



« *In silico* clinical trials
for optimal treatment of
viral infections »

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À l'invitation de la professeure Fahima Nekka

In infectious diseases, traditional pharmacokinetic (PK) and pharmacodynamic (PD) models are routinely used to establish concentration dependent effects of a drug on pathogen replication. Yet, these models ignore the complex and dynamic interplay between a pathogen and the host immune system. Using chronic HSV-2 infection as an example, I will demonstrate that synthesis of viral dynamic models with PK / PD equations allows for highly predictive *in silico* clinical trials. Model simulations allow for a more precise estimation of drug parameters necessary for complete viral containment, and may allow for optimized dosing strategies in future antimicrobial trials. I will conclude by highlighting similar approaches that are in development to inform the design of future therapeutic vaccine and viral eradication studies.