 9].
104 In this study, the age-specific SEIARW model was developed based on two transmission routes (form
105 market to person and person to person). In the model, people were divided into five compartments:

106 susceptible (S), exposed (E), symptomatic (I), asymptomatic (A), recovered (R), and the seafood
107 market were defined as reservoir (W). The definitions of the six compartments were shown in [Table 1](#).

108 The model was based on following assumptions:

109 a) Susceptible individuals become infected by contact with infected/asymptomatic people;

110 b) SARS-CoV-2 can transmit within each age group. The transmission rate of age group i and j are
111 β_{ij} and β_{ji} respectively.

112 c) SARS-CoV-2 can be transmitted between different age groups. The transmission rate from age
113 group i to j is β_{ij} and from j to i is β_{ji} .

114 d) Susceptible people will be infected after contact with seafood market, and the infection rate
115 coefficient is β_w ;

116 e) All the newborn individuals which were assumed as susceptible were added into age group 1.
117 Each age group has a natural mortality rate. We set the natural birth rate is br , and the natural mortality
118 rate is dr ;

119 f) The incubation period of exposed person is $1/\omega$. The exposed person will become asymptomatic
120 people after a latent period of $1/\omega'$. We describe p ($0 \leq p \leq 1$) as the proportion of asymptomatic
121 infection. Exposed individuals will become asymptomatic person A with a daily rate of pE , and become
122 symptomatic person with a daily rate of $(1-p)E$;

123 g) The transmissibility of A is κ times ($0 \leq \kappa \leq 1$) of that of I .

124 h) The individuals I and A will become recovered person (R) after an infectious period of $1/\gamma$ and
125 $1/\gamma'$. A part of I would die due to the infection. We assumed that the case fatality rate was f .

126 i) I and A individuals can shed pathogens into W with the shedding rate of μI and $\mu' A$, where μ and
127 μ' are the shedding coefficients;

128 j) SARS-CoV-2 will remove in the market after a given period (the life time of the virus is $1/\varepsilon$), and
 129 the daily decreasing rate of the pathogen is εW .

130 The flowchart of the model was shown in [Figure 1](#). The equations of the age-specific SEIARW
 131 model were shown as follows:

$$\frac{dS_i}{dt} = brN - \beta_{ii}S_i(I_i + \kappa A_i) - \beta_{ji}S_i(I_j + \kappa A_j) - \beta_w S_i W - drS_i$$

$$\frac{dE_i}{dt} = \beta_{ii}S_i(I_i + \kappa A_i) + \beta_{ji}S_i(I_j + \kappa A_j) - (1-p)\omega E_i - p\omega' E_i - drE_i$$

$$\frac{dI_i}{dt} = (1-p)\omega E_i - \gamma I_i - (dr + f)I_i$$

$$\frac{dA_i}{dt} = p\omega' E_i - \gamma' A_i - drA_i$$

$$\frac{dR_i}{dt} = \gamma I_i + \gamma' A_i - drR_i$$

$$\frac{dS_j}{dt} = brN - \beta_{jj}S_j(I_j + \kappa A_j) - \beta_{ji}S_j(I_i + \kappa A_i) - \beta_w S_j W - drS_j$$

$$\frac{dE_j}{dt} = \beta_{jj}S_j(I_j + \kappa A_j) + \beta_{ji}S_j(I_i + \kappa A_i) + \beta_w S_j W - (1-p)\omega E_j - p\omega' E_j - drE_j$$

$$\frac{dI_j}{dt} = (1-p)\omega E_j - \gamma I_j - (dr + f)I_j$$

$$\frac{dA_j}{dt} = p\omega' E_j - \gamma' A_j - drA_j$$

$$\frac{dR_j}{dt} = \gamma I_j + \gamma' A_j - drR_j$$

$$\frac{dW}{dt} = \mu(I_i + I_j) + \mu'(A_i + A_j) - \varepsilon W$$

$$N = S_i + E_i + I_i + A_i + R_i + S_j + E_j + I_j + A_j + R_j$$

132
 133 Since the different dimension of people and the virus, we adopt the following sets to perform the
 134 normalization:

135 $s_i = S_i/N$, $e_i = E_i/N$, $i_i = I_i/N$, $a_i = A_i/N$, $r_i = R_i/N$, $s_j = S_j/N$, $e_j = E_j/N$, $i_j = I_j/N$, $a_j = A_j/N$,

136 $r_j = R_j/N$, $w = \varepsilon W/\mu N$, $\mu' = c\mu$, $b_{ii} = \beta_{ii}N$, $b_{ij} = \beta_{ij}N$, $b_{jj} = \beta_{jj}N$, $b_{ji} = \beta_{ji}N$, $b_w = \mu\beta_w N/\varepsilon$.

