One or many models? Modeling infectious disease across scales

Juan B. Gutiérrez

University of Georgia, 200 D.W. Brooks Dr, Athens, GA, US, 30602

`jgutierr@uga.edu`

Recent acceleration in the rate of collection of molecular data, and the broad availability of sources of information at all other scales, have forced the quantitative biology community to rethink how to conceive, build, validate, and use mathematical models. A natural question is how to link scales, e.g. molecular, cellular, vector, inter-host, etc. in meaningful ways that provide insight that individual scales could not yield. In this talk I will showcase an approach aiming to explain how molecular and cellular processes are related to epidemiological dynamics, and *vice versa*. The context will be given by malaria, but the general principles are applicable to a large number of diseases. The conclusion of this exercise is that it possible to link scales in insightful ways only when a deep understanding of biology cooperates with mathematical modeling. It might not be possible to produce a single model of multi-scale infectious diseases, but instead, it is possible to inform and articulate phenomena occurring at a different scale by carrying information from one scale to the next in a structured way. This perspective demands a transdisciplinary approach to multi-scale modeling, integrating tools from mathematics, bioinformatics, biology, computer science, and statistics.

⋆Mini-Symposium: Modeling Infection Dynamics Across the Scales