Transient sensitivity analysis for developing pandemic disease prevention strategies

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#### Dikkat!

Bu raporda sunulan hesaplar kesin değildir. Verilecek kararlara yardımcı olması için hazırlanmıştır. Kullanılan hesap yöntemi ve model katsayıları, literatürdeki araştırmalara göre tutucu bir şekilde seçilmiştir.

# World is shaking

- Infected and death patients will increase continuously.
- Health system will collapse or collapsing in many countries.
- Lock-down measures are back and economy experiences the second shock.
- Pandemic will continue to exists until most of the people become immune.







### **Time-scales of the disease**





## **Probabiliy distributions of time scales**



### **Possible paths of disease development**





Susceptible Exposed Infective Removed Equation System (post-symptomatic transmission  $\tau_{transmission \ start} > 0$ )  $\frac{dS}{dt} = -\bar{\beta}(t)\frac{SI}{N} + \alpha(t)S$  $\frac{dE}{dt} = \bar{\beta}(t)\frac{SI}{N} - \frac{shvr test_{ac}}{\tau_{sypmtom onset}}E - \frac{shvr(1 - test_{ac})}{\tau_{latent}}E - \frac{(1 - shvr)}{\tau_{latent}}E$  $\frac{dI}{dt} = \frac{shvr(1 - test_{ac})}{\tau_{latent}}E + \frac{(1 - shvr)}{\tau_{latent}}E - \frac{shvr(1 - test_{ac})}{\tau_{infective}}I - \frac{(1 - shvr)}{\tau_{infective}}I$  $\frac{dQ}{dt} = \frac{shvr \ test_{ac}}{\tau_{sypmtom \ onset}} E - \frac{1}{\tau_{postsymptom}} Q$  $\frac{d\mathbf{R}}{dt} = \frac{\left(1 - dr_q\right)}{\tau_{postsymptom}}\mathbf{Q} + \frac{\left(1 - dr_q\right)shvr\left(1 - test_{ac}\right)}{\tau_{infective}}\mathbf{I} + \frac{\left(1 - dr_i\right)\left(1 - shvr\right)}{\tau_{infective}}\mathbf{I}$  $\frac{d\mathbf{D}}{dt} = \frac{dr_q}{\tau_{postsymptom}}\mathbf{Q} + \frac{dr_q \ shvr \ (1 - test_{ac})}{\tau_{infective}}\mathbf{I} + \frac{dr_i(1 - shvr)}{\tau_{infective}}\mathbf{I}$  $\frac{d\boldsymbol{P}}{dt} = -\alpha \boldsymbol{S}$ Katsavı Anlamı Birim zamanda ortalama bulaşan insan  $\bar{\beta}(t)$ Birim zamanda korumaya alınma katsayısı  $\alpha(\mathbf{t})$ Semptom göstermeye başlayanların hastaneye gitme oranı. SHVR Instantaneous population N = S + P + E + I + R - DYapılan testlerin doğruluk oranı. testac Ağır semptom gösterip, hastanade yatan ve karantinaya  $dr_q$ alınan hastaların ölüm oranı. -ÖZYEĞİN— Karantinaya girmeden bulaşıcılığı geçmiş hastaların ölüm --ÜNİVERSİTESİ  $dr_i$ oranı, normal ölüm oranı olrak alınmıştır.



Unknown model parameters are found by using GA optimization algorithms.

### **Distributions of time scales**



### Robust optimization algorithm under uncertain conditions



### Robust optimization algorithm under uncertain conditions





# Robust optimization algorithm under uncertain conditions Solution 14



### Robust optimization algorithm under uncertain conditions: Solution 14 (min rms error of detected patients)





### Robust optimization algorithm under uncertain conditions: Solution 1 (mid error for detected and death patients)





### **Transient sensitivity analysis algorithm**





Marino, S., Hogue, I. B., Ray, C. J., & Kirschner, D. E. (2008). A methodology for performing global uncertainty and sensitivity analysis in systems biology. Journal of Theoretical Biology, 254(1), 178–196. https://doi.org/10.1016/j.jtbi.2008.04.011

### **PRCC** and **P** value for infective patients (new)



- Parameters related to clinical parameters show always significant correlation.
- Since the number of susceptible are still too large, parameters related to death, as expected, appear to be insignificant.
- Sypmtom onset time scale takes very high P-value, when the PRCC for the same variable takes zero value.
- An interesting observation is that the –correlation of the symptom onset time-scale becomes + at the post peak phase.

### **PRCC and P value for daily died patients**



- Even if the health system works as desired, <u>clinical success is not the most</u> <u>influential parameter on the # of deaths</u>.
- In other words, prevention is the most influential strategy to decrease to number of death patients.
- If there were no patient, there would be no death.