137
 7

138 In the normalization, parameter c refers to relative shedding coefficients of A compared to I . The
 139 normalized model is expressed as follows:

$$\frac{ds_i}{dt} = brn - b_{ii}s_i(i_i + \kappa a_i) - b_{ji}s_i(i_j + \kappa a_j) - b_w s_i w - drs_i$$

$$\frac{de_i}{dt} = b_{ii}s_i(i_i + \kappa a_i) + b_{ji}s_i(i_j + \kappa a_j) - (1 - p)\omega e_i - p\omega' e_i - dre_i$$

$$\frac{di_i}{dt} = (1 - p)\omega e_i - \gamma i_i - (dr + f)i_i$$

$$\frac{da_i}{dt} = p\omega' e_i - \gamma' a_i - dra_i$$

$$\frac{dr_i}{dt} = \gamma i_i + \gamma' a_i - drr_i$$

$$\frac{ds_j}{dt} = brn - b_{jj}s_j(i_j + \kappa a_j) - b_{ji}s_j(i_i + \kappa a_i) - b_w s_j w - drs_j$$

$$\frac{de_j}{dt} = b_{jj}s_j(i_j + \kappa a_j) + b_{ji}s_j(i_i + \kappa a_i) + b_w s_j w - (1 - p)\omega e_j - p\omega' e_j - dre_j$$

$$\frac{di_j}{dt} = (1 - p)\omega e_j - \gamma i_j - (dr + f)i_j$$

$$\frac{da_j}{dt} = p\omega' e_j - \gamma' a_j - dra_j$$

$$\frac{dr_j}{dt} = \gamma i_j + \gamma' a_j - drr_j$$

$$\frac{dw}{dt} = \varepsilon(i_i + i_j + c(a_i + a_j) - w)$$

$$n = s_i + e_i + j_i + a_i + r_i + s_j + e_j + i_j + a_j + r_j$$

140 The left side of the equation shows the instantaneous rate of change of S , E , I , A , R and W at time
 141 t . The subscript i and j ($i \neq j$) represent age group 1 to 4/5 in the equation, respectively.

142 Parameters estimation

143 The mean incubation period was 5.2 days (95% confidence interval [CI]: 4.1–7.0) [2]. As reported
 144 by Xu *et al* [10], the median time from exposure to onset of illness (infected) was 4 days (interquartile
 145 range 3-5 days). Another study showed that the mean of incubation period was around 5 days and the
 146 period falls within the range of 2-14 days [11]. We set the 5-day as the incubation period and the latent
 147 period in this study. Thus, $\omega = \omega' = 0.2$.

148 Since there was no data on the proportion of asymptomatic infection of the virus, we simulated the
149 baseline value of proportion of 0.5 ($p = 0.5$). Since there was no evidence about the transmissibility of
150 asymptomatic infection, we assumed that the transmissibility of asymptomatic infection was 0.5 times
151 that of symptomatic infection ($\kappa = 0.5$), which was the similar value as influenza[12]. We assumed that
152 the relative shedding rate of A compared to I was 0.5. Thus, $c = 0.5$. Since the SARS-CoV-2 is an RNA
153 virus, we assumed that it could be died in the environment in a short time, but it could stay for a longer
154 time (10 days) in the unknown hosts in the market. We set $\varepsilon = 0.1$.

155 There is a mean 5-day delay from symptom onset to detection/hospitalization of a case (the cases
156 detected in Thailand and Japan were hospitalized from 3-7 days after onset, respectively) [13-15].
157 Another study showed that the mean time from illness onset to hospital admission (for treatment and/or
158 isolation) was estimated at 3-4 days without truncation and at 5-9 days when right truncated[11]. As
159 reported by Xu *et al*[10], the median time from onset of illness to first hospital admission was 2 (range
160 from 1-4) days. A study including 45 patients diagnosed before January 1 was estimated to have a
161 mean of 5.8 days (95% *CI*: 4.3–7.5) from illness onset to first medical visit[2]. In our model, we set the
162 infectious period of the cases as 6 days. Therefore, $\gamma = \gamma' = 0.1667$.

163 According the official report by National Health Commission of the People's Republic of China, we
164 collected the data of daily fatality from January 24th to 30th, 2020[16]. Therefore, we set f as 0.02348
165 (range: 0.02198-0.03186). In this study, we set the total population as 11,081,000 so that $br = 4.266 \times$
166 10^{-5} and $dr = 3.184 \times 10^{-5}$ based on the 2018 Wuhan Statistical Yearbook (Table 2).

167 A two-step curve fitting method was adopted to estimate the parameter b_W , b_{ii} , b_{jj} , b_{ij} , and b_{ji} . At the
168 first step, we used the mix-age SEIARW model to fit the data and to estimate the parameter b_W and
169 mix-age b (named as b_p). At the second step, we used the age-specific SEIARW model to fit the data

170 and to estimate the parameter b_{ii} , b_{jj} , b_{ij} , and b_{ji} .

171 **Quantification of the age-specific transmissibility of SARS-CoV-2**

172 In the model the age-specific secondary attack rate (SAR) was employed to quantify the
173 transmissibility of SARS-CoV-2. They were calculated as follows:

$$SAR_{ii} = \beta_{ii}/\gamma$$

$$SAR_{ij} = \beta_{ij}/\gamma$$

$$SAR_{ji} = \beta_{ji}/\gamma$$

$$SAR_{jj} = \beta_{jj}/\gamma$$

174 In the equations, SAR_{ii} , SAR_{ij} , SAR_{ji} , and SAR_{jj} refer to the age-specific SAR among age group i ,
175 from age group i to j , from age group j to i , and among age group j , respectively.

176 To quantify the age-specific transmissibility of SARS-CoV-2, we also performed a simulation which
177 was named as “knock-out” simulation in our previous study[17]. In this study, the “knock-out” simulation
178 was defined as cutting off the route of transmission between or within different age groups, and was
179 performed in the following scenarios: A) $\beta_{ii} = 0$; B) $\beta_{ij} = 0$; C) $\beta_{ji} = 0$; D) $\beta_{jj} = 0$; E) control (no cutting off
180 transmission route).

