# Supplementary Information (SI)

The SI fills in details for the main article, which should be read first.

Sections and tables within this supplementary text are preceded by “S”, e.g., Section S1 and Table S1. Rather than explicitly and repeatedly referring the reader of the main text to the SI for mathematical details, the sections within the SI correspond to sections in the main text, and except for the prefix “S” are numbered similarly. Below, sections, figures, and tables without “S” refer to the main article.

# Methods and Materials

## S2.1 Parameter estimates

The sources below are not exhaustive, but they indicate the range of the parameter estimates.

**Basic reproduction number**. Representative estimates of the basic reproduction number *R*0 in early COVID-19 include: an initial estimate from the WHO of 1.4 to 2.5 ([Viceconte and Petrosillo, 2020](#_ENREF_28)); 1.74 to 2.91 and 1.84 to 3.18 ([Xu et al., 2021](#_ENREF_30)); 1.85 (95% CI 1.37 to 2.60) ([Ma et al., 2020](#_ENREF_23)); 1.9 to 3.6 ([Zhao et al., 2021](#_ENREF_31)); 90% credible interval 2-2.7 ([Abbott et al., 2020](#_ENREF_1))**;** from Figure 1 in a review, 2 to 4 ([Bar-On et al., 2020](#_ENREF_4)); 2 to 5 ([Linka et al., 2020](#_ENREF_19)); from the first 425 laboratory-confirmed cases before 2020.01.22 in Wuhan, 2.2 (95% CI 1.4 to 3.9) ([Li et al., 2020a](#_ENREF_16)); 2.6 days (uncertainty range 1.5 to 3.5) ([Imai et al., 2020](#_ENREF_12)); 3 ([Lipsitch et al., 2003](#_ENREF_20)); in Wuhan up to 2020.01.18; 3.54 (95% CI 3.40 to 3.67) ([Hao et al., 2020](#_ENREF_9)); and 15.4 (CI 5.5 to 25.4) ([Aguilar et al., 2020](#_ENREF_2)). Finally, Table 1 in a review ([Liu et al., 2020](#_ENREF_21)) included: 1.5 to 6.49, with an average of 4.2 (six studies with mathematical methods); 2.2 to 2.68 with an average 2.67 (two studies with stochastic methods); and 2.2 to 3.58, with an average of 2.67 (three studies with statistical methods). The review concluded that *R*0 was expected to be 2 to 3, “broadly consistent with the WHO estimate”.

**Latent period**. The latent period occurs after infection but before infectiousness. Following conventions in epidemiological modeling, it corresponds to the exposed compartment  in Figure 1. Estimates of the mean latent period include 3 days with dispersion 4 ([Davies et al., 2020](#_ENREF_8); [Kucharski et al., 2020](#_ENREF_13)); 3.3 days (95% CI 0.2 to 7.9) with dispersion about 0.1 to 10 from Figure 3 ([Zhao et al., 2021](#_ENREF_31)); 3.69 days ([Li et al., 2020b](#_ENREF_17)); and 4 days ([Read et al., 2021](#_ENREF_26)).

**Infectious** **period**. The infectious period averaged five to six days for earlier strains ([Control, 2023](#_ENREF_7)) with a 4 day interval of half-maximum infectiousness ([Bar-On et al., 2020](#_ENREF_4)). Under a model of constant transmissibility  and a gamma-distributed infectious period ( and  in Figure 1), the dispersion *k* of the infectious period and the individual reproduction number are the same ([Lloyd-Smith et al., 2005](#_ENREF_22)). Contact tracing estimated the dispersion parameter *k* of the individual reproduction number variously, at 0.3 ([Sun et al., 2020](#_ENREF_27)); 0.51 (95% CI 0.49 to 0.52) ([Laxminarayan et al., 2020](#_ENREF_15)); 0.58 (95% CI 0.35-1.18) when *R*0=0.4 under non-pharmaceutical interventions in Shenzen 2020.01.14 to 2020.02.12 ([Bi et al., 2020](#_ENREF_5)); and 0.70 (95% CI 0.59 to 0.98) ([He et al., 2020](#_ENREF_10)).

**Ascertainment rate**. The case ascertainment rate  is the fraction of infections ascertained through healthcare and community testing ([Colman et al., 2023](#_ENREF_6)), and it likely varied greatly throughout early COVID-19, as diagnosis moved from symptomatology to laboratory testing ([Hao et al., 2020](#_ENREF_9)). Given as an (approximate) subclinical fraction , the approximate ascertainment rate of asymptomatic COVID-19, early estimates include: the consensus values from a review, 0.40 to 0.45 ([Oran and Topol, 2020](#_ENREF_25)); from an early study in Vo, Italy, 0.425 (95% CI 0.315 to 0.546) ([Lavezzo et al., 2020](#_ENREF_14)); on the Diamond Princess, 0.50 ([Ooi and Low, 2020](#_ENREF_24)); also on the Diamond Princess, 0.67 ([Hung et al., 2020](#_ENREF_11)); 0.87 with an lower bound 0.53 ([Hao et al., 2020](#_ENREF_9)).