# Conclusions

- In order to cease the pandemic nationally, it is shown quantitatively that transmission process has to be broken.
- Transmission can be broken now by
  - Lock down
  - Contact tracing and effective quarantine measures (works best when exposed patients are low). This will reduce new transmissions at pre and post symptomatic phase.
  - Personal measures
    - Mask, hygiene, social distance
    - Less social activity
    - Avoiding closed and crowded environments
  - Institutional measures
    - Regulations for public transport
    - Regulations for closed room usage, esp. regarding airborne transmission.
  - Vaccine (When will it resolve the pandemic?)
- Even if the health system works as desired, clinical success is not the most influential parameter on the # of deaths.



### References

[1] World Health Organization. (2009). Pandemic influenza preparedness and response, https://www.who.int/influenza/resources/documents/pandemic\_guidance\_04\_2009/en/ [2] Dong, E., Du, H., & Gardner, L. (2020). An interactive web-based dashboard to track COVID-19 in real time. The Lancet Infectious Diseases, 20(5), 533-534. https://doi.org/10.1016/S1473-3099(20)30120-1 [3] Kissler, S. M., Tedijanto, C., Goldstein, E., Grad, Y. H., & Lipsitch, M. (2020). Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. Science, 5793(February 2019), eabb5793. https://doi.org/10.1126/science.abb5793 [4] Peng, L., Yang, W., Zhang, D., Changjing, Z., & Hong, L. (2020). Epidemic analysis of COVID-19 in China by dynamical modeling. MedRxiv, February. https://doi.org/https://doi.org/10.1101/2020.02.16.20023465 [5] Prem, K., Liu, Y., Russell, T. W., Kucharski, A. J., Eggo, R. M., Davies, N., Flasche, S., Clifford, S., Pearson, C. A. B., Munday, J. D., Abbott, S., Gibbs, H., Rosello, A., Quilty, B. J., Jombart, T., Sun, F., Diamond, C., Gimma, A., van Zandvoort, K., ... Klepac, P. (2020). The effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan, China: a modelling study. The Lancet Public Health, 2667(20), 1–10. https://doi.org/10.1016/S2468-2667(20)30073-6 [6] Roda, W. C., Varughese, M. B., Han, D., & Li, M. Y. (2020). Why is it difficult to accurately predict the COVID-19 epidemic? Infectious Disease Modelling, 5(March), 271-281. https://doi.org/10.1016/j.idm.2020.03.001 [7] European Center for Disease Prevention and Control. (2020). Coronavirus disease 2019 (COVID-19) in the EU / EEA and the UK: eighth update (Issue 8th April). https://www.ecdc.europa.eu/En/Publications-Data/Rapid-Risk-Assessment-Coronavirus-Disease-2019-Covid-19-Pandemic-Eighth-Update [8] He, X., Lau, E. H. Y., Wu, P., Deng, X., Wang, J., Hao, X., Lau, Y. C., Wong, J. Y., Guan, Y., Tan, X., Mo, X., Chen, Y., Liao, B., Chen, W., Hu, F., Zhang, Q., Zhong, M., Wu, Y., Zhao, L., ... Leung, G. M. (2020). Temporal dynamics in viral shedding and transmissibility of COVID-19. Nature Medicine. https://doi.org/10.1038/s41591-020-0869-5 [9] Wölfel, R., Corman, V. M., Guggemos, W., Seilmaier, M., Zange, S., Müller, M. A., Niemeyer, D., Jones, T. C., Vollmar, P., Rothe, C., Hoelscher, M., Bleicker, T., Brünink, S., Schneider, J., Ehmann, R., Zwirglmaier, K., Drosten, C., & Wendtner, C. (2020). Virological assessment of hospitalized patients with COVID-2019. Nature. https://doi.org/10.1038/s41586-020-2196-x [10] Diekmann, O., Heesterbeek, J. A. P., & Metz, J. A. J. (1990). On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous pupulations. Journal of Mathematical Biology, 28, 365–382. [11] Haupt, R. L., & Haupt, S. E. (2004). Practical genetic algorithms (2nd Editio). John Wiley & Sons, Inc. [12] Holland, J. H. (1962). Outline for a logical theory of adaptive systems. Journal of the ACM, 9(3), 297–314. [13] Holland, J. H. (1973). Genetic algorithms and the optimal allocation of trials. SIAM Journal on Computing, 2(2), 88–105. [14] Holland, J. H. (1975). Adaptation in Natural and Artificial Systems: An Introductory Analysis with Applications to Biology, Control, and Artificial Intelligence. University of Michigan Press, Ann Arbor, MI. [15] Marino, S., Hogue, I. B., Ray, C. J., & Kirschner, D. E. (2008). A methodology for performing global uncertainty and sensitivity analysis in systems biology. Journal of Theoretical Biology, 254(1), 178–196. https://doi.org/10.1016/j.jtbi.2008.04.011