181 **Simulation method and statistical analysis**

182 Berkeley Madonna 8.3.18 (developed by Robert Macey and George Oster of the University of
183 California at Berkeley. Copyright ©1993-2001 Robert I. Macey & George F. Oster) was employed to
184 perform the curve fitting and the simulation. The simulation methods (Runge-Kutta method of order four
185 with tolerance set at 0.001) were the same as the previously published researches [18-24]. The data
186 was analyzed and figured by using Microsoft Office Excel 2010 (Microsoft, Redmond, WA, USA) and
187 GraphPad Prism 7.0 (GraphPad Software, La Jolla, CA). The goodness of fit was judged by coefficient

188 of determination (R^2) and Chi-square (χ^2) value calculated by SPSS 21.0 (IBM Corp, Armonk, NY,
189 USA).

190 **Sensitivity analysis**

191 Since nine parameters (p , κ , c , ε , ω , ω' , γ , γ' and f) in the models were collected from literatures,
192 there might be some uncertainties in our model. Therefore, we performed sensitivity analysis of
193 parameters p , κ , c , ε , ω , ω' , γ , γ' and f by splitting them into 1,000 values ranging from 0 – 0.9, 0 – 1, 0 –
194 1, 0 – 1, 0.1428 – 0.25, 0.1428 – 0.25, 0.125 – 0.25, 0.125 – 0.25, 0.02198 – 0.03186, respectively
195 (Table 2).

196

197 **Results**

198 **Epidemiological characteristics and curve fitting of SARS-CoV-2**

199 There were 29 COVID-19 cases data collected in Wuhan City from 26 November, 2019 to 23
200 December, 2019, among which 10 cases had a history of the seafood market exposure and 19 cases
201 had no history of the exposure (Figure 2).

202 The mix-age SEIARW model including all age groups fitted the reported data well ($\chi^2 = 4.77 \times 10^{-6}$,
203 $P > 0.999$). The results of the curve fitting were shown in Figure 3. The results also showed that the b_p
204 = 1.1329 and $b_W = 0.5255$. The age-specific SEIARW model fitted with the reported data well by
205 dividing the population into four age groups ($\chi^2 = 4.99 \times 10^{-6}$, $P > 0.999$), and five age groups ($\chi^2 = 4.85$
206 $\times 10^{-6}$, $P > 0.999$). Thus, the prevalence of COVID-19 in each age group was simulated in Figure 4.

207 **Transmissibility of SARS-CoV-2**

208 Based on the four-age-group SEIARW model, the highest transmissibility occurred from age group
209 2 to 3 ($SAR_{23} = 17.56$ per 10 million persons), followed by from age group 3 to 2 ($SAR_{32} = 10.17$ per 10

210 million persons), from age group 4 to 4 ($SAR_{44} = 6.99$ per 10 million persons), and from age group 3 to
211 4 ($SAR_{34} = 5.69$ per 10 million persons). The lowest transmissibility occurred from age group 1 to 2
212 ($SAR_{12} = 0.002$ per 10 million persons), followed by from age group 3 to 1 ($SAR_{31} = 0.003$ per 10 million
213 persons), from age group 4 to 2 ($SAR_{42} = 0.52$ per 10 million persons), and from age group 1 to 3
214 ($SAR_{13} = 1.08$ per 10 million persons) (Figure 5-A).

215 Based on the five-age-group SEIARW model, the highest transmissibility occurred from age group
216 4 to 5 ($SAR_{45} = 12.40$ per 10 million persons), followed by from age group 5 to 4 ($SAR_{54} = 6.61$ per 10
217 million persons), from age group 4 to 4 ($SAR_{44} = 5.08$ per 10 million persons), and from age group 2 to
218 1 ($SAR_{21} = 4.90$ per 10 million persons). The lowest transmissibility occurred from age group 3 to 4
219 ($SAR_{34} = 0.0002$ per 10 million persons), followed by from age group 1 to 1 ($SAR_{11} = 0.22$ per 10 million
220 persons), from age group 1 to 3 ($SAR_{13} = 1.54$ per 10 million persons), and from age group 1 to 2
221 ($SAR_{12} = 1.59$ per 10 million persons) (Figure 5-B).

222 The results of the “knock-out” simulation showed that, based on the four-age-group SEIARW
223 model, the scenarios $b_{23} = 0$, $b_{32} = 0$, and $b_{22} = 0$ led to the highest decrease for the number of cases.
224 However, the scenarios $b_{12} = 0$, $b_{31} = 0$, and $b_{11} = 0$ led to the lowest decrease for the number of cases
225 (Figure 6-A). Based on the five-age-group SEIARW model, the scenarios $b_{44} = 0$, $b_{45} = 0$, and $b_{54} = 0$
226 led to the highest decrease for the number of cases. However, the scenarios $b_{12} = 0$, $b_{31} = 0$, and $b_{11} = 0$
227 led to the lowest decrease for the number of cases (Figure 6-B).

228 Sensitivity analysis

229 The results of sensitivity analysis showed that the models were slightly sensitive to parameters p ,
230 ω , and γ but not sensitive to parameters κ , c , ε , f , ω' , and γ' (Figures 7 – 8).