## S2.2 Epidemic Exponential Growth as a Function of Latent and Infectious Periods

For a specific infected individual, let  be the latent period; , the infectious period. Consider introducing an infected individual into a completely susceptible population in our model. Given , secondary infections are uniformly distributed during the infectious period, because they arrive as a Poisson process of constant rate within the infectious period. Thus, the generation time , where  is an independent uniform variate. The relationship  holds ([Wallinga and Lipsitch, 2007](#_ENREF_29)), with , where . To calculate  from , note that . Then,

.

Because  is a Laplace transform, , easing numerical solution of  for the constant  in the epidemic exponential growth .

## S3.1 Numerical Check of Simulated Extinction Probabilities

Section 2.1 of the Methods and Materials implies that the offspring distribution of the Galton-Watson branching process corresponding to the epidemic model is Negative Binomial:  ([Lloyd-Smith et al., 2005](#_ENREF_22)). A numerical rootfinder yields the extinction probability as the root of the equation

.

**Table S1. Extinction probabilities for Galton-Watson processes corresponding to the simulated epidemics**.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Number**  **of**  **ancestors** | **Basic**  **reprod**  **number** | **Dispersion** | **Extinction**  **prob**  **numerical** | **Extinction**  **prob**  **simulated** | |
|  | ***R*0** | ***k*** | **p=any** | **p=0.4** | **p=0.8** |
| 1 | 3 | 0.7 | 0.416 | 0.418 | 0.415 |
| 1 | 3 | 0.3 | 0.628 | 0.625 | 0.624 |
| 1 | 2 | 0.7 | 0.571 | 0.570 | 0.573 |
| 1 | 2 | 0.3 | 0.739 | 0.736 | 0.734 |
| 2 | 3 | 0.7 | 0.173 | 0.173 | 0.171 |
| 2 | 3 | 0.3 | 0.394 | 0.318 | 0.330 |
| 2 | 2 | 0.7 | 0.326 | 0.392 | 0.392 |
| 2 | 2 | 0.3 | 0.546 | 0.550 | 0.543 |
| 3 | 3 | 0.7 | 0.072 | 0.070 | 0.071 |
| 3 | 3 | 0.3 | 0.247 | 0.238 | 0.248 |
| 3 | 2 | 0.7 | 0.187 | 0.183 | 0.192 |
| 3 | 2 | 0.3 | 0.404 | 0.406 | 0.413 |

Table S1 plots the extinction probabilities for different numbers of primary infections  and different combinations of the basic reproduction number *R*0 and dispersion *k*. From top to bottom, within the 4 rows for each number of ancestors, the order parallels the order in Figure 3. The top 2 rows represent basic reproduction number *R*0=3; the bottom 2, *R*0=2. Within each 2 rows, the top represents dispersion *k*=0.7; the bottom, *k*=0.3. The early stage of each hypothesized epidemic corresponds to a Galton-Watson branching process ([Ball and Donnelly, 1992](#_ENREF_3)) whose extinction probability can be computed numerically, as shown above. The numerically computed extinction probability appears in Column 4 for comparison with its estimate from the simulation in Columns 5 and 6 for the subclinical fractions *p*=0.4 and 0.8. In the model of Figure 1, the subclinical fraction *p* only affects the ascertainment of an infection, so it does not influence the estimated extinction probability. The two estimates agree well with the numerical computation, disagreeing only in the third decimal, as might be expected in a simulation with 10000 realizations.

## S3.2 The Probabilistic Coupling Argument

A probabilistic coupling argument ([Lindvall, 1992](#_ENREF_18)) can formalize the similarity of the epidemic evolutions for . Epidemic evolution, upon reaching , would be identical if the epidemic model had only one infected compartment and did not remember its past.

# References

Abbott, S., Hellewell, J., Munday, J., Funk, S., 2020. The transmissibility of novel Coronavirus in the early stages of the 2019-20 outbreak in Wuhan: Exploring initial point-source exposure sizes and durations using scenario analysis. Wellcome Open Res 5, 17.

Aguilar, J.B., Faust, J.S., Westafer, L.M., Gutierrez, J.B., 2020. Investigating the Impact of Asymptomatic Carriers on COVID-19 Transmission, pp. 1-21. doi: 10.1101/2020.03.18.20037994.

Ball, F., Donnelly, P., 1992. Branching-process approximation of epidemic models. Theory Prob. Appl. 37, 119-121.

Bar-On, Y.M., Flamholz, A., Phillips, R., Milo, R., 2020. SARS-CoV-2 (COVID-19) by the numbers. Elife 9.

