

LOCAL SENSITIVITY ANALYSIS OF A CO-INFECTION MODEL OF MALARIA AND CHOLERA DISEASES

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Several mathematical models found in the literature have been formulated to describe the transmission of malaria and cholera. Multi-strain complex dynamics are generally modeled with extended Susceptible-Infected-Recovered (SIR-type) models, and have demonstrated qualitatively good results when comparing empirical data and model simulations.

In this work, we perform a local sensitivity study taking into account the variation of the parameters and initial conditions applied to a SIR-type model (introduced in [4]) for malaria-cholera co-infection. The model sub-divides the total human population, denoted by N_h , into sub-populations of susceptible humans S_h , individuals infected with malaria only I_m , individuals infected with cholera only I_c , individuals infected with both malaria and cholera G_{mc} , individuals who recovered from malaria only R_m , individuals who recovered from cholera only R_c , individuals who recovered from both malaria and cholera R_{mc} . Therefore $N_h = S_h + I_m + I_c + G_{mc} + R_m + R_c + R_{mc}$. The total vector population, denoted by N_v , is sub-divided into susceptible mosquitoes S_v , and mosquitoes infected with malaria I_v . Thus, $N_v = S_v + I_v$. There are two assumptions in the model: mosquitoes do not suffer mosquito-induced death, and individuals infected with both malaria and cholera can only infect mosquitoes with malaria parasites. Also taking into account the bacterial population B_c , the model is defined by a system of ten ordinary differential equations describing rates of variation for each population.

Using QR factorization with column pivoting to the relative sensitivity matrix, we compute the relative identifiability and sensitivity of the parameters, and establish orderings with respect to their identifiability. Numerical simulations corresponding to different values of the parameters are discussed.

References

- [1] C. Cobelli and J.J. DiStefano. (1980). *Parameter and structural identifiability concepts and ambiguities: a critical review and analysis*, Am. J. Physiol. Regul. Integr. Comp. Physiol., 239, R7–R24.
- [2] G. Dimitriu. (2017). *Identifiability and Sensitivity Analyses for a Chronic Myelogenous Leukemia Model with T Cell Interaction*, Proceedings of the 21st International Conference on System Theory, Control and Computing (ICSTCC), 19-21 October 2017, Sinaia, Romania, 709–715.
- [3] M. Fink, A. Attarian, and H. Tran. (2007). *Subset selection for parameter estimation in an HIV model*, Proc. Appl. Math. Mech., 7 (1), 1121501–1121502.
- [4] K.O. Okosun and O.D. Makinde. (2014). *A co-infection model of malaria and cholera diseases with optimal control*, Math. Biosci., 258, 19–32.
- [5] K. Thomaseth and C. Cobelli. (1999). *Generalized sensitivity functions in physiological system identification*, Annals of Biomedical Engineering, 1999.