231

232 Discussion

233 This is the first study to develop an age-specific SEIARW model to quantify the transmissibility of
234 COVID-19 among different age groups. The results showed that our model fitted the reported data well,
235 thus has the capability of estimating or predicting? the age-specific transmissibility of the virus.

236 Based on the four-age-group SEIARW model, the highest transmissibility occurred between the
237 age groups 15 – 44 years and 45 – 64 years, among those ≥ 65 years, or from 45 – 64 years to ≥ 65
238 years. The lowest transmissibility occurred from age group 0-14 years to 15 – 44 years, or from 45 – 64
239 years to ≤ 14 years. Based on the five-age-group SEIARW model, the highest transmissibility occurred
240 between age group 25 – 59 years and ≥ 60 years, or among 25 – 59 years. The lowest transmissibility
241 occurred from age group 15 – 24 years to 25 – 59 years, or from age group 0-5 years to 6-14 years, or
242 to 15-24 years. The “knock-out” simulation had the similar results. We concluded that the virus was
243 more likely to transmit among older population.

244 These results revealed that SARS-CoV-2 has high transmissibility among adult older than 25 years
245 old or elder people, but has low transmissibility among children or people younger than 14 years.
246 These results were similar to the age-specific transmissibility of influenza A (H1N1)[4]. The age-specific
247 control and prevention interventions are needed.

248 The reasons for the difference of age-specific transmissibility remain unclear. It might be related to
249 the different contact characteristics among different age groups. Adults were more likely to work outside
250 and came into contact with different individuals in work places, buses, subways, or even airplanes.
251 However, children or younger people could stay at home during the outbreak, and they were less likely
252 to get infected, or if they were infected, it was mostly from adults or elder people in the same family.

253 Our findings were based on the parameter estimation and the data from literatures. It is known that

254 the asymptomatic infection of COVID-19 exists. As reported by Bai *et al*[25], 1 of 6 cases was
255 asymptomatic infected, with the proportion of asymptomatic of 0.17. As reported by Pan *et al*[26], 2 of 3
256 cases was asymptomatic infected, with the proportion of asymptomatic of 0.67. There was a research
257 showed that the asymptomatic infection would shed SARS-CoV-2 for 5 days[27]. However, there was
258 not enough evidence to provide the clear epidemiological estimates of the parameters ρ , κ , ω' , and γ'
259 which were related to asymptomatic characteristics. Although there was clinical evidence to calculate
260 the parameters related to symptomatic cases such as incubation period, fatality rate, and duration from
261 symptoms onset to diagnosis[1, 2], more epidemiological data are needed to explore the parameters.
262 However, we performed a sensitivity analysis of all the nine parameters from the literatures, and we
263 found that the models was slightly sensitive to parameters ρ , ω , and γ but not sensitive to parameters κ ,
264 c , ε , f , ω' , and γ' . Therefore, our results might be affected slightly by the parameter estimation.

265 Since we could not obtain the first-hand data, the results of our findings might have some
266 uncertainties. However, our study aimed to develop and provide an age-specific transmission model for
267 the public health department who has the big data to investigate the age-specific transmissibility in
268 real world scenarios.

269 **Conclusions**

270 By calculating the published data, our model showed that SARS-CoV-2 has a high transmissibility
271 among adults and elder people but low transmissibility among children and young people. Our results
272 provide a mathematical model for investigating the age-specific transmissibility of SARS-CoV-2. More
273 data and studies are needed to estimate the age-specific transmissibility in real world scenarios to
274 better understand the characteristics of the widely spread virus.

275

276 **Abbreviations**

277 SARS-CoV-2: severe acute respiratory syndrome coronavirus 2; COVID-19: coronavirus disease 2019;
278 R_0 : basic reproduction number; CI: confidence interval; BHRP: Bats-Hosts-Reservoir-People; RP:
279 Reservoir-People; SEIARW: susceptible – exposed – symptomatic – asymptomatic – recovered –
280 reservoir; SAR: secondary attack rate; R^2 : coefficient of determination.

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288 **Availability of data and materials**

289 Not applicable.

290 **Authors' contributions**

291 TMC and ZYZ designed research; TMC, YHS, BHZ, and ZYZ conceived the experiments, TMC, ZYZ,
292 YZZ, JWX, ZL, JR, XCL, YW, MY, LL, SSY, JL, RYL, FX, YYS, and YCC conducted the experiments
293 and analyzed the results; TMC, ZYZ, and QQH wrote the manuscript. All authors read and approved
294 the final manuscript.