Bi, Q., Wu, Y., Mei, S., Ye, C., Zou, X., Zhang, Z., Liu, X., Wei, L., Truelove, S.A., Zhang, T., Gao, W., Cheng, C., Tang, X., Wu, X., Wu, Y., Sun, B., Huang, S., Sun, Y., Zhang, J., Ma, T., Lessler, J., Feng, T., 2020. Epidemiology and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a retrospective cohort study. Lancet Infect Dis 27, 30287-30285.

Colman, E., Puspitarani, G.A., Enright, J., Kao, R.R., 2023. Ascertainment rate of SARS-CoV-2 infections from healthcare and community testing in the UK. Journal of Theoretical Biology 558, 111333.

Control, E.C.f.D.P.a., 2023. Transmission of COVID-19.

Davies, N.G., Klepac, P., Liu, Y., Prem, K., Jit, M., Eggo, R.M., 2020. Age-dependent effects in the transmission and control of COVID-19 epidemics. Nat Med 26, 1205-1211.

Hao, X., Cheng, S., Wu, D., Wu, T., Lin, X., Wang, C., 2020. Reconstruction of the full transmission dynamics of COVID-19 in Wuhan. Nature 584, 420-424.

He, D., Zhao, S., Xu, X., Lin, Q., Zhuang, Z., Cao, P., Wang, M.H., Lou, Y., Xiao, L., Wu, Y., Yang, L., 2020. Low dispersion in the infectiousness of COVID-19 cases implies difficulty in control. BMC Public Health 20, 1558.

Hung, I.F., Cheng, V.C., Li, X., Tam, A.R., Hung, D.L., Chiu, K.H., Yip, C.C., Cai, J.P., Ho, D.T., Wong, S.C., Leung, S.S., Chu, M.Y., Tang, M.O., Chen, J.H., Poon, R.W., Fung, A.Y., Zhang, R.R., Yan, E.Y., Chen, L.L., Choi, C.Y., Leung, K.H., Chung, T.W., Lam, S.H., Lam, T.P., Chan, J.F., Chan, K.H., Wu, T.C., Ho, P.L., Chan, J.W., Lau, C.S., To, K.K., Yuen, K.Y., 2020. SARS-CoV-2 shedding and seroconversion among passengers quarantined after disembarking a cruise ship: a case series. Lancet Infect Dis.

Imai, N., Cori, A., Dorigatti, I., Baguelin, M., Donnelly, C.A., Riley, S., N.M., F., 2020. Transmissibility of 2019-nCoV. Imperial College London. doi: 10.25561/77148.

Kucharski, A.J., Russell, T.W., Diamond, C., Liu, Y., Edmunds, J., Funk, S., Eggo, R.M., 2020. Early dynamics of transmission and control of COVID-19: a mathematical modelling study. Lancet Infect Dis 20, 553-558.

Lavezzo, E., Franchin, E., Ciavarella, C., Cuomo-Dannenburg, G., Barzon, L., Del Vecchio, C., Rossi, L., Manganelli, R., Loregian, A., Navarin, N., Abate, D., Sciro, M., Merigliano, S., De Canale, E., Vanuzzo, M.C., Besutti, V., Saluzzo, F., Onelia, F., Pacenti, M., Parisi, S., Carretta, G., Donato, D., Flor, L., Cocchio, S., Masi, G., Sperduti, A., Cattarino, L., Salvador, R., Nicoletti, M., Caldart, F., Castelli, G., Nieddu, E., Labella, B., Fava, L., Drigo, M., Gaythorpe, K.A.M., Ainslie, K.E.C., Baguelin, M., Bhatt, S., Boonyasiri, A., Boyd, O., Cattarino, L., Ciavarella, C., Coupland, H.L., Cucunubá, Z., Cuomo-Dannenburg, G., Djafaara, B.A., Donnelly, C.A., Dorigatti, I., van Elsland, S.L., FitzJohn, R., Flaxman, S., Gaythorpe, K.A.M., Green, W.D., Hallett, T., Hamlet, A., Haw, D., Imai, N., Jeffrey, B., Knock, E., Laydon, D.J., Mellan, T., Mishra, S., Nedjati-Gilani, G., Nouvellet, P., Okell, L.C., Parag, K.V., Riley, S., Thompson, H.A., Unwin, H.J.T., Verity, R., Vollmer, M.A.C., Walker, P.G.T., Walters, C.E., Wang, H., Wang, Y., Watson, O.J., Whittaker, C., Whittles, L.K., Xi, X., Ferguson, N.M., Brazzale, A.R., Toppo, S., Trevisan, M., Baldo, V., Donnelly, C.A., Ferguson, N.M., Dorigatti, I., Crisanti, A., Imperial College, C.-R.T., 2020. Suppression of a SARS-CoV-2 outbreak in the Italian municipality of Vo. Nature.