295 **Competing interests**

296 The authors declare that they have no competing interests.

297 **Consent for publication**

298 Not applicable.

299 **Ethics approval and consent to participate**

300 Not applicable.

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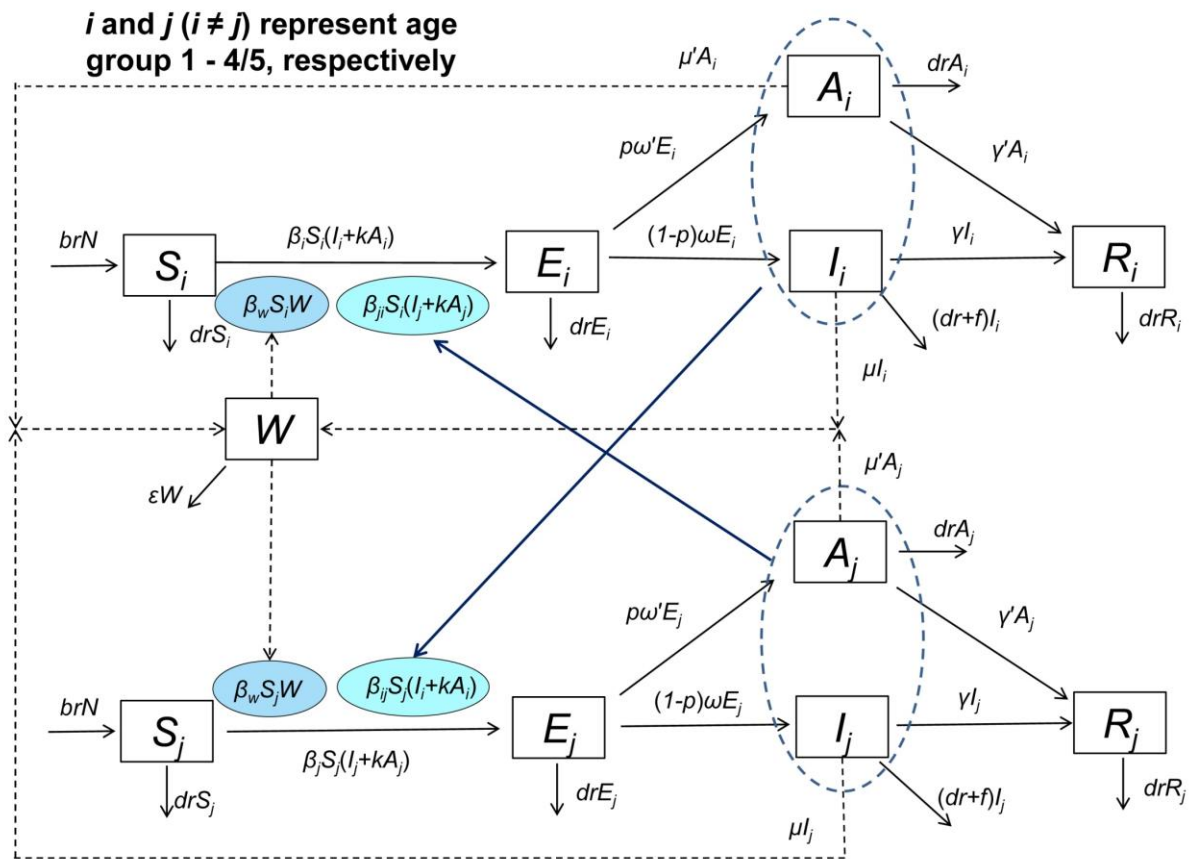
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381 **Figures**

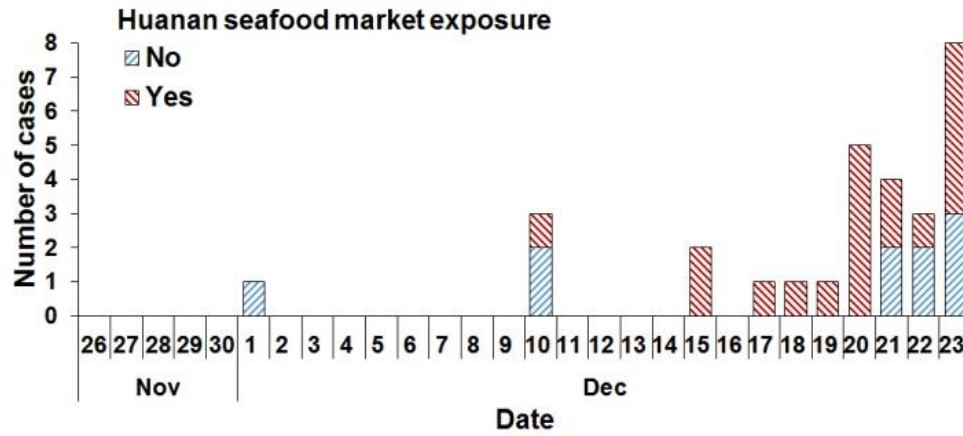
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384 **Figure 1. Flowchart of the age-specific SEIARW model**

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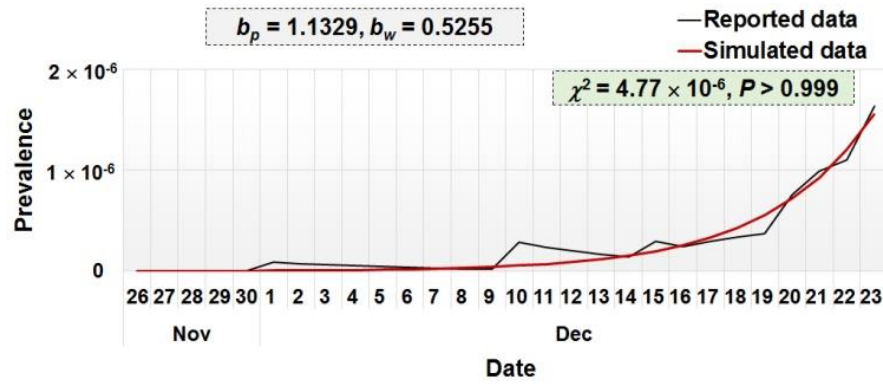


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387 **Figure 2. Epidemic curve of collected data of reported COVID-19 cases in Wuhan City from 26**

388 **November, 2019 to 23 December, 2019**

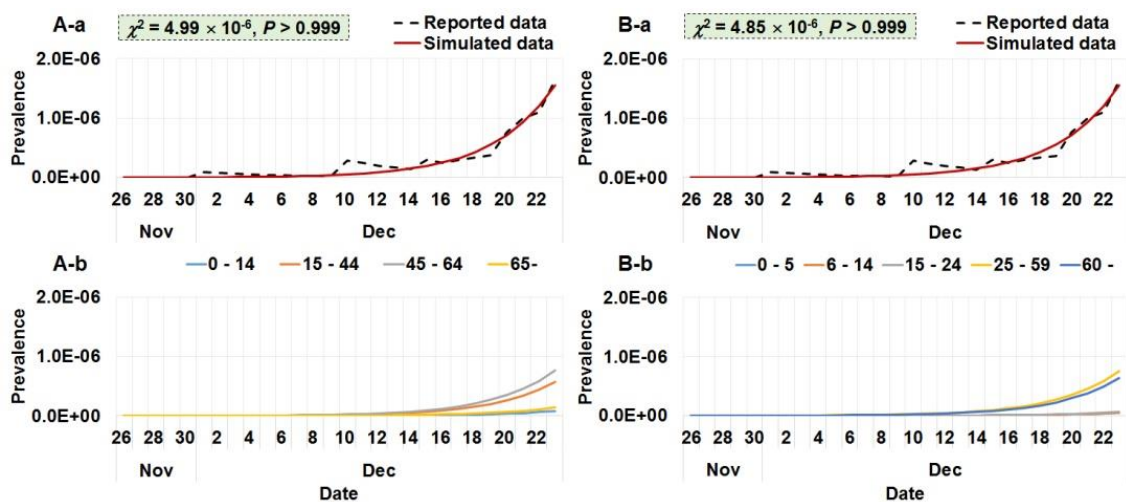
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391 **Figure 3. Results of curve fitting of the mix age SEIARW model to the reported data**

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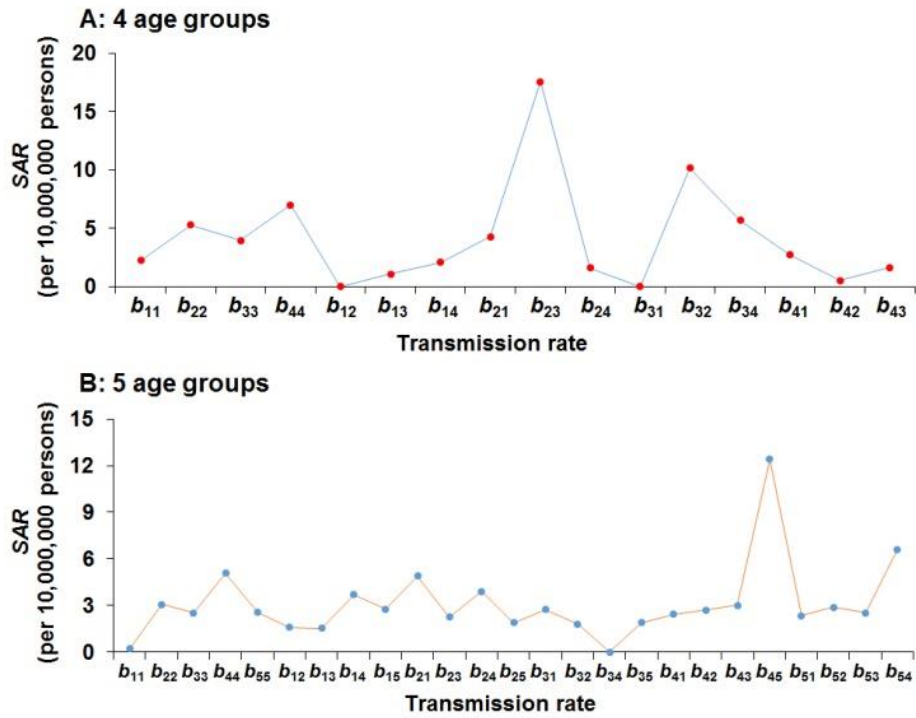
394 **Figure 4. Results of curve fitting of the age-specific SEIARW model to the reported data. A-a:**

395 curve fitting based on four age groups; A-b: the simulated prevalence by the age-specific SEIARW

396 model based on the four age groups; B-a: curve fitting based on five age groups; B-b: the simulated

397 prevalence by the age-specific SEIARW model based on the five age groups.