Laxminarayan, R., Wahl, B., Dudala, S.R., Gopal, K., Mohan, B.C., Neelima, S., Jawahar Reddy, K.S., Radhakrishnan, J., Lewnard, J.A., 2020. Epidemiology and transmission dynamics of COVID-19 in two Indian states. Science 370, 691-697.

Li, Q., Guan, X., Wu, P., Wang, X., Zhou, L., Tong, Y., Ren, R., Leung, K.S.M., Lau, E.H.Y., Wong, J.Y., Xing, X., Xiang, N., Wu, Y., Li, C., Chen, Q., Li, D., Liu, T., Zhao, J., Liu, M., Tu, W., Chen, C., Jin, L., Yang, R., Wang, Q., Zhou, S., Wang, R., Liu, H., Luo, Y., Liu, Y., Shao, G., Li, H., Tao, Z., Yang, Y., Deng, Z., Liu, B., Ma, Z., Zhang, Y., Shi, G., Lam, T.T.Y., Wu, J.T., Gao, G.F., Cowling, B.J., Yang, B., Leung, G.M., Feng, Z., 2020a. Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. N Engl J Med 382, 1199-1207.

Li, R., Pei, S., Chen, B., Song, Y., Zhang, T., Yang, W., Shaman, J., 2020b. Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2). Science 16.

Lindvall, T., 1992. Lectures on the Coupling Method. Wiley and Sons, New York.

Linka, K., Peirlinck, M., Kuhl, E., 2020. The reproduction number of COVID-19 and its correlation with public health interventions, pp. 1-15. doi: 10.1101/2020.05.01.20088047.

Lipsitch, M., Cohen, T., Cooper, B., Robins, J.M., Ma, S., James, L., Gopalakrishna, G., Chew, S.K., Tan, C.C., Samore, M.H., Fisman, D., Murray, M., 2003. Transmission dynamics and control of severe acute respiratory syndrome. Science 300, 1966-1970.

Liu, Y., Gayle, A.A., Wilder-Smith, A., Rocklov, J., 2020. The reproductive number of COVID-19 is higher compared to SARS coronavirus. Journal of Travel Medicine 27, taaa021.

Lloyd-Smith, J.O., Schreiber, S.J., Kopp, P.E., Getz, W.M., 2005. Superspreading and the effect of individual variation on disease emergence. Nature 438, 355-359.

Ma, S., Zhang, J., Zeng, M., Yun, Q., Guo, W., Zheng, Y., Zhao, S., Wang, M.H., Yang, Z., 2020. Epidemiological Parameters of COVID-19: Case Series Study. J Med Internet Res 22, e19994.

Ooi, E.E., Low, J.G., 2020. Asymptomatic SARS-CoV-2 infection. Lancet Infect Dis 20, 996-998.

Oran, D.P., Topol, E.J., 2020. Prevalence of Asymptomatic SARS-CoV-2 Infection: A Narrative Review. Ann Intern Med.

Read, J.M., Bridgen, J.R.E., Cummings, D.A.T., Ho, A., Jewell, C.P., 2021. Novel coronavirus 2019-nCoV (COVID-19): early estimation of epidemiological parameters and epidemic size estimates. Philos Trans R Soc Lond B Biol Sci 376, 20200265.

Sun, K., Wang, W., Gao, L., Wang, Y., Luo, K., Ren, L., Zhan, Z., Chen, X., Zhao, S., Huang, Y., Sun, Q., Liu, Z., Litvinova, M., Vespignani, A., Ajelli, M., Viboud, C., Yu, H., 2020. Transmission heterogeneities, kinetics, and controllability of SARS-CoV-2. eabe2424.

Viceconte, G., Petrosillo, N., 2020. COVID-19 R0: Magic number or conundrum? Infectious Disease Reports 12, 1-2.

Wallinga, J., Lipsitch, M., 2007. How generation intervals shape the relationship between growth rates and reproductive numbers. Proc Biol Sci 274, 599-604.

Xu, H., Zhang, Y., Yuan, M., Ma, L., Liu, M., Gan, H., Liu, W., Lum, G.G.A., Tao, F., 2021. Basic Reproduction Number of the 2019 Novel Coronavirus Disease in the Major Endemic Areas of China: A Latent Profile Analysis. Frontiers in Public Health 9.

Zhao, S., Tang, B., Musa, S.S., Ma, S., Zhang, J., Zeng, M., Yun, Q., Guo, W., Zheng, Y., Yang, Z., Peng, Z., Chong, M.K.C., Javanbakht, M., He, D., Wang, M.H., 2021. Estimating the generation interval and inferring the latent period of COVID-19 from the contact tracing data. Epidemics 36, 100482.