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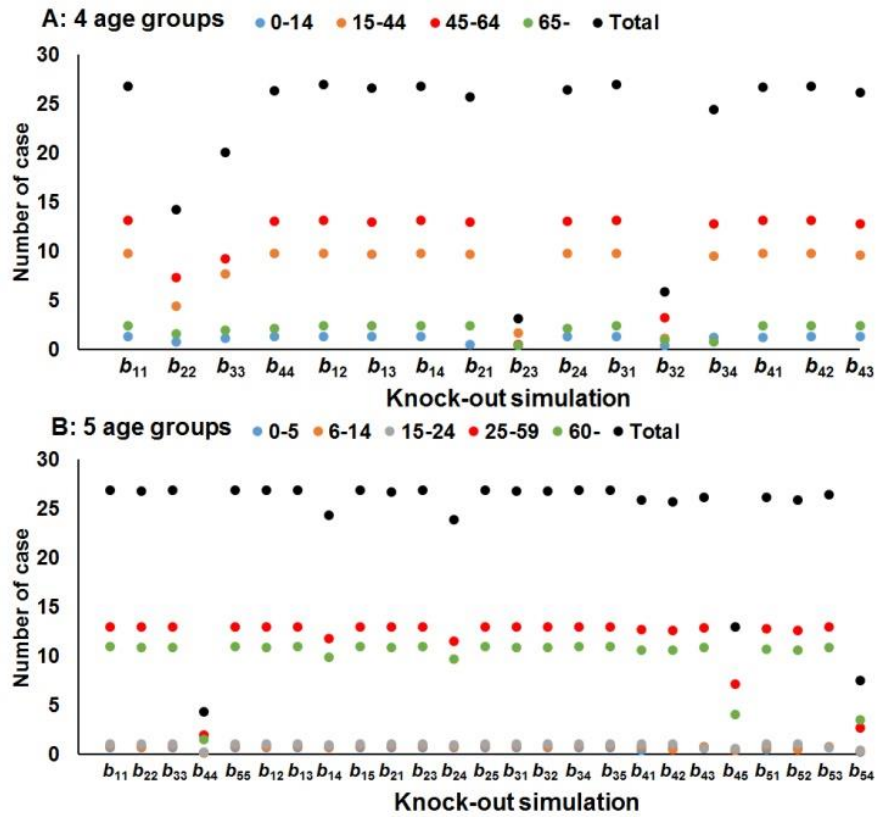


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400 **Figure 5. SAR simulated from the age-specific SEIARW model. A: SAR based on four age groups;**

401 B: SAR based on five age groups.

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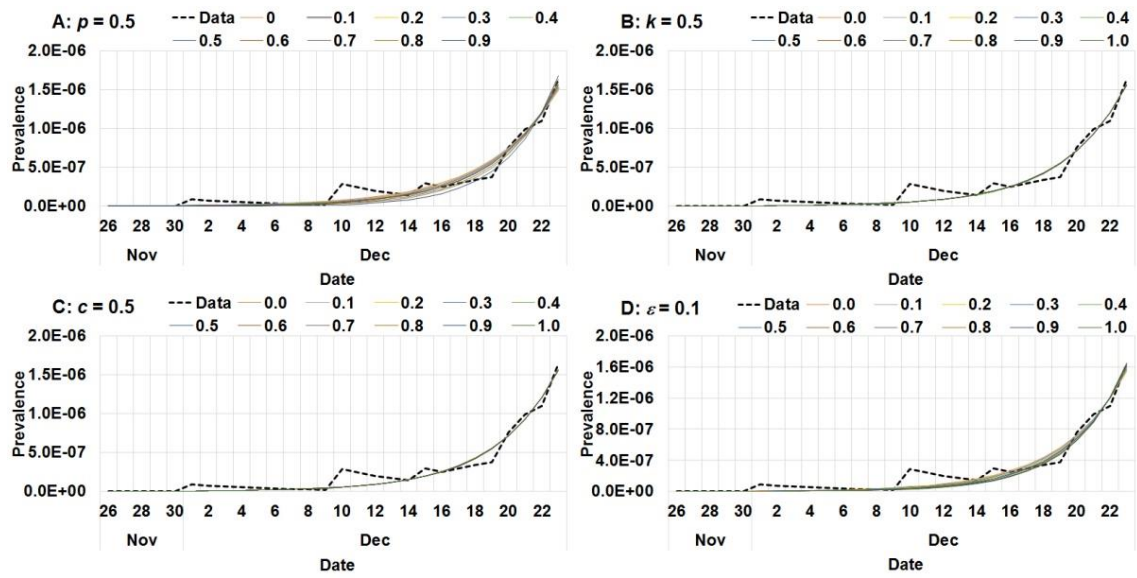


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404 **Figure 6. Results of the “knock-out” simulation from the age-specific SEIARW model. A: results**

405 based on four age groups; B: results based on five age groups.

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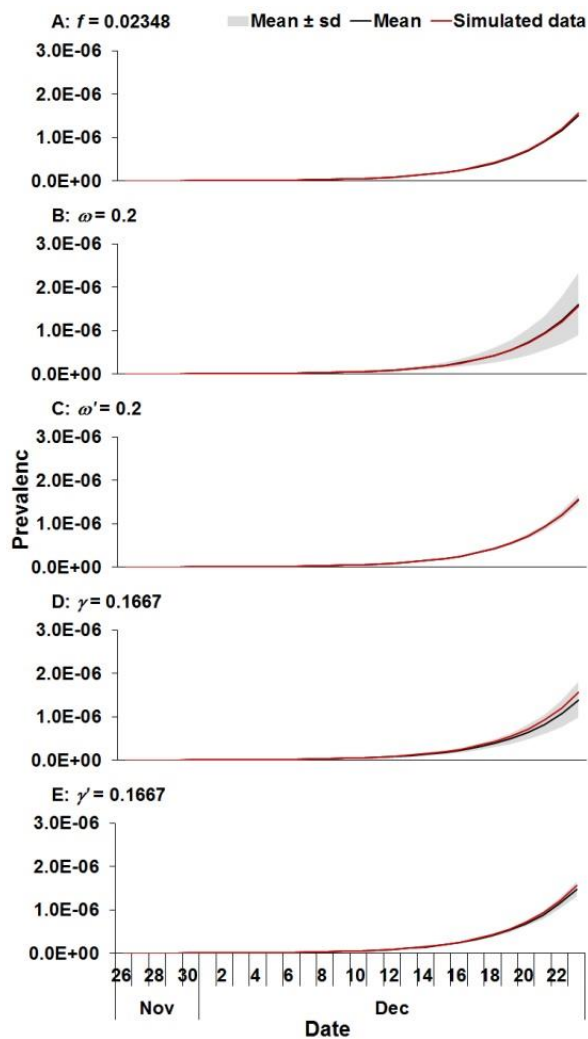


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408 **Figure 7. Results of sensitivity analysis of p , κ , c , and ϵ .** A: sensitivity analysis of p ; B: sensitivity

409 analysis of κ ; C: sensitivity analysis of c ; D: sensitivity analysis of ϵ .

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412 **Figure 8. Results of sensitivity analysis of ω , ω' , γ , γ' and f .** A: sensitivity analysis of ω ; B:

413 sensitivity analysis of ω' ; C: sensitivity analysis of γ ; D: sensitivity analysis of γ' ; F: sensitivity analysis of

414 f .

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417 **Tables**

418 **Table 1. Variables in the age-specific SEIARW model**

Variables	Description	Unit
S_i	Susceptible individuals density of age group i	Individuals·km ⁻²
S_j	Susceptible individuals density of age group j	Individuals·km ⁻²
E_i	Exposed individuals density of age group i	Individuals·km ⁻²
E_j	Exposed individuals density of age group j	Individuals·km ⁻²
I_i	Infectious individuals density age group i	Individuals·km ⁻²
I_j	Infectious individuals density age group j	Individuals·km ⁻²
A_i	Asymptomatic individuals density age group i	Individuals·km ⁻²
A_j	Asymptomatic individuals density age group j	Individuals·km ⁻²
R_i	Recovered individuals density age group i	Individuals·km ⁻²
R_j	Recovered individuals density age group j	Individuals·km ⁻²
W	Pathogen concentration in the seafood market	Viruses·mL ⁻³
N	Total number of population density	Individuals·km ⁻²

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420

421 **Table 2. Description and values of parameters in the age-specific SEIARW model**

Parameter	Description	Unit	Value	Range	Method
β_{ii}^*	Transmission relative rate among age group i	Individuals ⁻¹ ·days ⁻¹	-	-	-
b_{ii}^*	Scaled i -to- i contact rate	days ⁻¹	-	≥ 0	Curve fitting
β_{ij}^*	Transmission relative rate from age group i to j	Individuals ⁻¹ ·days ⁻¹	-	-	-
b_{ij}^*	Scaled i -to- j contact rate	days ⁻¹	-	≥ 0	Curve fitting
β_{ji}^*	Transmission relative rate from age group j to i	Individuals ⁻¹ ·days ⁻¹	-	-	-
b_{ji}^*	Scaled j -to- i contact rate	days ⁻¹	-	≥ 0	Curve fitting
β_{jj}^*	Transmission relative rate among age group j	Individuals ⁻¹ ·days ⁻¹	-	-	-
b_{jj}^*	Scaled j -to- j contact rate	days ⁻¹	-	≥ 0	Curve fitting
β_w	Seafood market contact rate	mL ⁻³ ·cells ⁻¹ ·days ⁻¹	-	-	-
b_w	Scaled market-to-person contact rate	days ⁻¹	0.9122	≥ 0	Curve fitting
κ	Relative transmissibility rate of asymptomatic to symptomatic individuals	1	0.5	0-1	Reference [12]

p	Proportion of the asymptomatic	1	0.5	0-1	Reference [12]
ω	Incubation relative rate	days ⁻¹	0.2	0.1428-0.25	References [2, 10, 11]
ω'	Latent relative rate	days ⁻¹	0.2	0.1428-0.25	References [2, 10, 11]
γ	Removed rate of the infectious	days ⁻¹	0.1667	0.125-0.25	References [2, 10, 11, 13-15]
γ'	Removed rate of the asymptomatic	days ⁻¹	0.1667	0.125-0.25	References [2, 10, 11, 13-15]
f	Fatality of the disease	1	0.02348	0.02198-0.03186	References [12]
ε	Pathogen lifetime relative rate	days ⁻¹	0.1	-	Assumption
μ	Person-to-reservoir contact rate (“shedding” by Infectious)	cells·mL ⁻³ ·day ⁻¹ ·km ² ·individuals ⁻¹	-	-	-
μ'	Person-to-reservoir contact rate (“shedding” by	cells·mL ⁻³ ·day ⁻¹ ·km ² ·individuals ⁻¹	-	-	-

	Asymptomatic)				
<i>c</i>	Relative shedding rate of asymptomatic compared to infectious	1	0.5	0-1	Reference [12]
<i>br</i>	Birth rate of the population	1	0.00004266	-	Wuhan Statistical Yearbook
<i>dr</i>	Death rate of the population	1	0.00003184	-	Wuhan Statistical Yearbook

422 *: *i* and *j* represent age group 1 to 4/5, respectively, and $i \neq j$

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